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QY  SEQUENCE  9 AA: 1182 MW: 31746990AMSD457 CRC64.
Query Match      16.2% Score 2: DP 1: Length 9:
Best Local Similarity 100.0% Pred. No. 1: 1e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 KP 6
DB  1
    4 KP 2

RESULT 24
FARP ASNSC
AC  F43172
DT  01 NOV 1995 (Rel. 42, Created)
DI  01 NOV 1995 (Rel. 42, Last sequence update)
DE  01 FEB 1996 (Rel. 43, Last annotation update)
DE  FMRFamide-like neuropeptide AF5.
OS  Ascaris suum (Pig Roundworm) (Ascaris lumbricoides).
OC  Eukaryota; Metazoa; Nematoda; Chordata; Ascaridae; Ascarididae; Ascaris.
OX  NCBI_TaxID: 6253;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE:95480462; PubMed 7651904;
RA  Cowden C, Strutton A.O.W.;
RT  "Eight novel FMRFamide-like neuropeptides isolated from the neocate-
RI  "Ascaris suum."
RI  Peptides 16:491-500(1995).
CC  1. SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
    FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD_RES  9 AA: 1052 MW: 342604615764 CRC64;
SQ  SEQUENCE  9 AA: 1052 MW: 342604615764 CRC64;

Query Match      18.2% Score 2: DP 1: Length 9:
Best Local Similarity 100.0% Pred. No. 1: 1e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 KP 6
DB  1
    4 KP 4

RESULT 24
FARP ASNSC
AC  F43172
DT  01 NOV 1995 (Rel. 42, Created)
DI  01 NOV 1995 (Rel. 42, Last sequence update)
DE  01 FEB 1996 (Rel. 43, Last annotation update)
DE  FMRFamide-like neuropeptide AF5.
OS  Ascaris suum (Pig Roundworm) (Ascaris lumbricoides).
OC  Eukaryota; Metazoa; Nematoda; Chordata; Ascaridae; Ascarididae; Ascaris.
OX  NCBI_TaxID: 6253;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE:95480462; PubMed 7651904;
RA  Cowden C, Strutton A.O.W.;
RT  "Eight novel FMRFamide-like neuropeptides isolated from the neocate-
RI  "Ascaris suum."
RI  Peptides 16:491-500(1995).
CC  1. SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
    FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD_RES  9 AA: 1012 MW: 544104714414615764 CRC64;
SQ  SEQUENCE  9 AA: 1012 MW: 544104714414615764 CRC64;

Query Match      18.2% Score 2: DP 1: Length 9:
Best Local Similarity 100.0% Pred. No. 1: 1e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  8 KP 9
DB  1
    4 KP 5

RESULT 25
FARP CALSI
AC  P48455
DT  01 OCT 1994 (Rel. 40, Created)
DI  01 OCT 1994 (Rel. 40, Last sequence update)
DE  01 NOV 1995 (Rel. 42, Last annotation update)
DE  FMRFamide-like neuropeptide.
OS  Callinectes sapidus (Blue crab).
OC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
    Decapoda; Brachyura;
OX  NCBI_TaxID: 6763;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE:92270479; PubMed 1615216;
RA  Krahnak K.G.;
RT  "The identification and structure-activity relations of a
RI  cardioactive FMRFamide related peptide from the blue crab Callinectes
RI  sapidus."
RI  Peptides 12:1295-1302(1991)
CC  1. FUNCTION: CARDIOACTIVE PEPTIDE.
    1. SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
    FAMILY.
KW  Neuropeptide; Amidation.
FT  MOD_RES  9 AA: 1159 MW: 1346072905A045B CRC64;
SQ  SEQUENCE  9 AA: 1159 MW: 1346072905A045B CRC64;

Query Match      18.2% Score 2: DP 1: Length 9:
Best Local Similarity 100.0% Pred. No. 1: 1e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  10 KP 11
DB  1
    4 KP 5

RESULT 26
FARP KLEAE
AC  P12387
DT  01 OCT 1989 (Rel. 42, Created)
DI  01 OCT 1989 (Rel. 42, Last sequence update)
DE  25 FEB 2003 (Rel. 43, Last annotation update)
DE  L-proline hydrolase (EC 4.2.1.49) (Protease) (Imidazolonepropionate
    hydrolase) (Protein).
OS  Klebsiella aerogenes.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
    Enterobacteriaceae; Klebsiella.
OX  NCBI_TaxID: 28451;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE:88798518; PubMed 2841445;
RA  Nienkoop A.J., Balduf S.A., Hodspeith M.E.S., Bender R.A.;
RT  "Bidirectional promoter in the htr(P) region of the histidine
RI  utilization (hut) operon from Klebsiella aerogenes."
RI  J. Bacteriol. 172:5477-5481(1990).
CC  1. CATALYTIC ACTIVITY: 3 (5-oxo-4,5-dihydro-3-H-imidazol-4-
    yl)propanoate + acetate -> H(2)O.

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RESULT 29  
 MEDO CAVP  
 ID MEDO\_CAVP0 STANDARD: PRL 9 AA  
 AC P44766  
 DT 01 FEB 1994 (Rel. 28, Created)  
 DT 01 FEB 1994 (Rel. 28, Last sequence update)  
 DT 28 FEB 2003 (Rel. 41, Last annotation update)  
 DE Neurotensin 6-9 (NM0-9)  
 GN NMD  
 OS *Capra falgariferus* (Goat) (P44766)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Mysticeti; Capri, Bov, Cervi  
 CX NCBI TaxID: 10147  
 RN 11  
 RP SEQUENCE  
 RC MEDLINE: 86242180; PubMed 2387627  
 RA Murphy R., Turner C.A., Kirsch J.H., Parker L., Giraud A.  
 RT "Isolation and amino acid sequence analysis of a novel form of neurotensin C peptide from quinea pig small intestine."  
 RL Peptides 11:513-517(1990).  
 CT 1- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES SELECTIVE VASOCONSTRICTION.  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- SIMILARITY: BELONGS TO THE NMD FAMILY.  
 DR InterPro: IPR001942; NMD.  
 DR Pfam: PF02070; NMD; 1.  
 DR PROSITE: PS00967; NMD; 1.  
 KW Amidation; Hormone.  
 FT MDL RES 9 AA: 1169 MW: 1617.43672928 CRC64:  
 SQ SEQUENCE 9 AA: 1169 MW: 1617.43672928 CRC64:  
 Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1; 3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PR 9  
 DB 7 PR 8  
 RESULT 30  
 MEDO\_HUMAN  
 ID MEDO\_HUMAN0 STANDARD: PRL 9 AA  
 AC P44777  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neurotensin, related peptide (NRP) (Kobayashi, 1986).  
 OS Homo sapiens (human), and Bos taurus (bovine), and Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catartia; Mammalia; Homo.  
 CX NCBI TaxID: 9606, 9913, 9986;  
 RN 11  
 RP SEQUENCE  
 RC MEDLINE: 86242180; PubMed 9087772  
 RA Woodard W.H., Kobayashi K., Chen C.F., Lee L.H., Kowen D.K., Jr., Shively J.E., Walsh J.H.  
 RT "The amino acid sequence of neurotensin, a neuropeptide associated with pepsin-treated human plasma: identical with human serum albumin, neurotensin and angiotensin."  
 RL Biochem. Biophys. Res. Commun. 136:943-952(1986).  
 RN 121  
 RP SEQUENCE  
 RC SPECIES: Human, Bovine, and Rabbit.  
 RA Carraway R.E., Mitra S.P., Cochran E.E.  
 RT "Structure of a biologically active neurotensin-related peptide obtained from pepsin-treated albumin(s)."

J. Biol. Chem. 262:5668-5674(1987).  
 CC 1- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND BLOOD FLOW (POTENTIAL).  
 DR PIR: A38895; ABBOS.  
 DR GO: GO:0055576; Catecholaminergic; NAS.  
 DR GO: GO:0055180; Prolactin hormone; NAS.  
 DR GO: GO:0037599; Prolactinase; DA.  
 DR GO: GO:0066629; Lipid metabolism; NAS.  
 KW Hormone.  
 SQ SEQUENCE 9 AA: 1172 MW: 12404.476141400 CRC64:  
 Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1; 3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PR 2  
 DB 2 PR 3  
 RESULT 31  
 OXYT\_CYPCA  
 ID OXYT\_CYPCA0 STANDARD: PRL 9 AA  
 AC P23879;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Vasotocin.  
 OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinus.  
 CX NCBI TaxID: 7982, 7757;  
 RN 111  
 RP SEQUENCE  
 RC SPECIES: Cyprinus; Petromyzon.  
 RA Acher R., Chauvet J., Chauvet M., Croty D.  
 RT "Characterization of neurohypophyseal hormones from a fresh water bony fish, the carp (Cyprinus carpio): Comparison with hormones from sea water bony fishes."  
 RL Comp. Biochem. Physiol. 14:245-254(1965).  
 RN 121  
 RP SEQUENCE  
 RC SPECIES: Petromyzon; Tissue: Pituitary.  
 RX MEDLINE: 88225975; PubMed 371646;  
 RA Lane I.F., Sower S.A., Kawauchi H.  
 RT "Arginine vasotocin from the pituitary gland of the lamprey (Petromyzon marinus): isolation and amino acid sequence."  
 RL Gen. Comp. Endocrinol. 70:152-157(1988).  
 CC 1- FUNCTION: ANTI-DIURETIC HORMONE.  
 CC 1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR: B01364; B01364.  
 DR PIR: S06375; S06375.  
 DR InterPro: IPR000981; Neurohyp\_horm.  
 DR Pfam: PF00220; Hormone4; 1.  
 DR PROSITE: PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT EUSLEFID 9 AA: 1053 MW: 17684560348 CRC64:  
 SQ SEQUENCE 9 AA: 1053 MW: 17684560348 CRC64:  
 Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1; 3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PR 9  
 DB 7 PR 8  
 RESULT 32  
 FPK1\_PERAM







01 SEQ ID# 10 10  
 02 SEQUENCE 10 AA: 1027 MW: 20625.656 Da (100% identity)  
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 04 Query Match 18.2% Score 21 DB 11 Length 10  
 05 Best Local Similarity 130.0% Ident. No. 10004  
 06 Matches 21 Conservative 0 Mismatches 0 Gaps 0  
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01 MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
 02 THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
 03 CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
 04 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
 05 INTERPRO: IP0002191; FIBRINOGEN.  
 06 PROSITE: PS00554; FIBRIN A3 C-TERMINAL DOMAIN; PARTIAL.  
 07 KW: Based on calculation: Plasma.  
 08 FT: RESIDUES 1 10 F1851N-PEPTIDE B.  
 09 NON TER 10  
 10 SEQUENCE 10 AA: 1097 MW: 94624.20000000000 CRC64:  
 11  
 12 Query Match 18.2% Score 21 DB 11 Length 10  
 13 Best Local Similarity 130.0% Ident. No. 10004  
 14 Matches 21 Conservative 0 Mismatches 0 Gaps 0  
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RX MEDLINE: 84204263; PubMed: 2452451;  
 RA Confusion M., Katsoulis S., Schmidt W.E., Chum L.  
 FT "[Ara] substance P and neurexin A from chicken small intestine."  
 RL Reg. J. Pept. 20:171-180(1998).  
 CL FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC 1. SUBCELLULAR LOCATION: Secreted  
 CC 1. SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR: JN0024; JN0024.  
 DR Cationic: PR002040; tachykinin.  
 DR PR00: PR0202; tachykinin.  
 DR PROSITE: PS00257; TACHYKININ: 1.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT M02 RES 10 10 AMIDATION N  
 SQ SEQUENCE 10 AA: 114 MW: 84606.20(46AA) (Ref.1)

Query Match 18.2% Score 21. DR 10. (ambig. 10)  
 Best Local Similarity 100.0%; Pred. No. gaps 0.  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0.

CY 4 K1 5  
 LU 2 K1 4

RESULT 1:  
 LAU GREEN  
 LD TACHYKININ STANDARD: 1973 10 AA.  
 AC P02763.  
 DI 01 FEB 1999 (Ref. 32; Created)  
 DT 01 FEB 1999 (Ref. 32; Last sequence added)  
 TI 16 SEP 2004 (Ref. 42; Last annotation update)  
 LE 1981 tachykinin I.  
 OS Crochis antrictus.  
 OC Eukaryota; Metazoa; Echinura; Xosipneusta; Trochodonta; Trochodas.  
 OX N01 LUX10 6432;  
 RN [1]  
 RP SEQUENCE AND SYNTHESIS.  
 RC TISSUE: Ventral nerve cord.  
 RX MEDLINE 94236558; PubMed: 8475470;  
 RA Koda T., Mitsuoka H., Nomoto K., Kubota T., Marukawa Y.  
 RT "Two novel tachykinin-related neuropeptides in the cephalopod mollusc,  
 KT Crochis antrictus."  
 SI PROCEED. BIOPHYS. RES. COMMUN. 1921:1 (1993)  
 DI FUNCTION CONTRACTILE ACTION IN THE TACHYKININ RECEPTOR-  
 CC MUSCLE OF THE ANIMAL.  
 CC 1. SUBCELLULAR LOCATION: Secreted.  
 CC 1. SIMILARITY SOME SIMILARITY TO TACHYKININ  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT M02 RES 10 10 AMIDATION  
 SQ SEQUENCE 10 AA: 117 MW: 84606.20(46AA) (Ref.1)

Query Match 18.2% Score 21. DR 10. (ambig. 10)  
 Best Local Similarity 100.0%; Pred. No. gaps 0.  
 Matches 2: Conservative 0; Mismatches 0; Gaps 0.

CY 4 K1 5  
 LU 2 K1 4

Search completed: September 30, 2003, 10:28:04  
 Gap time: 7.25 secs

GenScore version 3.0.0  
Copyright (c) 1995 - 2003, GenScore Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:37:04 : search time 41 min 7 seconds  
(with an additional 18)  
89.439 bits in total, 450000 queries/sec

File: US-09-787-443-12

Perfect score: 11 AKKTKPKERS 11

Sequence:

Scoring table: all10  
Gapop: 60.0, Gapext: 4.0

Sequences: 89,525 seqs, 2586,52004 residues

Word size: 3

Total number of hits satisfying chosen parameters: 459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post processing: testing first 500 similarities

Database: 1: SPKEMBL23;\*

2: sp.archaea;\*

3: sp.bacteria;\*

4: sp.fungi;\*

5: sp.invertebrate;\*

6: sp.mammal;\*

7: sp.mhc;\*

8: sp.orquelet;\*

9: sp.phage;\*

10: sp.plant;\*

11: sp.rent;\*

12: sp.virus;\*

13: sp.vertebrate;\*

14: sp.unclassified;\*

15: sp.viruses;\*

16: sp.bacterioph;\*

17: sp.archaeop;\*

Prod. No. is the number of results produced by the search. The score greater than of equal to the score of the best hit found printed, and is derived by analysis of the full database.

Summary:

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	8	9	Q58340
2	3	27.3	8	9	Q58341
3	3	27.3	9	2	Q54320
4	3	27.3	9	7	Q78425
5	3	27.3	1	2	Q47345
6	3	27.3	11	8	Q58344
7	3	27.3	12	2	Q53574
8	3	27.3	13	14	Q55431
9	3	27.3	14	2	Q71599
10	3	27.3	14	3	Q81362
11	3	27.3	14	19	Q94562
12	3	27.3	14	15	Q10235
13	3	27.3	14	15	Q10229
14	3	27.3	14	15	Q10234
15	3	27.3	14	15	Q10233
16	3	27.3	14	15	Q10234

17	3	27.3	14	15	Q10233	human immun
18	3	27.3	14	15	Q10229	human immun
19	3	27.3	14	15	Q10230	human immun
20	3	27.3	14	15	Q10227	human immun
21	3	27.3	14	15	Q10226	human immun
22	3	27.3	15	2	Q54298	salmonella
23	3	27.3	15	2	Q58386	serratia mu
24	3	27.3	15	2	Q58342	mycobacteri
25	3	27.3	15	2	Q54580	rhodobacter
26	3	27.3	15	2	Q46013	caulobacter
27	3	27.3	15	2	Q81171	thermopae
28	3	27.3	15	4	Q503A5	homo sapien
29	3	27.3	15	5	Q57883	axinella po
30	3	27.3	15	10	Q583A5	gossypium h
31	3	27.3	15	10	Q583A5	eschlerichia
32	3	27.3	15	10	Q583A5	eschlerichia
33	3	27.3	15	10	Q583A5	eschlerichia
34	3	27.3	15	10	Q583A5	eschlerichia
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85	3	27.3	15	10	Q583A5	eschlerichia
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88	3	27.3	15	10	Q583A5	eschlerichia
89	3	27.3	15	10	Q583A5	eschlerichia





276	2	18.2	10	8	Q94VH1	Q94VH1 varanus gle	309	2	18.2	10	15	Q85619	Q85619 moloney mu
277	2	18.2	10	8	Q95915	Q95915 leiocephis b	310	2	18.2	10	15	Q90K30	Q90K30 human immu
278	2	18.2	10	8	Q94VH5	Q94VH5 varanus oli	311	2	18.2	10	15	Q8Q318	Q8Q318 human immu
279	2	18.2	10	8	Q8SH3	Q8SH3 calanca tar	312	2	18.2	10	15	Q75595	Q75595 human immu
280	2	18.2	10	8	Q8SHK1	Q8SHK1 calanca tas	313	2	18.2	10	15	Q87617	Q87617 chimpanzee
281	2	18.2	10	8	Q95610	Q95610 madonia po	314	2	18.2	11	2	Q9R790	Q9R790 borrelia qa
282	2	18.2	10	8	Q94VH7	Q94VH7 batista mb	315	2	18.2	11	2	Q8RKN1	Q8RKN1 escherichia
283	2	18.2	10	8	Q950S8	Q950S8 madonia do	316	2	18.2	11	2	Q8L274	Q8L274 neisseria m
284	2	18.2	10	8	Q95289	Q95289 madonia sp	317	2	18.2	11	2	Q9R708	Q9R708 pseudomonas
285	2	18.2	10	8	Q95830	Q95830 bradyrhiza	318	2	18.2	11	2	Q9S618	Q9S618 prochloroc
286	2	18.2	10	8	Q9T0D6	Q9T0D6 tetastocine	319	2	18.2	11	2	Q77404	Q77404 escherichia
287	2	18.2	10	8	Q94VH4	Q94VH4 opheusa mus	320	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
288	2	18.2	10	8	Q9SHM2	Q9SHM2 calandma leo	321	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
289	2	18.2	10	8	Q9SHM2	Q9SHM2 calandma las	322	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
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314	2	18.2	10	8	Q95613	Q95613 madonia po	347	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
315	2	18.2	10	8	Q95613	Q95613 madonia po	348	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
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317	2	18.2	10	8	Q95613	Q95613 madonia po	350	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
318	2	18.2	10	8	Q95613	Q95613 madonia po	351	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
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325	2	18.2	10	8	Q95613	Q95613 madonia po	358	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
326	2	18.2	10	8	Q95613	Q95613 madonia po	359	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
327	2	18.2	10	8	Q95613	Q95613 madonia po	360	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
328	2	18.2	10	8	Q95613	Q95613 madonia po	361	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
329	2	18.2	10	8	Q95613	Q95613 madonia po	362	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
330	2	18.2	10	8	Q95613	Q95613 madonia po	363	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
331	2	18.2	10	8	Q95613	Q95613 madonia po	364	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
332	2	18.2	10	8	Q95613	Q95613 madonia po	365	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
333	2	18.2	10	8	Q95613	Q95613 madonia po	366	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
334	2	18.2	10	8	Q95613	Q95613 madonia po	367	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
335	2	18.2	10	8	Q95613	Q95613 madonia po	368	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
336	2	18.2	10	8	Q95613	Q95613 madonia po	369	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
337	2	18.2	10	8	Q95613	Q95613 madonia po	370	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
338	2	18.2	10	8	Q95613	Q95613 madonia po	371	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
339	2	18.2	10	8	Q95613	Q95613 madonia po	372	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
340	2	18.2	10	8	Q95613	Q95613 madonia po	373	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
341	2	18.2	10	8	Q95613	Q95613 madonia po	374	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
342	2	18.2	10	8	Q95613	Q95613 madonia po	375	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
343	2	18.2	10	8	Q95613	Q95613 madonia po	376	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
344	2	18.2	10	8	Q95613	Q95613 madonia po	377	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
345	2	18.2	10	8	Q95613	Q95613 madonia po	378	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
346	2	18.2	10	8	Q95613	Q95613 madonia po	379	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
347	2	18.2	10	8	Q95613	Q95613 madonia po	380	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
348	2	18.2	10	8	Q95613	Q95613 madonia po	381	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
349	2	18.2	10	8	Q95613	Q95613 madonia po	382	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
350	2	18.2	10	8	Q95613	Q95613 madonia po	383	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
351	2	18.2	10	8	Q95613	Q95613 madonia po	384	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
352	2	18.2	10	8	Q95613	Q95613 madonia po	385	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
353	2	18.2	10	8	Q95613	Q95613 madonia po	386	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
354	2	18.2	10	8	Q95613	Q95613 madonia po	387	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
355	2	18.2	10	8	Q95613	Q95613 madonia po	388	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
356	2	18.2	10	8	Q95613	Q95613 madonia po	389	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
357	2	18.2	10	8	Q95613	Q95613 madonia po	390	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
358	2	18.2	10	8	Q95613	Q95613 madonia po	391	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
359	2	18.2	10	8	Q95613	Q95613 madonia po	392	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
360	2	18.2	10	8	Q95613	Q95613 madonia po	393	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
361	2	18.2	10	8	Q95613	Q95613 madonia po	394	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
362	2	18.2	10	8	Q95613	Q95613 madonia po	395	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
363	2	18.2	10	8	Q95613	Q95613 madonia po	396	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
364	2	18.2	10	8	Q95613	Q95613 madonia po	397	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
365	2	18.2	10	8	Q95613	Q95613 madonia po	398	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
366	2	18.2	10	8	Q95613	Q95613 madonia po	399	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
367	2	18.2	10	8	Q95613	Q95613 madonia po	400	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
368	2	18.2	10	8	Q95613	Q95613 madonia po	401	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
369	2	18.2	10	8	Q95613	Q95613 madonia po	402	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
370	2	18.2	10	8	Q95613	Q95613 madonia po	403	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
371	2	18.2	10	8	Q95613	Q95613 madonia po	404	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
372	2	18.2	10	8	Q95613	Q95613 madonia po	405	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
373	2	18.2	10	8	Q95613	Q95613 madonia po	406	2	18.2	11	2	Q9RQ66	Q9RQ66 buchura ap
374	2	18.2	10										

362	2	18.2	11	8	Q8SK01	Q8SK01 eteophorus	455	2	18.2	12	5	Q17140	Q17140 crassostrea
363	2	18.2	11	8	Q72639	Q72639 laudakia lae	456	2	18.2	12	5	Q8MY01	Q8MY01 drosophila
364	2	18.2	11	8	Q46236	Q46236 aphelophorus	457	2	18.2	12	5	Q26429	Q26429 drosophila
365	2	18.2	11	8	Q35374	Q35374 laudakia st	458	2	18.2	12	5	Q9TW00	Q9TW00 fasciola he
366	2	18.2	11	8	Q96590	Q96590 laudakia st	459	2	18.2	12	5	Q9N289	Q9N289 gorilla gor
367	2	18.2	11	8	Q96581	Q96581 tetrachlorus	460	2	18.2	12	5	Q9XT42	Q9XT42 canis fami
368	2	18.2	11	8	Q96582	Q96582 eteophorus	461	2	18.2	12	5	Q8WNN9	Q8WNN9 avis arles
369	2	18.2	11	8	Q96583	Q96583 eteophorus	462	2	18.2	12	5	Q9T818	Q9T818 bos taurus
370	2	18.2	11	8	Q96584	Q96584 eteophorus	463	2	18.2	12	5	Q9N289	Q9N289 pan troglod
371	2	18.2	11	8	Q96585	Q96585 eteophorus	464	2	18.2	12	5	Q96584	Q96584 canis fami
372	2	18.2	11	8	Q96586	Q96586 eteophorus	465	2	18.2	12	5	Q9T818	Q9T818 bos indicus
373	2	18.2	11	8	Q96587	Q96587 eteophorus	466	2	18.2	12	5	Q9T818	Q9T818 petunia hyb
374	2	18.2	11	8	Q96588	Q96588 eteophorus	467	2	18.2	12	5	Q96585	Q96585 eteophorus
375	2	18.2	11	8	Q96589	Q96589 eteophorus	468	2	18.2	12	5	Q96585	Q96585 eteophorus
376	2	18.2	11	8	Q96590	Q96590 eteophorus	469	2	18.2	12	5	Q96585	Q96585 eteophorus
377	2	18.2	11	8	Q96591	Q96591 eteophorus	470	2	18.2	12	5	Q96585	Q96585 eteophorus
378	2	18.2	11	8	Q96592	Q96592 eteophorus	471	2	18.2	12	5	Q96585	Q96585 eteophorus
379	2	18.2	11	8	Q96593	Q96593 eteophorus	472	2	18.2	12	5	Q96585	Q96585 eteophorus
380	2	18.2	11	8	Q96594	Q96594 eteophorus	473	2	18.2	12	5	Q96585	Q96585 eteophorus
381	2	18.2	11	8	Q96595	Q96595 eteophorus	474	2	18.2	12	5	Q96585	Q96585 eteophorus
382	2	18.2	11	8	Q96596	Q96596 eteophorus	475	2	18.2	12	5	Q96585	Q96585 eteophorus
383	2	18.2	11	8	Q96597	Q96597 eteophorus	476	2	18.2	12	5	Q96585	Q96585 eteophorus
384	2	18.2	11	8	Q96598	Q96598 eteophorus	477	2	18.2	12	5	Q96585	Q96585 eteophorus
385	2	18.2	11	8	Q96599	Q96599 eteophorus	478	2	18.2	12	5	Q96585	Q96585 eteophorus
386	2	18.2	11	8	Q96600	Q96600 eteophorus	479	2	18.2	12	5	Q96585	Q96585 eteophorus
387	2	18.2	11	8	Q96601	Q96601 eteophorus	480	2	18.2	12	5	Q96585	Q96585 eteophorus
388	2	18.2	11	8	Q96602	Q96602 eteophorus	481	2	18.2	12	5	Q96585	Q96585 eteophorus
389	2	18.2	11	8	Q96603	Q96603 eteophorus	482	2	18.2	12	5	Q96585	Q96585 eteophorus
390	2	18.2	11	8	Q96604	Q96604 eteophorus	483	2	18.2	12	5	Q96585	Q96585 eteophorus
391	2	18.2	11	8	Q96605	Q96605 eteophorus	484	2	18.2	12	5	Q96585	Q96585 eteophorus
392	2	18.2	11	8	Q96606	Q96606 eteophorus	485	2	18.2	12	5	Q96585	Q96585 eteophorus
393	2	18.2	11	8	Q96607	Q96607 eteophorus	486	2	18.2	12	5	Q96585	Q96585 eteophorus
394	2	18.2	11	8	Q96608	Q96608 eteophorus	487	2	18.2	12	5	Q96585	Q96585 eteophorus
395	2	18.2	11	8	Q96609	Q96609 eteophorus	488	2	18.2	12	5	Q96585	Q96585 eteophorus
396	2	18.2	11	8	Q96610	Q96610 eteophorus	489	2	18.2	12	5	Q96585	Q96585 eteophorus
397	2	18.2	11	8	Q96611	Q96611 eteophorus	490	2	18.2	12	5	Q96585	Q96585 eteophorus
398	2	18.2	11	8	Q96612	Q96612 eteophorus	491	2	18.2	12	5	Q96585	Q96585 eteophorus
399	2	18.2	11	8	Q96613	Q96613 eteophorus	492	2	18.2	12	5	Q96585	Q96585 eteophorus
400	2	18.2	11	8	Q96614	Q96614 eteophorus	493	2	18.2	12	5	Q96585	Q96585 eteophorus
401	2	18.2	11	8	Q96615	Q96615 eteophorus	494	2	18.2	12	5	Q96585	Q96585 eteophorus
402	2	18.2	11	8	Q96616	Q96616 eteophorus	495	2	18.2	12	5	Q96585	Q96585 eteophorus
403	2	18.2	11	8	Q96617	Q96617 eteophorus	496	2	18.2	12	5	Q96585	Q96585 eteophorus
404	2	18.2	11	8	Q96618	Q96618 eteophorus	497	2	18.2	12	5	Q96585	Q96585 eteophorus
405	2	18.2	11	8	Q96619	Q96619 eteophorus	498	2	18.2	12	5	Q96585	Q96585 eteophorus
406	2	18.2	11	8	Q96620	Q96620 eteophorus	499	2	18.2	12	5	Q96585	Q96585 eteophorus
407	2	18.2	11	8	Q96621	Q96621 eteophorus	500	2	18.2	12	5	Q96585	Q96585 eteophorus
408	2	18.2	11	8	Q96622	Q96622 eteophorus	501	2	18.2	12	5	Q96585	Q96585 eteophorus
409	2	18.2	11	8	Q96623	Q96623 eteophorus	502	2	18.2	12	5	Q96585	Q96585 eteophorus
410	2	18.2	11	8	Q96624	Q96624 eteophorus	503	2	18.2	12	5	Q96585	Q96585 eteophorus
411	2	18.2	11	8	Q96625	Q96625 eteophorus	504	2	18.2	12	5	Q96585	Q96585 eteophorus
412	2	18.2	11	8	Q96626	Q96626 eteophorus	505	2	18.2	12	5	Q96585	Q96585 eteophorus
413	2	18.2	11	8	Q96627	Q96627 eteophorus	506	2	18.2	12	5	Q96585	Q96585 eteophorus
414	2	18.2	11	8	Q96628	Q96628 eteophorus	507	2	18.2	12	5	Q96585	Q96585 eteophorus
415	2	18.2	11	8	Q96629	Q96629 eteophorus	508	2	18.2	12	5	Q96585	Q96585 eteophorus
416	2	18.2	11	8	Q96630	Q96630 eteophorus	509	2	18.2	12	5	Q96585	Q96585 eteophorus
417	2	18.2	11	8	Q96631	Q96631 eteophorus	510	2	18.2	12	5	Q96585	Q96585 eteophorus
418	2	18.2	11	8	Q96632	Q96632 eteophorus	511	2	18.2	12	5	Q96585	Q96585 eteophorus
419	2	18.2	11	8	Q96633	Q96633 eteophorus	512	2	18.2	12	5	Q96585	Q96585 eteophorus
420	2	18.2	11	8	Q96634	Q96634 eteophorus	513	2	18.2	12	5	Q96585	Q96585 eteophorus
421	2	18.2	11	8	Q96635	Q96635 eteophorus	514	2	18.2	12	5	Q96585	Q96585 eteophorus
422	2	18.2	11	8	Q96636	Q96636 eteophorus	515	2	18.2	12	5	Q96585	Q96585 eteophorus
423	2	18.2	11	8	Q96637	Q96637 eteophorus	516	2	18.2	12	5	Q96585	Q96585 eteophorus
424	2	18.2	11	8	Q96638	Q96638 eteophorus	517	2	18.2	12	5	Q96585	Q96585 eteophorus
425	2	18.2	11	8	Q96639	Q96639 eteophorus	518	2	18.2	12	5	Q96585	Q96585 eteophorus
426	2	18.2	11	8	Q96640	Q96640 eteophorus	519	2	18.2	12	5	Q96585	Q96585 eteophorus
427	2	18.2	11	8	Q96641	Q96641 eteophorus	520	2	18.2	12	5	Q96585	Q96585 eteophorus
428	2	18.2	11	8	Q96642	Q96642 eteophorus	521	2	18.2	12	5	Q96585	Q96585 eteophorus
429	2	18.2	11	8	Q96643	Q96643 eteophorus	522	2	18.2	12	5	Q96585	Q96585 eteophorus
430	2	18.2	11	8	Q96644	Q96644 eteophorus	523	2	18.2	12	5	Q96585	Q96585 eteophorus
431	2	18.2	11	8	Q96645	Q96645 eteophorus	524	2	18.2	12	5	Q96585	Q96585 eteophorus
432	2	18.2	11	8	Q96646	Q96646 eteophorus	525	2	18.2	12	5	Q96585	Q96585 eteophorus
433	2	18.2	11	8	Q96647	Q96647 eteophorus	526	2	18.2	12	5	Q96585	Q96585 eteophorus
434	2	18.2	11	8	Q96648	Q96648 eteophorus	527	2	18.2	12	5	Q96585	Q96585 eteophorus
435	2	18.2	11	8	Q96649	Q96649 eteophorus	528	2	18.2	12	5	Q96585	Q96585 eteophorus
436	2	18.2	11	8	Q96650	Q96650 eteophorus	529	2	18.2	12	5	Q96585	Q96585 eteophorus
437	2	18.2	11	8	Q96651	Q96651 eteophorus	530	2	18.2	12	5	Q96585	Q96585 eteophorus
438	2	18.2	11	8	Q96652	Q96652 eteophorus	531	2	18.2	12	5	Q96585	Q96585 eteophorus
439	2	18.2	11	8	Q96653	Q96653 eteophorus	532	2	18.2	12	5	Q96585	Q96585 eteophorus
440	2	18.2	11	8	Q96654	Q96654 eteophorus	533	2	18.2	12	5	Q96585	Q96585 eteophorus
441	2	18.2	11	8	Q96655	Q96655 eteophorus	534	2	18.2	12	5	Q96585	Q96585 eteophorus
442	2	18.2	11	8	Q96656	Q96656 eteophorus	535	2	18.2	12	5	Q96585	Q96585 eteophorus
443	2	18.2	11	8	Q96657	Q96657 eteophorus	536	2	18.2	12	5	Q96585	Q96585 eteophorus
444	2	18.2	11	8	Q96658	Q96658 eteophorus	537	2	18.2	12	5	Q96585	Q96585 eteophorus
445	2	18.2	11	8	Q96659	Q96659 eteophorus	538	2	18.2	12	5	Q96585	Q96585 eteophorus
446	2	18.2	11	8	Q96660	Q96660 eteophorus	539	2	18.2	12	5	Q96585	Q96585 eteophorus
447	2	18.2	11	8	Q96661	Q96661 eteophorus	540	2	18.2	12	5	Q96585	Q96585 eteophorus
448	2	18.2	11	8	Q96662	Q96662 eteophorus	541	2	18.2	12	5	Q96585	Q96585 eteophorus
449	2	18.2	11	8	Q96663	Q96663 eteophorus	542	2	18.2	12	5	Q96585	Q96585 eteophorus
450	2	18.2	11	8	Q96664	Q96664 eteophorus	543	2	18.2	12	5	Q96585	Q96585 eteophorus
451	2	18.2	11	8	Q96665	Q96665 eteophorus	544	2	18.2	12	5	Q96585	Q96585 eteophorus
452	2	18.2	11	8	Q96666	Q96666 eteophorus	545	2	18.2	12	5	Q96585	Q96585 eteophorus
453	2	18.2	11	8	Q96667	Q96667 eteophorus	546	2	18.2	12	5	Q96585	Q96585 eteophorus
454	2	18.2	11	8	Q96668	Q96668 eteophorus	547	2	18.2	12	5	Q96585	Q96585 eteophorus

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRI:	8 AA.
Q8SK01	Q8SK01	Q8SK01	Q8SK







OS Human immunodeficiency virus 1.  
 AC Viruses: Retroviridae; Lentivirus.  
 CX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuzia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor."  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U89851; AAC26091.1;  
 DR EMBL: U89851; AAC26091.1;  
 DR InterPro: IPR00428; Env\_GP41.  
 DR Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1691 MW: 15874719(4556566) Ck64;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 LB 2 PER 4

## RESULT 15

OT 010244 PRELIMINARY: PRI: 14 AA.  
 AC 010244;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DT 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 AC Viruses: Retroviridae; Lentivirus.  
 CX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuzia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor."  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U89851; AAC26091.1;  
 DR InterPro: IPR00428; Env\_GP41.  
 DR Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1733 MW: 15874690(4556566) Ck64;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 LB 2 PER 4

## RESULT 16

OT 010245 PRELIMINARY: PRI: 14 AA.  
 AC 010245;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DT 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.

OS Human immunodeficiency virus 1.  
 AC Viruses: Retroviridae; Lentivirus.  
 CX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuzia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor."  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U89851; AAC26091.1;  
 DR InterPro: IPR00428; Env\_GP41.  
 DR Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1691 MW: 15874719(4556566) Ck64;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 LB 2 PER 4

## RESULT 17

OT 010241 PRELIMINARY: PRI: 14 AA.  
 AC 010241;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DT 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 AC Viruses: Retroviridae; Lentivirus.  
 CX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuzia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor."  
 RL J. Virol. 72:3646-3657(1998).  
 DR EMBL: U89851; AAC26091.1;  
 DR InterPro: IPR00428; Env\_GP41.  
 DR Pfam: PF0517; GP41.1;  
 KW Transmembrane.  
 FT NON-TER 1  
 SQ SEQUENCE 14 AA: 1693 MW: 15874708(4556566) Ck64;

Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 LB 1  
 LB 2 PER 4

## RESULT 18

OT 010229 PRELIMINARY: PRI: 14 AA.  
 AC 010229;  
 DT 01-JUL-1997 (EMBLrel. 04, Created)  
 DT 01-JUL-1997 (EMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (EMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus  
 OX NCRL\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RR EMBL: U99849; AAC26085.1;  
 RR InterPro: IPR000428; Env\_GP41.  
 RR Pfam: PF00517; GP41; 1.  
 RW Transmembrane.  
 KW NON-TER  
 FT [1]  
 SQ SEQUENCE 14 AA: 1691 MW: 1567566-9557645; DB 15; Length 14;  
 Query Match 27.3% Score 4; DB 15; Length 14;  
 Best Local Similarity 100.0% Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 II  
 ZD 2 PER 4

RESULT 19  
 O10226 PRELIMINARY; PRT; 14 AA.  
 AC O10226;  
 DT 01-JUN-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCRL\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RR EMBL: U99849; AAC26085.1;  
 RR InterPro: IPR000428; Env\_GP41.  
 RR Pfam: PF00517; GP41; 1.  
 RW Transmembrane.  
 KW NON-TER  
 FT [1]  
 SQ SEQUENCE 14 AA: 1721 MW: 1567566-9557645; DB 15; Length 14;  
 Query Match 27.3% Score 4; DB 15; Length 14;  
 Best Local Similarity 100.0% Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 II  
 ZD 2 PER 4

RESULT 20  
 O10227 PRELIMINARY; PRT; 14 AA.  
 AC O10227;  
 DT 01-JUN-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCRL\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RR EMBL: U99849; AAC26085.1;  
 RR InterPro: IPR000428; Env\_GP41.  
 RR Pfam: PF00517; GP41; 1.  
 RW Transmembrane.  
 KW NON-TER  
 FT [1]  
 SQ SEQUENCE 14 AA: 1691 MW: 15674719-4503566 CRC64;  
 Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0% Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 II  
 ZD 2 PER 4

RESULT 21  
 O10226 PRELIMINARY; PRT; 14 AA.  
 AC O10226;  
 DT 01-JUN-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN ENV.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.  
 OX NCRL\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 98216723; PubMed 9557645;  
 RA Salvi R., Garbuglia A.R., Di Caro A., Pulciani S., Montella F.,  
 RA Benedetto A.  
 RT "Grossly defective net gene sequences in a human immunodeficiency  
 RT virus type 1 seropositive long-term nonprogressor";  
 RL J. Virol. 72:3646-3657(1998).  
 RR EMBL: U99849; AAC26085.1;  
 RR InterPro: IPR000428; Env\_GP41.  
 RR Pfam: PF00517; GP41; 1.  
 RW Transmembrane.  
 KW NON-TER  
 FT [1]  
 SQ SEQUENCE 14 AA: 1691 MW: 15674719-4503566 CRC64;  
 Query Match 27.3% Score 3; DB 15; Length 14;  
 Best Local Similarity 100.0% Pred. No. 7.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PER 10  
 II  
 ZD 2 PER 4

RESULT 22  
 O54298 PRELIMINARY; PRT; 15 AA.  
 AC O54298;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE RNA polymerase alpha subunit (Fragment).  
 GN RPOA.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Salmonella.





Q91161

ID Q91161 PRELIMINARY: PRT: 15 AA.  
 AC Q91161  
 DT 01-MAY-2000 (TrEMBLrel. 22, Last sequence update)  
 DI 01-MAY-2000 (TrEMBLrel. 22, Last annotation update)  
 DE Putative formase (Fragment).  
 GN K04P.  
 OS The cyanobacter *Prochlorococcus* (Chlorophyta: Cyanophyta).  
 OC Bacteria; Firmicutes; Clostridia; Firmicutes; Clostridia.  
 OX NCBI\_TaxID: 2424.  
 KW III  
 SEQUENCE FROM N.A.  
 RC STRAIN: A295b.  
 RA Maruta K., Mukai K., Kikuchi H., Nakada S., Kurumada R.  
 RT "The genes encoding a trehalose phosphorylase and a KdsA-like  
 K1 phosphorylase from *Thermotoga* sp. (Firmicutes).  
 RG Submitted (Nov-2001) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: AB076331; BAB97302.1;  
 FI NCBIFR 15  
 SQ SEQUENCE 15 AA: 1894 MW: 45606.62; 244.6 kDa.

Query Match: 27.4% Score 4. DB 5: Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 0 FRK 7  
 DI III  
 DI 0 FRK 8

RESULT 28

Q91043

ID Q91043 PRELIMINARY: PRT: 15 AA.  
 AC Q91043  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Putative formase (Fragment).  
 GN K04P.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Echinostoma.  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID: 9606.  
 KW III  
 SEQUENCE FROM N.A.  
 RC STRAIN: A295b.  
 RA Maruta K., Mukai K., Kikuchi H., Nakada S., Kurumada R.  
 RT "The genes encoding a trehalose phosphorylase and a KdsA-like  
 K1 phosphorylase from *Thermotoga* sp. (Firmicutes).  
 RG Submitted (Nov-2001) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: AB076331; BAB97302.1;  
 FI NCBIFR 15  
 SQ SEQUENCE 15 AA: 1604 MW: 45061.62; 244.6 kDa.

Query Match: 27.4% Score 4. DB 5: Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 0 FRK 13  
 DI III  
 DI 0 FRK 14

RESULT 29

Q91043

ID Q91043 PRELIMINARY: PRT: 15 AA.  
 AC Q91043  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Putative formase (Fragment).  
 GN K04P.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Echinostoma.  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID: 9606.  
 KW III  
 SEQUENCE FROM N.A.  
 RC STRAIN: A295b.  
 RA Maruta K., Mukai K., Kikuchi H., Nakada S., Kurumada R.  
 RT "The genes encoding a trehalose phosphorylase and a KdsA-like  
 K1 phosphorylase from *Thermotoga* sp. (Firmicutes).  
 RG Submitted (Nov-2001) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: AB076331; BAB97302.1;  
 FI NCBIFR 15  
 SQ SEQUENCE 15 AA: 1604 MW: 45061.62; 244.6 kDa.

Query Match: 27.4% Score 4. DB 5: Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 0 FRK 13  
 DI III  
 DI 0 FRK 14

QY Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorphia;  
 OC Haliacanthidae; Axinellidae; Axinella.  
 OX NCBI\_TaxID: 12959.  
 KW III  
 SEQUENCE FROM N.A.  
 RC STRAIN: A295b.  
 RA Maruta K., Mukai K., Kikuchi H., Nakada S., Kurumada R.  
 RT "The genes encoding a trehalose phosphorylase and a KdsA-like  
 K1 phosphorylase from *Thermotoga* sp. (Firmicutes).  
 RG Submitted (Nov-2001) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: AB076331; BAB97302.1;  
 FI NCBIFR 15  
 SQ SEQUENCE 15 AA: 177. MW: 45867.65; 244.6 kDa.

Query Match: 27.4% Score 4. DB 5: Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 0 FRK 4  
 DI III  
 DI 0 FRK 9

RESULT 30

Q91043

ID Q91043 PRELIMINARY: PRT: 15 AA.  
 AC Q91043  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Putative formase (Fragment).  
 GN K04P.  
 OS Gossypium hirsutum (Plantae).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 OX NCBI\_TaxID: 3635.  
 KW III  
 SEQUENCE FROM N.A.  
 RC STRAIN: A295b.  
 RA Maruta K., Mukai K., Kikuchi H., Nakada S., Kurumada R.  
 RT "The genes encoding a trehalose phosphorylase and a KdsA-like  
 K1 phosphorylase from *Thermotoga* sp. (Firmicutes).  
 RG Submitted (Nov-2001) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: AB076331; BAB97302.1;  
 FI NCBIFR 15  
 SQ SEQUENCE 15 AA: 1689 MW: 10679508; 46.99 kDa.

Query Match: 27.4% Score 4. DB 5: Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRK 4  
 DI III  
 DI 1 FRK 15

RESULT 31

Q91043

ID Q91043 PRELIMINARY: PRT: 8 AA.  
 AC Q91043  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Putative formase (Fragment).  
 GN K04P.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID: 562.  
 KW III  
 SEQUENCE FROM N.A.  
 RC STRAIN: A295b.  
 RA Maruta K., Mukai K., Kikuchi H., Nakada S., Kurumada R.  
 RT "The genes encoding a trehalose phosphorylase and a KdsA-like  
 K1 phosphorylase from *Thermotoga* sp. (Firmicutes).  
 RG Submitted (Nov-2001) to the EMBL/GenBank/CCDS databases.  
 DR EMBL: AB076331; BAB97302.1;  
 FI NCBIFR 15  
 SQ SEQUENCE 8 AA: 1689 MW: 10679508; 46.99 kDa.

Query Match: 27.4% Score 4. DB 5: Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRK 4  
 DI III  
 DI 1 FRK 15

Query Match: 27.4% Score 4. DB 5: Length 15;  
 Best Local Similarity: 100.0%; Pred. No. 7.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FRK 4  
 DI III  
 DI 1 FRK 15



```

ID Q54258 PRELIMINARY: PRT: 8 AA.
AC Q54258.
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DI 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE N11H (Fragment).
GN N11H.
OS Synchococcus sp. (strain POC 4801 / RF 1) (cyanobacterium)
OC Bacteria; Cyanobacteria; Chroococcales; Cyanophyceae
CX NCBI_TaxID:41431
LN 111
DR EMBL: D00113; RAA00067.1; -
DR EMBL: X04609; CAA24278.1; -
FT NON_TER 8
RP SEQUENCE FROM N.A.
RC STRAIN: RF 1.
RA MEDLINE: 99251861; PubMed: 10217599.
RA Huang L., Lin R.F., Chu M.K., Chou R.N.
RC "Genetization and expression of nitrogen fixation genes in the aerobic
RT nitrogen fixing unicellular cyanobacterium Synchococcus sp. strain
RT RF-1."
RI Microbiology 145:743-751(1999).
DR EMBL: AF001780; AAC33369.1; -
FT NON_TER 8
RP SEQUENCE 8 AA: 985 MW: 116354; GI: 4046; CR: 64.

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8; 05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PK 3
DB 2 PK 3

RESULT 37
Q54258 PRELIMINARY: PRT: 8 AA.
AC Q54258.
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P4G protein (Fragment).
GN P4G
OS Lactobacillus collinoides.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae
CX NCBI_TaxID: 339507
LN 111
DR EMBL: A120774; CAG31093.1; -
FT NON_TER 8
RP SEQUENCE FROM N.A.
RC STRAIN LMG 18853.
RA Saeysquet N., Goulet K., Laplace J.M., Audray Y.
RT "Characterisation of the G40 dehydratase gene product of Lactobacillus
PT collinoides."
RL FEBS Microbiol. Lett. 019:1-6(01).
DR EMBL: A120774; CAG31093.1; -
FT NON_TER 8
RP SEQUENCE 8 AA: 862 MW: 87450; GI: 66818; CR: 64.

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8; 05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RS 11
DB 7 RS 9

RESULT 38
Q54246 PRELIMINARY: PRT: 8 AA.
ID Q54246
AC Q54246; Q52412;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Thermophilic proton ATPase epsilon subunit amino terminal (fragment).

```

```

OS thermophilic bacterium PS3.
OC Bacteria; Firmicutes; Bacillales.
CX NCBI_TaxID:2334;
LN 111
DR EMBL: X04609; CAA24278.1; -
FT NON_TER 8
RP SEQUENCE FROM N.A.
RC STRAIN: PS3.
RA MEDLINE: 87137359; PubMed: 2880841;
RA Kagawa Y., Ishizaka M., Saishu I., Nakao S.
RC "Stable structure of the thermophilic proton ATPase beta subunit."
RI J. Biochem. 100:923-934(1986).
DR EMBL: D00113; RAA00067.1; -
DR EMBL: X04609; CAA24278.1; -
FT NON_TER 8
RP SEQUENCE 8 AA: 914 MW: 87551; GI: 4046; CR: 64.

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8; 05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MK 7
DB 1 MK 2

RESULT 39
Q54250 PRELIMINARY: PRT: 8 AA.
ID Q54250
AC Q54250.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Stage V spotolation protein E (Fragment).
GN SpvE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID:1423;
LN 111
DR EMBL: A120774; CAG31093.1; -
FT NON_TER 8
RP SEQUENCE FROM N.A.
RC STRAIN: 168.
RA MEDLINE: 93004529; PubMed: 1391053;
RA Henriques A.O., de Lencastre H., Piquot P.J.
RT "A Bacillus subtilis morphotype cluster that includes spvE is
RI homologous to the mid region of Escherichia coli."
RI Biochimie 74:735-748(1992).
DR EMBL: X64258; CAA45556.1; -
FT NON_TER 8
RP SEQUENCE 8 AA: 853 MW: 87551; GI: 4046; CR: 64.

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8; 05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KI 5
DB 5 KI 6

RESULT 40
Q54252 PRELIMINARY: PRT: 8 AA.
ID Q54252
AC Q54252.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Quaternary ammonium compound-resistance protein QacEdelta1
DE (Fragment).
GN QACDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales.
CX NCBI_TaxID:287;
LN 111
DR EMBL: X04609; CAA24278.1; -
FT NON_TER 8
RP SEQUENCE FROM N.A.

```

$\psi$       6 MK 7  
         ||  
 00      ; MK 2

RESULT: 43  
Q9P057  
ID: Q9R057  
PRELIMINARY: 8 AA.

Dataset	Time Period	Annotation Type	Update Status
DE	01-MAY-2009	(REMLAB)	13, created
DE	01-MAY-2010	(REMLAB)	13, last sequence update
DE	01-JUN-2021	(REMLAB)	17, last annotation update

GN  
NHS  
MCH  
OS  
VAC

OX NOB2\_TaxID 9;  
RN 111  
RP SEQUENCE FROM N.A.

Clark M.A., Moran N.A., Edmunds P.J.  
"Sequence evolution in bacterial endosymbionts having extreme base  
K: compositions." *J. Mol. Evol.* 16: 366-376 (1982).

DR	EMBS:	AE1A0B12	AA13797	1	8	
FI	NON TER					
SQ	SEQUENCE	B	AA:	940	MW:	FA73504771A356 CRC64;

```
Query Match: 18.247 Score 2: DB 2: Length 83
Best Local Similarity: 100.000 Pred. No. 8.3e+05
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
```

QY
2 MK 7
1 MK 2
1 MK 2

RESULT 44  
Q9S443  
ID Q9S443  
PRELIMINARY  
PRT: 8 AA.

DT	MAY-2000	(TREMbreRel, 1, 3, 5 treated)
DT	01-MAY-2000	(TREMbreRel, 1, 3, 5 last sequence update)
DT	01-MAY-2000	(TREMbreRel, 1, 3, 5 last generation update)
DT	01-MAY-2000	(TREMbreRel, 1, 3, 5 last generation update)

[illegible]

EX NCHI\_taxid=287;  
END  
SEQUENCE FROM N.A.  
END

ROY D., COLLEGE M., PERION K., ROY P.H.:  
RA  
RI  
RI  
RI  
RI

"Characterization of a novel 6'-N-aminoglycoside acetyltransferase gene *aac(6')* IIc from the integron of a Chinese *Pseudomonas aeruginosa*

RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
 RR EMBL: AF142771; AAL44628.1;  
 FT N-TER 6 Amino Acids  
 SS SEQUENCE 6 AA; 66.66% IDENTITY WITH EMBL:AF142771.1; AAL44628.1

```
Query Match      18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0% Pred. NG: 8.3e+05;
Matches 2: Compression 11: Mismatches 0: Indels 0: Gaps 0:
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6 MK 7  
11

31 1 MK 2

# RESULT 45

Q15900  
ID Q15900 PRELIMINARY: PRI: 8 AA  
AC Q15900  
DT 01-NOV-1999 (TREMBLrel. 01, Created)  
DT 01-NOV-1999 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-2001 (TREMBLrel. 19, Last annotation update)  
DE (Gene XP6A11b) (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TIGHE J.E., Galardi F.,  
RA Lee C.C., Yaddan A., Weinert M., Bailey J., Couch L., Xiong M.,  
RA Colbourne M.L., Chinault C.A., Baldwin A., Lindsay E.A., Zhao Z., Y.,  
RA Caskey C.J.H.  
RT "Isolation of chromosome specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995)  
ER EMBL: 142079; AAA73885.1;  
FI NON-TER 1  
FT NON-TER 1  
SQ SEQUENCE 8 AA: 921 MW: 667053.00(CAA CRC64)

Query Match 18.2% Score 2: DB 4: Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MK 7

DT 4 MK 5

# RESULT 46

Q15895  
ID Q15895 PRELIMINARY: PRI: 8 AA  
AC Q15895  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE (Gene XP6A11b) (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TIGHE J.E., Galardi F.,  
RA Lee C.C., Yaddan A., Weinert M., Bailey J., Couch L., Xiong M.,  
RA Colbourne M.L., Chinault C.A., Baldwin A., Lindsay E.A., Zhao Z., Y.,  
RA Caskey C.J.H.  
RT "Isolation of chromosome specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995)  
ER EMBL: 142075; AAA73885.1;  
FI NON-TER 1  
FT NON-TER 1  
SQ SEQUENCE 8 AA: 921 MW: 667053.00(CAA CRC64)

Query Match 18.2% Score 2: DB 4: Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MK 7

DT 4 MK 5

# RESULT 47

Q9Y4J4  
ID Q9Y4J4 PRELIMINARY: PRI: 8 AA  
AC Q9Y4J4  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE Runt/82nt/MT38  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE-95002916; PubMed 7919424;  
RA TIGHE J.E., Galardi F.,  
RA "Alternative, out-of-frame run1/MT38 transcripts are encoded by the  
RT derivative (8) chromosome in the t(8;21) of acute myeloid leukemia  
RT M2."  
RL EMBL: 841215-2121(1994);  
DR EMBL: S74092; AAA14144.1;  
FI NON-TER 1  
FT NON-TER 1  
SQ SEQUENCE 8 AA: 1667 MW: 20F414044B17244B CRC64;

Query Match 18.2% Score 2: DB 4: Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MK 10

DT 6 MK 7

# RESULT 48

Q15898  
ID Q15898 PRELIMINARY: PRI: 8 AA  
AC Q15898  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE (Gene XP6A11b) (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TIGHE J.E., Galardi F.,  
RA Lee C.C., Yaddan A., Weinert M., Bailey J., Couch L., Xiong M.,  
RA Colbourne M.L., Chinault C.A., Baldwin A., Lindsay E.A., Zhao Z., Y.,  
RA Caskey C.J.H.  
RT "Isolation of chromosome specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995)  
ER EMBL: 142078; AAA74888.1;  
FI NON-TER 1  
FT NON-TER 1  
SQ SEQUENCE 8 AA: 948 MW: 44A1140477B458B CRC64;

Query Match 18.2% Score 2: DB 4: Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RS 11

DT 7 RS 8

# RESULT 49

Q15888  
ID Q15888 PRELIMINARY: PRI: 8 AA  
AC Q15888

Search completed: September 30, 2003, 10:17:22  
Run time : 37.6667 secs

31 01-NV-1996 (TREMBLrel. 01, Complete)  
32 01-NV-1996 (TREMBLrel. 01, Last sequence update)  
33 01-DA-2001 (TREMBLrel. 19, Last annotation update)  
34 (Gene XP148A) (Fragment)  
35 B629 sapiens (human)  
36 Ekaryotid, Metazoa: Chordata: Vertebrata, Euteleostomi  
37 Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo  
38 NCBI TaxId:9606  
39 111  
40 SEQUENCE FROM N.A.  
41 TISSUE: Placenta  
42 Accession: U00001, Version: 1, Length: 10,000, 10,000 bp  
43 Cui, Hsueh-Ming, Chaudhry, A., Chaudhry, A., Chaudhry, A., Zhang, Y.  
44 Casky, J. et al.  
45 "Isolation of chromosome-specific genes by computer-aided hybrid  
46 arrays cDNAs and cosmid libraries."  
47 Hum. Mol. Genet. 9:1000-1005  
48 EMBL: U42067, AAA74878.1, 1, 1  
49 FT N=133  
50 N=133  
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52 SEQUENCE # AA: 1068 MW: 41025 MW: 41025 MW: 41025 MW: 41025

Query Match: 10.2%, Score: 21.10, E-value: 0  
Best local similarity: 10.0%, Pref. No. 6, Gap: 0  
Matches: 21 Conservative 0 Mismatches 0 Gaps 0  
37 3 KP 8  
38 11  
39 1 KP 2

RESULT: 0  
OUTLINE  
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41 01-NV-1996 (TREMBLrel. 01, Last sequence update)  
42 01-DA-2001 (TREMBLrel. 19, Last annotation update)  
43 (Gene XP148A) (Fragment)  
44 B629 sapiens (human)  
45 Ekaryotid, Metazoa: Chordata: Vertebrata, Euteleostomi  
46 Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo  
47 NCBI TaxId:9606  
48 111  
49 SEQUENCE FROM N.A.  
50 TISSUE: Placenta  
51 Accession: U00001, Version: 1, Length: 10,000, 10,000 bp  
52 Cui, Hsueh-Ming, Chaudhry, A., Chaudhry, A., Chaudhry, A., Zhang, Y.  
53 Casky, J. et al.  
54 "Isolation of chromosome-specific genes by computer-aided hybrid  
55 arrays cDNAs and cosmid libraries."  
56 Hum. Mol. Genet. 9:1000-1005  
57 EMBL: U42067, AAA74878.1, 1, 1  
58 FT N=133  
59 N=133  
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61 SEQUENCE # AA: 1068 MW: 41025 MW: 41025 MW: 41025 MW: 41025

Query Match: 10.2%, Score: 21.10, E-value: 0  
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Matches: 21 Conservative 0 Mismatches 0 Gaps 0  
37 3 KP 8  
38 11  
39 1 KP 2



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247	3	27.3	9	3	US-09-082-797-5	Sequence 5, Appl	320	3	27.3	9	4	US-09-229-037-6	Sequence 6, Appl
248	3	27.3	9	3	US-09-082-797-6	Sequence 6, Appl	321	3	27.3	9	4	US-09-311-784A-267	Sequence 267, App
249	3	27.3	9	3	US-09-082-797-7	Sequence 7, Appl	322	3	27.3	9	4	US-08-929-847-10	Sequence 10, Appl
250	3	27.3	9	3	US-09-082-797-8	Sequence 8, Appl	323	3	27.3	9	4	US-09-839-542B-503	Sequence 503, App
251	3	27.3	9	3	US-09-082-797-9	Sequence 9, Appl	324	3	27.3	9	4	US-09-839-542B-3074	Sequence 3074, App
252	3	27.3	9	3	US-09-082-797-13	Sequence 13, Appl	325	3	27.3	9	4	US-09-839-542B-3076	Sequence 3076, App
253	3	27.3	9	3	US-09-082-797-14	Sequence 14, Appl	326	3	27.3	9	4	US-09-839-542B-3119	Sequence 3119, App
254	3	27.3	9	3	US-09-082-797-15	Sequence 15, Appl	327	3	27.3	9	4	US-09-839-542B-3121	Sequence 3121, App
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256	3	27.3	9	3	US-09-082-797-17	Sequence 17, Appl	329	3	27.3	9	4	US-09-839-542B-3166	Sequence 3166, App
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259	3	27.3	9	3	US-09-139-802-4	Sequence 4, Appl	332	3	27.3	9	4	US-09-839-542B-3254	Sequence 3254, App
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262	3	27.3	9	3	US-09-112-206-22	Sequence 222, App	335	3	27.3	9	4	US-08-926-9-4-178	Sequence 178, App
263	3	27.3	9	3	US-09-112-206-22	Sequence 223, App	336	3	27.3	9	5	PCT-US93-11781-5	Sequence 5, Appl
264	3	27.3	9	3	US-09-112-206-24	Sequence 224, App	337	3	27.3	9	5	PCT-US94-01258-58	Sequence 58, Appl
265	3	27.3	9	3	US-09-112-206-24	Sequence 225, App	338	3	27.3	9	5	PCT-US94-09798-9	Sequence 9, Appl
266	3	27.3	9	3	US-09-112-206-24	Sequence 226, App	339	3	27.3	9	5	PCT-US95-00147-20	Sequence 20, Appl
267	3	27.3	9	3	US-09-112-206-22	Sequence 227, App	340	3	27.3	9	5	PCT-US95-00147-26	Sequence 26, Appl
268	3	27.3	9	3	US-09-177-246-4	Sequence 47, Appl	341	3	27.3	9	5	PCT-US95-02478-12	Sequence 12, Appl
269	3	27.3	9	3	US-09-263-976-33	Sequence 33, Appl	342	3	27.3	9	5	PCT-US95-11235-58	Sequence 58, Appl
270	3	27.3	9	3	US-09-131-643-31	Sequence 31, Appl	343	3	27.3	9	5	5171838-7	Patent No. 5171838
271	3	27.3	9	3	US-09-476-482-19	Sequence 19, Appl	344	3	27.3	10	1	US-07-666-719-7	Sequence 7, Appl
272	3	27.3	9	3	US-09-504-410-9	Sequence 9, Appl	345	3	27.3	10	1	US-07-714-540-1	Sequence 1, Appl
273	3	27.3	9	3	US-09-502-603-44	Sequence 44, Appl	346	3	27.3	10	1	US-08-128-971H-5	Sequence 5, Appl
274	3	27.3	9	3	US-09-518-046-41	Sequence 41, Appl	347	3	27.3	10	1	US-08-139-034-4	Sequence 4, Appl
275	3	27.3	9	3	US-08-278-865-4	Sequence 4, Appl	348	3	27.3	10	1	US-08-115-171-4	Sequence 4, Appl
276	3	27.3	9	3	US-09-492-543-32	Sequence 32, Appl	349	3	27.3	10	1	US-08-370-648-7	Sequence 7, Appl
277	3	27.3	9	4	US-09-492-543-58	Sequence 58, Appl	350	3	27.3	10	1	US-08-212-190A-9	Sequence 9, Appl
278	3	27.3	9	4	US-09-492-543-71	Sequence 71, Appl	351	3	27.3	10	1	US-08-462-917-9	Sequence 9, Appl
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293	3	27.3	9	4	US-09-187-859-576	Sequence 576, App	366	3	27.3	10	2	US-08-727-688-13	Sequence 13, Appl
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297	3	27.3	9	4	US-09-187-859-576	Sequence 576, App	370	3	27.3	10	2	US-08-482-228-209	Sequence 209, App
298	3	27.3	9	4	US-09-187-859-576	Sequence 576, App	371	3	27.3	10	2	US-08-900-321-9	Sequence 9, Appl
299	3	27.3	9	4	US-09-187-859-576	Sequence 576, App	372	3	27.3	10	2	US-08-669-161A-7	Sequence 7, Appl
300	3	27.3	9	4	US-09-187-859-576	Sequence 576, App	373	3	27.3	10	2	US-08-669-161A-28	Sequence 28, Appl
301	3	27.3	9	4	US-09-187-859-576	Sequence 576, App	374	3	27.3	10	3	US-08-482-528-209	Sequence 209, App
302	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	375	3	27.3	10	3	US-08-602-039-7	Sequence 7, Appl
303	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	376	3	27.3	10	3	US-09-247-146-1	Sequence 1, Appl
304	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	377	3	27.3	10	3	US-08-973-225-60	Sequence 60, Appl
305	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	378	3	27.3	10	3	US-09-007-020-3	Sequence 3, Appl
306	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	379	3	27.3	10	3	US-08-931-645-54	Sequence 54, Appl
307	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	380	3	27.3	10	3	US-09-188-579-66	Sequence 66, Appl
308	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	381	3	27.3	10	3	US-09-244-298A-60	Sequence 60, Appl
309	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	382	3	27.3	10	3	US-08-405-647B-6	Sequence 6, Appl
310	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	383	3	27.3	10	3	US-08-789-333F-9	Sequence 9, Appl
311	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	384	3	27.3	10	3	US-08-765-094C-27	Sequence 27, Appl
312	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	385	3	27.3	10	3	US-09-082-797-27	Sequence 27, Appl
313	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	386	3	27.3	10	3	US-09-169-015-19	Sequence 19, Appl
314	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	387	3	27.3	10	3	US-08-836-075A-199	Sequence 199, App
315	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	388	3	27.3	10	3	US-08-836-075A-200	Sequence 200, App
316	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	389	3	27.3	10	3	US-08-836-075A-201	Sequence 201, App
317	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	390	3	27.3	10	3	US-08-836-075A-202	Sequence 202, App
318	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	391	3	27.3	10	3	US-08-836-075A-203	Sequence 203, App
319	3	27.3	9	4	US-09-509-124-4	Sequence 4, App	392	3	27.3	10	3	US-08-602-999A-5	Sequence 5, Appl

443	3	27.3	10	3	US-08-085-449-6	Sequence 5, Appl1	466	3	27.3	10	6	5171838-8	Patent No. 5171838
444	3	27.3	10	3	US-09-113-921-62	Sequence 52, App1	467	3	27.3	10	6	5179097-17	Patent No. 5179097
445	3	27.3	10	3	US-09-113-921-63	Sequence 53, App1	468	3	27.3	10	6	5204096-31	Patent No. 5204096
446	3	27.3	10	3	US-09-486-443-11	Sequence 11, App1	469	3	27.3	11	1	US-07-666-719-18	Sequence 18, Appl
447	3	27.3	10	3	US-08-843-573-5	Sequence 5, Appl1	470	3	27.3	11	1	US-07-755-161A-9	Sequence 9, Appl1
448	3	27.3	10	3	US-09-315-344-66	Sequence 5, App1	471	3	27.3	11	1	US-07-841-474-9	Sequence 9, Appl1
449	3	27.3	10	3	US-09-320-934-20	Sequence 5, App1	472	3	27.3	11	1	US-08-646-538-1	Sequence 1, Appl1
400	3	27.3	10	3	US-09-253-945-22	Sequence 12, App1	473	3	27.3	11	1	US-08-197-795-5	Sequence 5, Appl1
461	3	27.3	10	3	US-09-263-975-34	Sequence 34, App1	474	3	27.3	11	1	US-08-128-971B-15	Sequence 15, Appl
462	3	27.3	10	3	US-09-263-975-34	Sequence 34, App1	475	3	27.3	11	1	US-08-476-875-3	Sequence 3, Appl1
463	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	476	3	27.3	11	1	US-08-318-935-3	Sequence 3, Appl1
464	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	477	3	27.3	11	1	US-08-483-232-3	Sequence 3, Appl1
465	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	478	3	27.3	11	1	US-08-256-771-32	Sequence 32, Appl
466	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	479	3	27.3	11	1	US-08-462-973-10	Sequence 10, Appl
467	3	27.3	10	3	US-08-278-805-5	Sequence 5, Appl1	480	3	27.3	11	1	US-08-483-140-3	Sequence 3, Appl1
468	3	27.3	10	3	US-09-017-63A-1	Sequence 6, Appl1	481	3	27.3	11	1	US-08-323-531-32	Sequence 32, Appl
469	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	482	3	27.3	11	1	US-08-548-540-145	Sequence 145, App
470	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	483	3	27.3	11	1	US-08-548-540-160	Sequence 160, App
471	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	484	3	27.3	11	1	US-08-198-094-32	Sequence 32, Appl
472	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	485	3	27.3	11	1	US-08-732-970-2	Sequence 2, Appl1
473	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	486	3	27.3	11	1	US-08-381-984-32	Sequence 32, Appl
474	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	487	3	27.3	11	2	US-08-669-721-16	Sequence 16, Appl
475	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	488	3	27.3	11	2	US-08-485-938A-3	Sequence 3, Appl1
476	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	489	3	27.3	11	2	US-08-464-182A-11	Sequence 11, Appl
477	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	490	3	27.3	11	2	US-08-464-182A-12	Sequence 12, Appl
478	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	491	3	27.3	11	2	US-08-693-274A-3	Sequence 3, Appl1
479	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	492	3	27.3	11	2	US-08-693-274A-4	Sequence 4, Appl1
480	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	493	3	27.3	11	2	US-08-637-759B-211	Sequence 211, App
481	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	494	3	27.3	11	2	US-08-679-865-35	Sequence 35, Appl
482	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	495	3	27.3	11	2	US-08-727-688-24	Sequence 24, Appl
483	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	496	3	27.3	11	2	US-08-406-271-11	Sequence 11, Appl
484	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	497	3	27.3	11	2	US-08-496-371-12	Sequence 12, Appl
485	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	498	3	27.3	11	2	US-08-680-876-35	Sequence 35, Appl
486	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	499	3	27.3	11	2	US-08-934-222-77	Sequence 77, Appl
487	3	27.3	10	3	US-09-167-859-40	Sequence 40, App1	500	3	27.3	11	2	US-08-934-402-77	Sequence 77, Appl

## ALIGNMENTS

## RESULT 1

US-09-016-466A-65  
Sequence 55, Application US/5906366A  
Patent No. 5955431  
GENERAL INFORMATION:  
APPLICANT: Stevens, Richard L.  
APPLICANT: Huang, Chifu  
TITLE OF INVENTION: FAST CELL PROTEASE PEPTIDE  
TITLE OF INVENTION: INHIBITORS  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: M&L Groenfield & Sacks, P.C.  
STREET: 603 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02210-2211  
COMPUTER READABLE FORM:  
COMPUTER TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,366A  
FILING DATE: January 30, 1998  
CLASSIFICATION: 53C  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/037,090  
FILING DATE: 05 FEB 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Plummer, Elizabeth R.  
REGISTRATION NUMBER: 36,637  
REFERENCE/DOCKET NUMBER: 80801/7093

1. TRANSMITTANCE INFORMATION  
 2. REF. NO. 617-720-4500  
 3. REF. NO. 617-720-2441  
 4. INDEX  
 5. INFORMATION FOR SEC ID NO. 65:  
 6. SPECIFIC CHARACTERISTICS:  
 7. LENGTH 8 amino acids  
 8. TYPE amino acid  
 9. STABILITY Stable  
 10. POLARITY Nonar  
 11. MOLECULAR WT 494.65  
 12. US 05 016 494A 65

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1  SEQ ID NO 8
2  LENGTH: 8
3  TYPE: PR1
4  ORGANISM: Artificial Sequence
5  NAME/KEY: SITE
6  LOCATION: (1)
7  OTHER INFORMATION: THIS IS D-GLUTAMINE
8  OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:ANALOG OF
9  OTHER INFORMATION: NEUROTENSIN
10 US 09 484 423 7

```

```

Query Match: 30.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Gaps 0;

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QY 7 KRR 10
RL 1 KRR 4

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## RESULT 3

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1  SEQ ID NO 8
2  LENGTH: 8
3  TYPE: PR1
4  ORGANISM: Artificial Sequence
5  NAME/KEY: SITE
6  LOCATION: (1)
7  OTHER INFORMATION: THIS IS D-GLUTAMINE
8  OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:ANALOG OF
9  OTHER INFORMATION: NEUROTENSIN
10 US 09 484 423 7

```

```

Query Match: 30.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Gaps 0;

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```

QY 7 KRR 10
RL 1 KRR 4

```

## RESULT 7

```

1  SEQ ID NO 8
2  LENGTH: 8
3  TYPE: PR1
4  ORGANISM: Artificial Sequence
5  NAME/KEY: SITE
6  LOCATION: (1)
7  OTHER INFORMATION: THIS IS D-GLUTAMINE
8  OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:ANALOG OF
9  OTHER INFORMATION: NEUROTENSIN
10 US 09 484 423 7

```

```

Query Match: 30.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Gaps 0;

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QY 7 KRR 10
RL 1 KRR 4

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## Query Match: 30.4%

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1  SEQ ID NO 8
2  LENGTH: 8
3  TYPE: PR1
4  ORGANISM: Artificial Sequence
5  NAME/KEY: SITE
6  LOCATION: (1)
7  OTHER INFORMATION: THIS IS D-GLUTAMINE
8  OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:ANALOG OF
9  OTHER INFORMATION: NEUROTENSIN
10 US 09 425 769 8

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```

Query Match: 30.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Gaps 0;

```

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QY 7 KRR 10
RL 1 KRR 4

```

## RESULT 8

```

1  SEQ ID NO 8
2  LENGTH: 8
3  TYPE: PR1
4  ORGANISM: Artificial Sequence
5  NAME/KEY: SITE
6  LOCATION: (1)
7  OTHER INFORMATION: THIS IS D-GLUTAMINE
8  OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:ANALOG OF
9  OTHER INFORMATION: NEUROTENSIN
10 US 09 436 170 7

```

```

Query Match: 30.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Gaps 0;

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QY 7 KRR 10
RL 1 KRR 4

```

## RESULT 9

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1  SEQ ID NO 8
2  LENGTH: 8
3  TYPE: PR1
4  ORGANISM: Artificial Sequence
5  NAME/KEY: SITE
6  LOCATION: (1)
7  OTHER INFORMATION: THIS IS D-GLUTAMINE
8  OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE:ANALOG OF
9  OTHER INFORMATION: NEUROTENSIN
10 US 09 436 170 7

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Query Match: 30.4%, Score 41, DP 4, Length 8;
Best Local Similarity: 100.0%, P-adj. No. 2.5e-05;
Matches: 4, Conservative 0, Mismatches 0, Gaps 0;

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QY 7 KRR 10
RL 1 KRR 4

```



```

1  TITLE OF INVENTION: MOLECULES
2  NUMBER OF SEQUENCES: 58
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: Arnold, White & Burke
5  STREET: P.O. Box 4433
6  CITY: Houston,
7  STATE: Texas
8  COUNTRY: USA
9  ZIP: 77210
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC DOS/MS DOS
14 SOFTWARE: Patent in Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/666,564
17 FILING DATE: 14 JUN 1996
18 CLASSIFICATION: 530
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: PCT/US97/12245
21 FILING DATE: 15 DEC 1993
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Kitchell, Barbara S.
24 REGISTRATION NUMBER: 33,928
25 REFERENCE/DOCKET NUMBER: US/08/666,564
26 TELEPHONE: 512/418-1000
27 TELEFAX: 512/418-1000
28 INFORMATION FOR SEQ ID NO: 52:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 12 amino acids
31 TYPE: amino acid
32 STRANDEDNESS:
33 TOPLOGY: Linear
34 US 08-666,564-52
35
36 Query Match: 36.4%, Score 4; DB 3; Length 12;
37 Best Local Similarity: 100.0%; Pred. No. 1.2e-02;
38 Matches: 4; Conservative 0; Mismatches 0; Indels 0;
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1 TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEGRADING ENZYME  
2 FILE REFERENCE: 1422-368P  
3 CURRENT APPLICATION NUMBER: US/09/404,812  
4 CURRENT FILING DATE: 1998-12-21  
5 NUMBER OF SEQ ID NOS: 17  
6 SOFTWARE: Patent In Ver. 2.0  
7 SEQ ID NO 4  
8 LENGTH: 12  
9 TYPE: ORF  
10 ORGANISM: Artificial Sequence  
11 FEATURE:  
12 OTHER INFORMATION: xaa - N-terminal amino acid  
13 FEATURE:  
14 OTHER INFORMATION: Description of Artificial Sequence: Referred to as  
15 OTHER INFORMATION: manufactured by peptide synthesis.  
16 US 09-202-842-4

Query Match: 36.4% Score 4: 36 4: 12 Length 12:  
Best Local Similarity 100.0% Pred. No. 1: 20-02  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PRRS 10  
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DB 5 PRRS 8

RESULT 15  
US-09-650-438-52  
1 Sequence 52: Application US/09/650-438  
2 Patent No. 6456529  
3 GENERAL INFORMATION:  
4 APPLICANT: Miller, Edmund J.  
5 HAYASHI, Shinichi  
6 TITLE OF INVENTION: PEPTIDE INHIBITING CELL GROWTH INHIBITORS  
7 NUMBER OF SEQUENCES: 58  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Arnold, White & Durkee  
10 STREET: P.O. Box 4433  
11 CITY: Houston  
12 STATE: Texas  
13 COUNTRY: USA  
14 ZIP: 77210  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Floppy disk  
17 COMPUTER: IBM PC compatible  
18 OPERATING SYSTEM: PC-DOS/MS-DOS  
19 SOFTWARE: Patent Reference #13, Version #1.0  
20 CURRENT APPLICATION DATA:  
21 APPLICATION NUMBER: US/09/560,414  
22 FILING DATE: 29-Aug-2000  
23 CLASSIFICATION: C08K6/00  
24 PRIOR APPLICATION DATA:  
25 APPLICATION NUMBER: 09/605,117  
26 FILING DATE: <Unknown>  
27 ATTORNEY/AGENT INFORMATION:  
28 NAME: Kitchell, Barbara S.  
29 REGISTRATION NUMBER: 33,928  
30 REFERENCE/DOCKET NUMBER: 0755-020  
31 TELECOMMUNICATION INFORMATION:  
32 TELEPHONE: 512/418-1600  
33 TELEFAX: 512/474-7577  
34 INFORMATION FOR SEQ ID NO: 52:  
35 SEQUENCE CHARACTERISTICS:  
36 LENGTH: 12 amino acids  
37 TYPE: amino acid  
38 STRANDEDNESS: <Unknown>  
39 TOPOLOGY: linear  
40 SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US 09-650-438-52

Query Match: 36.4% Score 4: 36 4: 12 Length 12:  
Best Local Similarity 100.0% Pred. No. 1: 20-02  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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1111  
DB 3 PRRS 6  
RESULT 17  
PCT US93-12245-52  
1 Sequence 52: Application PCT/US93/12245  
2 GENERAL INFORMATION:  
3 APPLICANT: Cohen, Allen B.  
4 APPLICANT: Miller, Edmund J.  
5 APPLICANT: KURAWSKA, Anna  
6 APPLICANT: HAYASHI, Shinichi  
7 APPLICANT: HITTLE, Ronald R.  
8 TITLE OF INVENTION: PEPTIDE INHIBITORS OF CXC  
9 TITLE OF INVENTION: INTERFERING MOLECULES  
10 NUMBER OF SEQUENCES: 58  
11 CORRESPONDENCE ADDRESS:  
12 ADDRESSEE: Arnold, White & Durkee  
13 STREET: P.O. Box 4433  
14 CITY: Houston  
15 STATE: Texas  
16 COUNTRY: USA  
17 ZIP: 77210  
18 COMPUTER READABLE FORM:  
19 MEDIUM TYPE: Floppy disk  
20 COMPUTER: IBM PC compatible  
21 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
22 SOFTWARE: WordPerfect 5.1  
23 CURRENT APPLICATION DATA:  
24 APPLICATION NUMBER: PCT/US93/12245  
25 FILING DATE: Concurrently herewith  
26 CLASSIFICATION:  
27 ATTORNEY/AGENT INFORMATION:  
28 NAME: Kitchell, Barbara S.  
29 REGISTRATION NUMBER: 33,928  
30 REFERENCE/DOCKET NUMBER: C1FN016PCT  
31 TELECOMMUNICATION INFORMATION:  
32 TELEPHONE: (512) 320-7200  
33 TELEFAX: (713) 789-2679  
34 TELE: 79-0924  
35 INFORMATION FOR SEQ ID NO: 52:  
36 SEQUENCE CHARACTERISTICS:  
37 LENGTH: 12 amino acids  
38 TYPE: amino acid  
39 STRANDEDNESS: single  
40 TOPOLOGY: linear  
41 MOLECULE TYPE: peptide  
42 PCT US93-12245-52

Query Match: 36.4% Score 4: 36 4: 12 Length 12:  
Best Local Similarity 100.0% Pred. No. 1: 20-02  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 PRRS 11  
1111  
DB 3 PRRS 6

RESULT 18  
US-07-714-540-8  
1 Sequence 6: Application US/97/14542  
2 Patent No. 5262521  
3 GENERAL INFORMATION:  
4 APPLICANT: Almquist, Ronald G.  
5 APPLICANT: Toll, Lawrence  
6 TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING  
7 TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF  
8 NUMBER OF SEQUENCES: 13  
9 CORRESPONDENCE ADDRESS:  
10 ADDRESSEE: Irell & Manella

```

1 STREET: 545 Middlefield Road, Suite 200
2 CITY: Menlo Park
3 STATE: California
4 COUNTRY: USA
5 ZIP: 94025
6
7 COMPILED REAMABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC DOS/MS DOS
11 SOFTWARE: Patent In Release #1.0, Version #
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/07/14,540
15 FILING DATE: 19910607
16 CLASSIFICATION: 514
17
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Reed, Glanville
20 REGISTRATION NUMBER: 41,492
21 REFERENCE/DOCKET NUMBER: 8500, 550,000
22
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 415-427-7259
25 TELEFAX: 415-427-2951
26 FAX: 706141
27
28 INFORMATION FOR SEQ ID NO: 5:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 13 amino acids
31 TYPE: AMINO ACID
32 STRANDEDNESS: Single
33 TOPOLOGY: Linear
34 MOLECULE TYPE: protein
35 US/07/14,540-B
36
37 Query Match: 36.4% Score 47 DB 1 Length 13
38 Best local Similarity: 100.0% Proj. No. 1 4e-02
39 Matches: 4: Conservative 0: Mismatches 0: Gaps 0:
40
41
42 27 7 KPRR 10
43 111
44 6 KPRR 9
45
46 RESULT 20
47 US 08-447-137-117
48 Sequence 117, Application US/08747117
49 Patent No. 5945034
50 GENERAL INFORMATION:
51 APPLICANT: YEN, Richard C.K.
52 TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
53 TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
54 NUMBER OF SEQUENCES: 184
55 CORRESPONDENCE ADDRESS:
56 ADDRESSEE: Townsend and Townsend and Crew LLP
57 STREET: Two Embarcadero Center, 8th Floor
58 CITY: San Francisco
59 STATE: CA
60 COUNTRY: USA
61 ZIP: 94111
62 COMPUTER READABLE FORM:
63 MEDIUM TYPE: Floppy disk
64 COMPUTER: IBM PC compatible
65 OPERATING SYSTEM: PC DOS/MS-DOS
66 SOFTWARE: Patent In Release #1.0, Version #1.30
67
68 CURRENT APPLICATION DATA:
69 APPLICATION NUMBER: US/08/147,137
70 FILING DATE: 12 NOV 1998
71 CLASSIFICATION: 424
72
73 PRIOR APPLICATION DATA:
74 APPLICATION NUMBER: US 08/212,546
75 FILING DATE: 14 MAR 1994
76
77 PRIOR APPLICATION DATA:
78 APPLICATION NUMBER: US 08/069,931
79 FILING DATE: 01 JUN 1994
80
81 PRIOR APPLICATION DATA:
82 APPLICATION NUMBER: US 07/959,560
83 FILING DATE: 13 OCT 1992
84
85 PRIOR APPLICATION DATA:
86 APPLICATION NUMBER: US 07/441,720
87 FILING DATE: 15 JAN 1991
88
89 ATTORNEY/AGENT INFORMATION:
90 NAME: Apple, Randolph L.
91 REGISTRATION NUMBER: 45,429
92 REFERENCE/DOCKET NUMBER: 616197-00084005
93
94 TELECOMMUNICATION INFORMATION:
95 TELEPHONE: 415-576-7200
96
97 INFORMATION FOR SEQ ID NO: 117:
98 SEQUENCE CHARACTERISTICS:
99 LENGTH: 13 amino acids
100 TYPE: amino acid
101 STRANDEDNESS: Not relevant

```

```

1 SEQUENCE CHARACTERISTICS:
2 LENGTH: 13 amino acids
3 TYPE: amino acid
4 STRANDEDNESS: Single
5 TOPOLOGY: Linear
6 MOLECULE TYPE: peptide
7 FEATURES:
8 NAME/KEY: Modified-site
9 LOCATION: 1
10 OTHER INFORMATION: /note "Position 1 p-Glu."
11 FEATURES:
12 NAME/KEY: Modified-site
13 LOCATION: 1
14 OTHER INFORMATION: /note "Position 13 Leu-OH."
15
16 US-08-428-488-11
17
18 Query Match: 36.4% Score 47 DB 1 Length 13
19 Best local Similarity: 100.0% Proj. No. 1 4e-02
20 Matches: 4: Conservative 0: Mismatches 0: Gaps 0:
21
22
23 27 7 KPRR 10
24 111
25 6 KPRR 9
26
27 RESULT 20
28 US-08-447-137-117
29 Sequence 117, Application US/08747117
30 Patent No. 5945034
31 GENERAL INFORMATION:
32 APPLICANT: YEN, Richard C.K.
33 TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
34 TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
35 NUMBER OF SEQUENCES: 184
36 CORRESPONDENCE ADDRESS:
37 ADDRESSEE: Townsend and Townsend and Crew LLP
38 STREET: Two Embarcadero Center, 8th Floor
39 CITY: San Francisco
40 STATE: CA
41 COUNTRY: USA
42 ZIP: 94111
43 COMPUTER READABLE FORM:
44 MEDIUM TYPE: Floppy disk
45 COMPUTER: IBM PC compatible
46 OPERATING SYSTEM: PC DOS/MS-DOS
47 SOFTWARE: Patent In Release #1.0, Version #1.30
48
49 CURRENT APPLICATION DATA:
50 APPLICATION NUMBER: US/08/147,137
51 FILING DATE: 12 NOV 1998
52 CLASSIFICATION: 424
53
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: US 08/212,546
56 FILING DATE: 14 MAR 1994
57
58 PRIOR APPLICATION DATA:
59 APPLICATION NUMBER: US 08/069,931
60 FILING DATE: 01 JUN 1994
61
62 PRIOR APPLICATION DATA:
63 APPLICATION NUMBER: US 07/959,560
64 FILING DATE: 13 OCT 1992
65
66 PRIOR APPLICATION DATA:
67 APPLICATION NUMBER: US 07/441,720
68 FILING DATE: 15 JAN 1991
69
70 ATTORNEY/AGENT INFORMATION:
71 NAME: Apple, Randolph L.
72 REGISTRATION NUMBER: 45,429
73 REFERENCE/DOCKET NUMBER: 616197-00084005
74
75 TELECOMMUNICATION INFORMATION:
76 TELEPHONE: 415-576-7200
77
78 INFORMATION FOR SEQ ID NO: 117:
79 SEQUENCE CHARACTERISTICS:
80 LENGTH: 13 amino acids
81 TYPE: amino acid
82 STRANDEDNESS: Not relevant

```



```

FEATURES: not relevant
NAME/KEY: Modified-site
LOCATION:
OTHER INFORMATION: /product "p-Glu"
US 58-742-137-117

Query Match: 36.4%; Score: 4; DB: 3; Length: 13;
Best Local Similarity: 100.0%; Pred. No. 1.3e+02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 7 KRR 10
111
1b 6 KRR 9

RESULT 23
US-08-787-443-1
Sequence 1: Application US/08787-443
Patent No. 6501970
GENERAL INFORMATION:
APPLICANT: STRASSER, CATHERINE D.
APPLICANT: CASCHER, MARGARET A.
APPLICANT: MAWELL, DOUGLAS A.
TITLE OF INVENTION: MODIFIED NEUROPEPTIDE Y RECEPTORS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAM H. McDONNELL BLVD.
STREET: 127 EAST LINCOLN AVENUE
CITY: RAINWAY
STATE: NEW JERSEY
COUNTRY: US
ZIP: 07069-1900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817-869
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/345,017
FILING DATE: 27 NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: NICHOLSON, WILLIAM H.
REGISTRATION NUMBER: 25,147
REFERENCE/DACKET NUMBER: 29419Y PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-1348
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-817-869-6

Query Match: 36.4%; Score: 4; DB: 3; Length: 13;
Best Local Similarity: 100.0%; Pred. No. 1.3e+02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 2 KRR 1
111
1b 9 KRR 12

RESULT 24
US-09-394-254A-1
Sequence 1: Application US/09394-254A
Patent No. 6194486
GENERAL INFORMATION:
APPLICANT: MERTENS et al.
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey S. Boone
STREET: 675 McDonnell Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

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1  SOFTWARE: Patent In Release #1.0, Version 1.1.0
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/09/787-443-12
4  FILING DATE:
5  CLASSIFICATION:
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: 09/787-443
8  FILING DATE:
9  ATTORNEY/AGENT INFORMATION:
10 NAME: Jeffrey S. Boone
11 REGISTRATION NUMBER: 29294
12 REFERENCE/DECKET NUMBER: M-093 W-05
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: 1 (314) 654-8955
15 TELEFAX: 1 (314) 654-3156
16 INFORMATION FOR SEQ ID NO: 1:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 14 amino acids
19 TYPE: amino acid
20 STRANDNESS: not relevant
21 TOPOLOGY: not relevant
22 MOLECULE TYPE: peptide
23 FRAGMENT TYPE: internal
24 FEATURE:
25 NAME/KEY: Modified site
26 LOCATION: 1
27 OTHER INFORMATION: /product: "PYROGLUTAMATE"
US-09-334-254A 1

```

```

Query Match: 96.4%; Score 4; DB 0; Length 14;
Best Local Similarity: 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

28 7 KPRR 10
29 111
30 6 KPRR 9

```

## RESULT 24

```

1  US-09-289-693-1
2  Sequence 1: Application US/09289693
3  Patent No. 6214790
4  GENERAL INFORMATION:
5  APPLICANT: Richardson, Elliott
6  APPLICANT: Casack, Bernadette Marie
7  APPLICANT: Egan, Jean-Paul
8  APPLICANT: McSwicker, Daniel J.
9  APPLICANT: Fard, Abdul
10 APPLICANT: Taylor, Beth Marie
11 APPLICANT: Boudreau, M.
12 FILE REFERENCE: 07509/04003
13 CURRENT APPLICATION NUMBER: US/09/289-693
14 CURRENT FILING DATE: 1998-04-09
15 EARLIER APPLICATION NUMBER: US 60/121479
16 EARLIER FILING DATE: 1998-02-14
17 EARLIER APPLICATION NUMBER: US 60/298109
18 EARLIER FILING DATE: 1998-08-27
19 EARLIER APPLICATION NUMBER: US 60/060100
20 EARLIER FILING DATE: 1998-07-09
21 EARLIER APPLICATION NUMBER: US 60/061000
22 EARLIER FILING DATE: 1998-04-20
23 NUMBER OF SEQ ID NOS: 30
24 SOFTWARE: FASTSQ for Windows Version 4
25 SEQ ID NO: 1
26 LENGTH: 14
27 TYPE: PSI
28 ORGANISM: Artificial Sequence
29 FEATURE:
30 OTHER INFORMATION: Synthesized by GenScript, Inc.
31 NAME/KEY: SITE
32 LOCATION: (1)-(11)

```

```

1  OTHER INFORMATION: Xaa - pyrrolidone carboxylic acid
2  US-09-289-693-1
3  Query Match: 96.4%; Score 4; DB 3; Length 13;
4  Best Local Similarity: 100.0%; Pred. No. 1.3e+02;
5  Matches 4; Conservative 0; Mismatches 0; Gaps 0;
6  QY 7 KPRR 10
7  11
8  6 KPRR 9
9  RESULT 25
10 US-09-355-869-2
11 Sequence 2: Application US/09035869
12 Patent No. 6332663
13 GENERAL INFORMATION:
14 APPLICANT: Regis, David Eugene
15 TITLE OF INVENTION: METHOD FOR THE DETECTION AND LOCALIZATION OF MALIGNANT
16 TITLE OF INVENTION: HUMAN TUMORS
17 FILE REFERENCE: 1608-04
18 CURRENT APPLICATION NUMBER: US/09/355-869
19 CURRENT FILING DATE: 1999-09-04
20 EARLIER APPLICATION NUMBER: PCT/US95/01964
21 EARLIER FILING DATE: 1996-02-02
22 EARLIER APPLICATION NUMBER: EP 97200247.6
23 EARLIER FILING DATE: 1997-02-04
24 NUMBER OF SEQ ID NOS: 4
25 SOFTWARE: Patent In Ver. 2.0
26 SEQ ID NO: 2
27 LENGTH: 14
28 TYPE: PSI
29 ORGANISM: Homo sapiens
30 FEATURE:
31 NAME/KEY: SITE
32 LOCATION: (1)
33 OTHER INFORMATION: This site is pyroglutamate.
US-09-355-869-2

```

```

Query Match: 96.4%; Score 4; DB 4; Length 13;
Best Local Similarity: 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 7 KPRR 10
11 11
12 6 KPRR 9

```

## RESULT 26

```

1  US-09-355-869-2
2  Sequence 3: Application US/09035869
3  Patent No. 6344551
4  GENERAL INFORMATION:
5  APPLICANT: Craib, A. Grey
6  APPLICANT: Griffin, David
7  APPLICANT: Oliveira, Baldemero M.
8  APPLICANT: Watkins, Maren
9  APPLICANT: Rillyard, David R.
10 APPLICANT: Impetrial, Julia
11 APPLICANT: Cruz, Lourdes J.
12 APPLICANT: Wainstaff, John D.
13 APPLICANT: Layer, Richard L.
14 APPLICANT: Jones, Robert M.
15 APPLICANT: McCabe, R. Tyler
16 APPLICANT: Cosmetix, Inc.
17 APPLICANT: University of Utah Research Foundation
18 APPLICANT: Salk Institute
19 TITLE OF INVENTION: Controlling
20 FILE REFERENCE: Controlling
21 CURRENT APPLICATION NUMBER: US/09/355-869
22 CURRENT FILING DATE: 2003-06-29
23 EARLIER APPLICATION NUMBER: US 09/420,797
24 EARLIER FILING DATE: 1999-10-19

```

1 PRIOR APPLICATION NUMBER: US 60/130,661  
 2 PRIOR FILING DATE: 1999-04-23  
 3 PRIOR APPLICATION NUMBER: US 60/126,561  
 4 PRIOR FILING DATE: 1999-04-09  
 5 PRIOR APPLICATION NUMBER: US 60/105,015  
 6 PRIOR FILING DATE: 1998-10-20  
 7 NUMBER OF SEQ ID NOS: 13  
 8 SOFTWARE: PatentIn Ver. 2.0  
 9 SEQ ID NO 8  
 10 LENGTH: 13  
 11 TYPE: PRT  
 12 ORGANISM: Bos sp.  
 13 FEATURES  
 14 NAME/KEY: PEPTIDE  
 15 LOCATION (1)  
 16 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 US-09-605,990-B

Query Match 36.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.0e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 KPRR 10  
 1111  
 6 KPRR 9

RESULT 27  
 US-09-420-797-B

1 Sequence 8, Application US/09420797-B  
 2 Patent No. 6525221  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Craig, A. Grey  
 5 APPLICANT: Griffin, David  
 6 APPLICANT: Olivera, Baldomero M.  
 7 APPLICANT: Watkins, Marc  
 8 APPLICANT: Hilliard, David R.  
 9 APPLICANT: Imperial, Julita  
 10 APPLICANT: Cruz, Lourdes J.  
 11 APPLICANT: Wagstaff, John D.  
 12 APPLICANT: Layer, Richard L.  
 13 APPLICANT: Jones, Robert M.  
 14 APPLICANT: McCabe, R. Tyler  
 15 APPLICANT: Cognetix, Inc.  
 16 APPLICANT: University of Utah Research Foundation  
 17 APPLICANT: Salk Institute  
 18 TITLE OF INVENTION: Conculakin G. Analogs thereof and Uses Thereof  
 19 FILE REFERENCE: Conculakin-G  
 20 CURRENT APPLICATION NUMBER: US 60/130,661  
 21 PRIOR FILING DATE: 1999-04-23  
 22 PRIOR APPLICATION NUMBER: US 60/126,561  
 23 PRIOR FILING DATE: 1999-04-09  
 24 PRIOR APPLICATION NUMBER: US 60/105,015  
 25 PRIOR FILING DATE: 1998-10-20  
 26 NUMBER OF SEQ ID NOS: 13  
 27 SOFTWARE: PatentIn Ver. 2.0  
 28 SEQ ID NO 8  
 29 LENGTH: 13  
 30 TYPE: PRT  
 31 ORGANISM: Bos sp.  
 32 FEATURES  
 33 NAME/KEY: PEPTIDE  
 34 LOCATION (1)  
 35 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 US-09-605,990-B

Query Match 36.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.0e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 KPRR 10  
 1111  
 6 KPRR 9

Query Match 36.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.0e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 KPRR 10

Db 1111  
 6 KPRR 9  
 RESULT 28  
 US-09-605,991-B

1 Sequence 8, Application US/09605991  
 2 Patent No. 6489298  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Craig, A. Grey  
 5 APPLICANT: Griffin, David  
 6 APPLICANT: Olivera, Baldomero M.  
 7 APPLICANT: Watkins, Marc  
 8 APPLICANT: Hilliard, David R.  
 9 APPLICANT: Imperial, Julita  
 10 APPLICANT: Cruz, Lourdes J.  
 11 APPLICANT: Wagstaff, John D.  
 12 APPLICANT: Layer, Richard L.  
 13 APPLICANT: Jones, Robert M.  
 14 APPLICANT: McCabe, R. Tyler  
 15 APPLICANT: Cognetix, Inc.  
 16 APPLICANT: University of Utah Research Foundation  
 17 APPLICANT: Salk Institute  
 18 TITLE OF INVENTION: Conculakin G. Analogs thereof and Uses Thereof  
 19 FILE REFERENCE: Conculakin-G  
 20 CURRENT APPLICATION NUMBER: US/09/605,991  
 21 PRIOR FILING DATE: 2000-06-29  
 22 PRIOR APPLICATION NUMBER: US/09/420,797  
 23 PRIOR FILING DATE: 1999-10-19  
 24 PRIOR APPLICATION NUMBER: US 60/130,661  
 25 PRIOR FILING DATE: 1999-04-23  
 26 PRIOR APPLICATION NUMBER: US 60/126,561  
 27 PRIOR FILING DATE: 1999-04-09  
 28 PRIOR APPLICATION NUMBER: US 60/105,015  
 29 PRIOR FILING DATE: 1998-10-20  
 30 NUMBER OF SEQ ID NOS: 13  
 31 SOFTWARE: PatentIn Ver. 2.0  
 32 SEQ ID NO 8  
 33 LENGTH: 13  
 34 TYPE: PRT  
 35 ORGANISM: Bos sp.  
 36 FEATURES  
 37 NAME/KEY: PEPTIDE  
 38 LOCATION (1)  
 39 OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.  
 US-09-605,991-B

Query Match 35.4% Score 41 DB 4 Length 13  
 Best Local Similarity 100.0% Pct. No. 1.0e-02  
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 KPRR 10  
 1111  
 6 KPRR 9

RESULT 29  
 US-09-609,934-B

1 Sequence 8, Application US/09609934  
 2 Patent No. 6525221  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Craig, A. Grey  
 5 APPLICANT: Griffin, David  
 6 APPLICANT: Olivera, Baldomero M.  
 7 APPLICANT: Watkins, Marc  
 8 APPLICANT: Hilliard, David R.  
 9 APPLICANT: Imperial, Julita  
 10 APPLICANT: Cruz, Lourdes J.  
 11 APPLICANT: Wagstaff, John D.  
 12 APPLICANT: Layer, Richard L.  
 13 APPLICANT: Jones, Robert M.  
 14 APPLICANT: McCabe, R. Tyler  
 15 APPLICANT: Cognetix, Inc.

```

1  APPLICANT: University of Utah Research Foundation
2  APPLICANT: Salk Institute
3  TITLE OF INVENTION: Confolakin-G; Analogs thereof and uses therefor
4  FILE REFERENCE: Confolakin-G CIP
5  CURRENT APPLICATION NUMBER: US/09/09,594
6  CURRENT FILING DATE: 2000-06-13
7  EARLIER APPLICATION NUMBER: US 60/133,661
8  EARLIER FILING DATE: 1999-04-23
9  EARLIER APPLICATION NUMBER: US 4,428,164
10 EARLIER FILING DATE: 1999-04-09
11 EARLIER APPLICATION NUMBER: US 13/105,113
12 EARLIER FILING DATE: 1998-10-20
13 EARLIER APPLICATION NUMBER: US 09/420,737
14 EARLIER FILING DATE: 1999-10-29
15 EARLIER APPLICATION NUMBER: US 09/
16 EARLIER FILING DATE: 2000-05-29
17 NUMBER OF SEQ ID NOS: 13
18 SOFTWARE: Patent In Ver. 2.0
19 SEQ ID NO: 1
20 LENGTH: 14
21 TYPE: LRP
22 ORGANISM: RUS SP.
23 FEATURE:
24 NAME/KEY: PEPTIDE
25 LOCATION: (1)
26 OTHER INFORMATION: Xaa at residue 1 is pyro D.
27 US 09 609 594 #

```

```

Query Match: 36.4%; Score 4; DB 4; Length 14;
Best Local Similarity: 100.0%; Pred. No. 1.4e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

CY 7 KERR 10
DB 1 1
5 KERR 9

```

```

RESULT 40
1  US-09-787-443-12
2  Sequence 6: Application PC/T055514-27
3  GENERAL INFORMATION:
4  APPLICANT: STRAUER, CATHERINE E.
5  APPLICANT: CASCIERI, MARGARET A.
6  APPLICANT: MACNELL, DOUGLAS J.
7  TITLE OF INVENTION: MODIFIED NEUREXIN-LIKE A RECEPTORS
8  NUMBER OF SEQUENCES: 11
9  CORRESPONDENT ADDRESS:
10 ADDRESSEE: MARY A. APOLLINA
11 STREET: 126 EAST LINCOLN AVENUE
12 CITY: RABWAY
13 STATE: NEW JERSEY
14 COUNTRY: US
15 ZIP: 07065-0000
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: PCT/US95/1477
23 FILING DATE:
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 PRIOR APPLICATION NUMBER: US 08/441,017
27 FILING DATE: 07-NOV-1994
28 ATTORNEY/AGENT INFORMATION:
29 NAME: APOLLINA, MARY A.
30 REGISTRATION NUMBER: 34,087
31 REFERENCE/DOCKET NUMBER: 19-188 17
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (908) 594-3462
34 TELEFAX: (908) 594-4720
35 INFORMATION FOR SEQ ID NO: 1:

```

```

1  SEQUENCE CHARACTERISTICS:
2  LENGTH: 13 amino acids
3  TYPE: amino acid
4  STRANDNESS: single
5  TOPOLOGY: linear
6  MOLECULE TYPE: peptide
7  PCT-US95-14577-6
8
9  Query Match: 36.4%; Score 4; DB 5; Length 13;
10 Best Local Similarity: 100.0%; Pred. No. 1.4e-02;
11 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

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CY 2 KERR 5
DB 9 KERR 12

```

```

RESULT 41
1  US-09-755-272-4
2  Sequence 4: Application US/09/255272
3  Patient No. 562269
4  GENERAL INFORMATION:
5  APPLICANT: Kumar, Ramesh
6  APPLICANT: Sharma, Ajay
7  APPLICANT: Khoury-Christianson, Anastasia
8  APPLICANT: M.
9  TITLE OF INVENTION: Production of therapeutic peptides in
10 TRANSGENIC ANIMALS as a fusion with Hemoglobin
11 NUMBER OF SEQUENCES: 42
12 CORRESPONDENT ADDRESS:
13 ADDRESSEE: PENNIE & EMMONS
14 STREET: 1155 Avenue of the Americas
15 CITY: New York
16 STATE: NY
17 COUNTRY: USA
18 ZIP: 10036-2711
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patent In Release #1.0, Version #1.25
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/09/255,272
26 FILING DATE:
27 CLASSIFICATION: 435
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Cotuzzi, Laura A.
30 REGISTRATION NUMBER: 30742
31 REFERENCE/DOCKET NUMBER: 5794 092
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (212) 793-9090
34 TELEFAX: (212) 659-9741/8864
35 INFORMATION FOR SEQ ID NO: 4:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 14 amino acids
38 TYPE: amino acid
39 TOPOLOGY: unknown
40 MOLECULE TYPE: Peptide
41 HYPOTHETICAL: NO
42 ANTI-SENSE: NO
43 US-08-255-272-4

```

```

Query Match: 36.4%; Score 4; DB 1; Length 14;
Best Local Similarity: 100.0%; Pred. No. 1.4e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

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CY 7 KERR 10
DB 7 KERR 10

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RESULT 42
1  US-07-420 917-2

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1 Sequence 2, Application US/07920457
2 Patent No. 5447915
3 GENERAL INFORMATION:
4 APPLICANT: Schreiber, Stuart
5 APPLICANT: Burakoff, Steven
6 TITLE OF INVENTION: Terminally-Blocked Anticatalytic Polypeptides
7 NUMBER OF SEQUENCES: 12
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Alligretti & Wilcoff, Ltd
10 STREET: 10 South Wacker Drive, Suite 600
11 CITY: Chicago
12 STATE: IL
13 COUNTRY: USA
14 ZIP: 60606
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.23
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/07/920,597
22 FILING DATE: 19920828
23 CLASSIFICATION: 514
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: WO/92/001142
26 FILING DATE: 28 FEB 1991
27 ATTORNEY/AGENT INFORMATION:
28 NAME: No. 5447915nan, Kevin E
29 REGISTRATION NUMBER: 45,904
30 REFERENCE/DOCKET NUMBER: #1,174-E
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 312-715-1000
33 TELEFAX: 312-715-1234
34 INFORMATION FOR SEQ ID NO: 2:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 9 amino acids
37 TYPE: amino acid
38 STRANDNESS: single
39 TOPOLOGY: linear
40 MOLECULE TYPE: peptide
41 US 07-920-597-2
42
43 Query Match 27.5% Score 3, DR 1, Length 8;
44 Best Local Similarity 100.0%, Pct. No. 2, 500, 60
45 Matches 37 Conservative 67 Mismatches 0 Gaps 0
46
47 QY 7 KPR 3
48 DB 6 KPR 6
49
50 RESULT 14
51 US-07-920-597-2
52 Sequence 3, Application US/07920457
53 Patent No. 5447915
54 GENERAL INFORMATION:
55 APPLICANT: Schreiber, Stuart
56 APPLICANT: Burakoff, Steven
57 TITLE OF INVENTION: Terminally-Blocked Anticatalytic Polypeptides
58 NUMBER OF SEQUENCES: 12
59 CORRESPONDENCE ADDRESS:
60 ADDRESSEE: Alligretti & Wilcoff, Ltd
61 STREET: 10 South Wacker Drive, Suite 600
62 CITY: Chicago
63 STATE: IL
64 COUNTRY: USA
65 ZIP: 60606
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: Floppy disk
68 COMPUTER: IBM PC compatible
69 OPERATING SYSTEM: PC DOS/MS-DOS
70 SOFTWARE: PatentIn Release #1.0, Version #1.23

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/07/920,597
3 FILING DATE: 19920828
4 CLASSIFICATION: 514
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: WO/92/001142
7 FILING DATE: 28 FEB 1991
8 ATTORNEY/AGENT INFORMATION:
9 NAME: No. 5447915nan, Kevin E
10 REGISTRATION NUMBER: 45,904
11 REFERENCE/DOCKET NUMBER: #1,174-E
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 312-715-1000
14 TELEFAX: 312-715-1234
15 INFORMATION FOR SEQ ID NO: 3:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 8 amino acids
18 TYPE: amino acid
19 STRANDNESS: single
20 TOPOLOGY: linear
21 MOLECULE TYPE: peptide
22 US 07-920-597-4
23
24 Query Match 27.5% Score 3, DR 1, Length 8;
25 Best Local Similarity 100.0%, Pct. No. 2, 500, 05
26 Matches 37 Conservative 37 Mismatches 0 Gaps 0
27
28 QY 7 KPR 9
29 DB 4 KPR 6
30
31 RESULT 34
32 US-08-178-570-51
33 Sequence 51, Application US/08178570
34 Patent No. 5542157
35 GENERAL INFORMATION:
36 APPLICANT: Lewis G. Cardley
37 APPLICANT: Zhou Song Yang
38 TITLE OF INVENTION: Substrate Specificity of Protein Kinases
39 NUMBER OF SEQUENCES: 77
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: LAHIVE & CACKFIELD
42 STREET: 60 STATE STREET, SUITE 510
43 CITY: BOSTON
44 STATE: MASSACHUSETTS
45 COUNTRY: USA
46 ZIP: 02109-1875
47 COMPUTER READABLE FORM:
48 MEDIUM TYPE: Floppy disk
49 COMPUTER: IBM PC compatible
50 OPERATING SYSTEM: PC-DOS/MS-DOS
51 SOFTWARE: ASCII text
52 CURRENT APPLICATION DATA:
53 APPLICATION NUMBER: US/08/178,570
54 FILING DATE: JANUARY 7, 1994
55 CLASSIFICATION: 435
56 ATTORNEY/AGENT INFORMATION:
57 NAME: DOUGELL, GIGLIO & J...
58 REGISTRATION NUMBER: 33,593
59 REFERENCE/DOCKET NUMBER: BBI-004
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (617) 227-7400
62 TELEFAX: (617) 227-5941
63 INFORMATION FOR SEQ ID NO: 51:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH: 8 amino acids
66 TYPE: amino acid
67 TOPOLOGY: linear
68 MOLECULE TYPE: peptide
69 FRAGMENT TYPE: internal
70 US-08-178-570-51

```

Query Match: 27.98% Sequence: 100% ID: 100%  
 Best Local Similarity: 100.00% Protein: 27.98%  
 Matches: 47 Conservative: 47 Mismatches: 0 Gaps: 0

QY 1 ABQ 3  
 DL 1 ABQ 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/08/20174  
 2 Patent No. 566745  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHELATING COMPOUNDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 300 N Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS/MS-DOS  
 16 SOFTWARE: Patent to Release #10, Version 1.0  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 435  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Scott, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/20-6A, F  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5300  
 26 TELEFAX: (202) 672-5355  
 27 TEXT: 004166  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 6 amino acids  
 31 TYPE: amino acid  
 32 TOPOLOGY: Linear  
 33 Molecule Type: peptide  
 34 US 09-787-443-12

QY 1 ABQ 3  
 DL 1 ABQ 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/08/20174  
 2 Patent No. 566745  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHELATING COMPOUNDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 300 N Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS  
 16 SOFTWARE: Patent to Release #10, Version 1.0  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 435  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Scott, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/20-6A, F  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5300  
 26 TELEFAX: (202) 672-5355  
 27 TEXT: 004166  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 6 amino acids  
 31 TYPE: amino acid  
 32 TOPOLOGY: Linear  
 33 Molecule Type: peptide  
 34 US 09-787-443-12

QY 1 ABQ 3  
 DL 1 ABQ 3

Result 6:  
 US 09-787-443-12

1 Sequence 10, Application US/08/20174  
 2 Patent No. 566745  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Godbody, Anne  
 5 TITLE OF INVENTION: PEPTIDE CHELATING COMPOUNDS  
 6 NUMBER OF SEQUENCES: 11  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Foley & Lardner  
 9 STREET: Suite 600, 300 N Street, N.W.  
 10 CITY: Washington, D.C.  
 11 COUNTRY: USA  
 12 ZIP: 20007-5109  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: floppy disk  
 15 OPERATING SYSTEM: PC-DOS  
 16 SOFTWARE: Patent to Release #10, Version 1.0  
 17 CURRENT APPLICATION DATA:  
 18 FILING DATE: 25-FEB-1994  
 19 CLASSIFICATION: 435  
 20 ATTORNEY/AGENT INFORMATION:  
 21 NAME: Scott, Stephen A.  
 22 REGISTRATION NUMBER: 29,768  
 23 REFERENCE/DOCKET NUMBER: 1177/20-6A, F  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: (202) 672-5300  
 26 TELEFAX: (202) 672-5355  
 27 TEXT: 004166  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 6 amino acids  
 31 TYPE: amino acid  
 32 TOPOLOGY: Linear  
 33 Molecule Type: peptide  
 34 US 09-787-443-12

1 STREET: P.O. Box 443  
 2 CITY: Houston  
 3 STATE: Texas  
 4 COUNTRY: USA  
 5 ZIP: 77270  
 6 COMPUTER READABLE FORM:  
 7 MEDIUM TYPE: floppy disk  
 8 OPERATING SYSTEM: PC-DOS/MS-DOS  
 9 SOFTWARE: Patent to Release #10, Version 1.0  
 10 CURRENT APPLICATION DATA:  
 11 FILING DATE: August 31, 1993  
 12 CLASSIFICATION: 424  
 13 ATTORNEY/AGENT INFORMATION:  
 14 NAME: Parker, David L.  
 15 REGISTRATION NUMBER: 42,435  
 16 REFERENCE/DOCKET NUMBER: 0780331/PAR  
 17 TELECOMMUNICATION INFORMATION:  
 18 TELEPHONE: 512-420-7400  
 19 TELEFAX: 512-424-7677  
 20 TEXT: No. 500933 Applicable  
 21 INFORMATION FOR SEQ ID NO: 1:  
 22 SEQUENCE CHARACTERISTICS:  
 23 LENGTH: 6 amino acid residues  
 24 TYPE: amino acid  
 25 STRANDEDNESS: Single  
 26 TOPOLOGY: Linear  
 27 Molecule Type: peptide  
 28 US-09-787-443-12

Query Match: 27.98% Sequence: 100% ID: 100%  
 Best Local Similarity: 100.00% Protein: 27.98%  
 Matches: 47 Conservative: 47 Mismatches: 0 Gaps: 0

QY 9 KRS 11  
 DL 6 KRS 8

Result 47  
 US 09-787-443-12  
 1 Sequence 47, Application US/08-070649  
 2 Patent No. 5648226  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Vanden Eynde, Olivier, LeBacker, Olivier,  
 5 TITLE OF INVENTION: Isolated, Tumor-Induced Nucleic Acid  
 6 NUMBER OF SEQUENCES: 19  
 7 CORRESPONDENCE ADDRESS:  
 8 ADDRESSEE: Polio & Lynch  
 9 STREET: 407 Third Avenue  
 10 CITY: New York City  
 11 STATE: New York  
 12 COUNTRY: USA  
 13 ZIP: 10022  
 14 COMPUTER READABLE FORM:  
 15 MEDIUM TYPE: Diskette, 5 1/4 inch, 960 kb storage  
 16 MAPPING: 100 PS/2  
 17 OPERATING SYSTEM: PC-DOS  
 18 SOFTWARE: WordPerfect  
 19 CURRENT APPLICATION DATA:  
 20 FILING DATE: 20 JANUARY 1995  
 21 CLASSIFICATION: 430  
 22 ATTORNEY/AGENT INFORMATION:  
 23 REFERENCE/DOCKET NUMBER: 06250162  
 24 TELECOMMUNICATION INFORMATION:  
 25 TELEPHONE: 212-693-1104  
 26 TELEFAX: 212-693-1104  
 27 TEXT: 00000000  
 28 INFORMATION FOR SEQ ID NO: 1:  
 29 SEQUENCE CHARACTERISTICS:  
 30 LENGTH: 27 amino acids  
 31 TYPE: amino acid  
 32 TOPOLOGY: Linear  
 33 Molecule Type: peptide  
 34 US-09-787-443-12

ATTORNEY/AGENT INFORMATION:  
 NAME: Hanson, No. 568226men b.  
 REGISTRATION NUMBER: 30,946  
 REFERENCE/Docket NUMBER: 130,523.2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-9864  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 SUBSTRATE: linear  
 US-09 370-628 4

Query Match: 27.3%, Score: 4, EP 1, Length: 8;  
 Best Local Similarity: 100.0%, Pred. No. 2.5e+05;  
 Matches: 3, Conservative: 0, Mismatches: 0, Indels: 0, Caps: 0;

QY 8 PER 10  
 20 5 PER 7

RESULT 4:  
 US-08 713 484-10  
 Sequence 10, Application US/08/71484  
 Patent No. 5679642  
 GENERAL INFORMATION:  
 APPLICANT: Goodbody, Agne  
 TITLE OF INVENTION: PEPTIDE-CELLULOSER CONJUGATES  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 900 K Street, N.W.  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/713,484  
 FILING DATE: 13-SEP-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/202,178  
 FILING DATE: 25-FEB-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bent, Stephen A.  
 REGISTRATION NUMBER: 29,766  
 REFERENCE/Docket NUMBER: 16777/293/ALLE  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5490  
 TELEFAX: (202) 672-5499  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 SUBSTRATE: linear  
 MEDIUM TYPE: floppy disk  
 US-08-713 484-10

Query Match: 27.3%, Score: 4, EP 1, Length: 8;  
 Best Local Similarity: 100.0%, Pred. No. 2.5e+05;  
 Matches: 3, Conservative: 0, Mismatches: 0, Indels: 0, Caps: 0;

QY 7 PER 5  
 20 2 PER 4

RESULT 40  
 US-08-754 173 45  
 Sequence 45, Application US/08/754170  
 Patent No. 5707626  
 GENERAL INFORMATION:  
 APPLICANT: Leuvas, Acetone  
 APPLICANT: Takehana, Yoshi  
 APPLICANT: Khresnam, Glenn  
 TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
 IMMUNOINFECTION: IMMUNOINFECTION STRATEGIES FOR  
 NUMBER OF SEQUENCES: 121  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Leuvas, Acetone  
 STREET: 201 No. 5707626th Fiquetod Street, Suite 500

ATTORNEY/AGENT INFORMATION:  
 NAME: Hanson, No. 568226men b.  
 REGISTRATION NUMBER: 30,946  
 REFERENCE/Docket NUMBER: 130,523.2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 688-9864  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 SUBSTRATE: linear  
 US-09 370-628 4

Query Match: 27.3%, Score: 4, EP 1, Length: 8;  
 Best Local Similarity: 100.0%, Pred. No. 2.5e+05;  
 Matches: 3, Conservative: 0, Mismatches: 0, Indels: 0, Caps: 0;

QY 8 PER 10  
 20 5 PER 7

RESULT 4:  
 US-08 713 484-10  
 Sequence 10, Application US/08/71484  
 Patent No. 5679642  
 GENERAL INFORMATION:  
 APPLICANT: Goodbody, Agne  
 TITLE OF INVENTION: PEPTIDE-CELLULOSER CONJUGATES  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 900 K Street, N.W.  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/713,484  
 FILING DATE: 13-SEP-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/202,178  
 FILING DATE: 25-FEB-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bent, Stephen A.  
 REGISTRATION NUMBER: 29,766  
 REFERENCE/Docket NUMBER: 16777/293/ALLE  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 672-5490  
 TELEFAX: (202) 672-5499  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 SUBSTRATE: linear  
 MEDIUM TYPE: floppy disk  
 US-08-713 484-10

Query Match: 27.3%, Score: 4, EP 1, Length: 8;  
 Best Local Similarity: 100.0%, Pred. No. 2.5e+05;  
 Matches: 3, Conservative: 0, Mismatches: 0, Indels: 0, Caps: 0;

QY 7 PER 5  
 20 2 PER 4

RESULT 40  
 US-08-754 173 45  
 Sequence 45, Application US/08/754170  
 Patent No. 5707626  
 GENERAL INFORMATION:  
 APPLICANT: Leuvas, Acetone  
 APPLICANT: Takehana, Yoshi  
 APPLICANT: Khresnam, Glenn  
 TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR  
 IMMUNOINFECTION: IMMUNOINFECTION STRATEGIES FOR  
 NUMBER OF SEQUENCES: 121  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Leuvas, Acetone  
 STREET: 201 No. 5707626th Fiquetod Street, Suite 500

CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90012  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 FILING DATE: 31 JAN 1996  
 CLASSIFICATION: 435  
 PREP APPLICATION DATA:  
 APPLICATION NUMBER: US 08/594,443  
 FILING DATE: 11 MAR 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Spitznagel, John P.  
 REGISTRATION NUMBER: 29,215  
 REFERENCE/ACKET NUMBER: 1929,400  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 977-1001  
 TELEFAX: (213) 977-1003  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MEDIUM TYPE: peptide  
 US-08-594,443-45

Query Match: 27.0% Score: 3; DB 1; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.5e-05;  
 Matches: 3; Conservative: 0; Mismatches: 0; Gaps: 0;

QY: 8 PER 40  
 DB: 1 PER 3

RESULT 47  
 US-08-594,443-45  
 Sequence 55, Application US/08/594443  
 Patent No. 5771216  
 GENERAL INFORMATION:  
 APPLICANT: ROLF, LOU  
 APPLICANT: Volschan, Eugene W  
 TITLE OF INVENTION: METHOD OF PREPARING A PEPTIDE  
 TITLE OF INVENTION: METHOD OF PREPARING A PEPTIDE  
 TITLE OF INVENTION: METHOD OF PREPARING A PEPTIDE  
 NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & MORRISON  
 STREET: 2000 Pennsylvania Avenue, NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20006-1888  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent in Release #1.0, Version #1.0  
 CURRENT APPLICATION DATA:  
 FILING DATE: 31 JAN 1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Marshfield, Kate H  
 REGISTRATION NUMBER: 29,959  
 REFERENCE/ACKET NUMBER: 22959,2002-21  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500  
 TELEFAX: (202) 622-0188  
 TELE: 90-4500 MRSNEPERSWSH  
 INFORMATION FOR SEQ ID NO: 51:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANGENESS: Single  
 TOPOLOGY: linear  
 MEDIUM TYPE: peptide  
 FEATUFE:  
 NAME/KEY: Peptide  
 LOCAL ID: 51  
 OTHER INFORMATION / deleted: 100.0% (2.2%)  
 US-08-594,443-51

Query Match: 27.0% Score: 3; DB 1; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.5e-05;  
 Matches: 3; Conservative: 0; Mismatches: 0; Gaps: 0;

QY: 5 QRT 5  
 DB: 2 QRT 4

RESULT 42  
 US-08-259,550A-55  
 Sequence 55, Application US/08259550A  
 Patent No. 5776892  
 GENERAL INFORMATION:  
 APPLICANT: GAMES, David F  
 APPLICANT: Gull, Ronald G  
 TITLE OF INVENTION: Anti Inflammatory Peptides  
 NUMBER OF SEQUENCES: 91  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PENNIE & PERMANIS  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 FILING DATE: 16 JUN 1994  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mison, Stephen  
 REGISTRATION NUMBER: 14,872  
 REFERENCE/ACKET NUMBER: 7142,021  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9040  
 TELEFAX: (212) 869-8864/9741  
 TELE: 66241 PENNIE  
 INFORMATION FOR SEQ ID NO: 55:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: unknown  
 MEDIUM TYPE: Peptide  
 HYPOTHECAL: NO  
 ANTI-SENSE: NO  
 US-08-259,550A-55

Query Match: 27.0% Score: 3; DB 1; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.5e-05;  
 Matches: 3; Conservative: 0; Mismatches: 0; Gaps: 0;

QY: 7 PER 9



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2  OTHER INFORMATION: /Notes: "Isolation occurred by an unknown (old)"
3  OTHER INFORMATION: /method: (med) or (ppd) from (ppd) residue"
4  FEATURE:
5  NAME/KEY: Modified site
6  LOCATION: 6
7  OTHER INFORMATION: /Label: sub-cloning p1
8  OTHER INFORMATION: /Notes: "Isolation occurred by an unknown (old)"
9  OTHER INFORMATION: /method: (med) or (ppd) from (ppd) residue"
10 FEATURE:
11 NAME/KEY: Modified site
12 LOCATION: 8
13 OTHER INFORMATION: /Label: sub-cloning p2
14 OTHER INFORMATION: /Notes: "Isolation occurred by an unknown (old)"
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16 US 08 717 2083
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19 Best Local Similarity: 100.0%, Pctd. No. 2.5e+05;
20 Matches: 3, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;
21
22 QY 3 KPS 5
23 ID 11
24 3 KPS 5
25
26 RESULT 44
27 US 08 693 234A 2
28 ? Sequence 10, Application US/08/43254A
29 ? Patent No. 5866549
30 ? GENERAL INFORMATION:
31 ? APPLICANT: Johnson, Jan H.
32 ? APPLICANT: Van Veen, Barry H
33 ? TITLE OF INVENTION: Isolation of lactoferrin B
34 ? NUMBER OF SEQUENCES: 17
35 ? CORRESPONDENCE ADDRESS:
36 ? ADDRESSEE: Townsend and Townsend and Client, LLP
37 ? STREET: Two Embarcadero Center, Embarcadero
38 ? CITY: San Francisco
39 ? STATE: California
40 ? COUNTRY: USA
41 ? ZIP: 94111-3834
42 ? COMPUTER READABLE FORM:
43 ? MEDIUM TYPE: Floppy disk
44 ? COMPUTER: IBM PC compatible
45 ? OPERATING SYSTEM: PC DOS/MS-DOS
46 ? SOFTWARE: Patent In Release #1.0, Version #1.0
47 ? CURRENT APPLICATION DATA:
48 ? APPLICATION NUMBER: US/08/43254A
49 ? FILING DATE: 15 OCT 1996
50 ? CLASSIFICATION: 530
51 ? PUBLICATION DATA:
52 ? APPLICATION NUMBER: US 08/43254A
53 ? FILING DATE: 05 JUN 1995
54 ? PUBLICATION NUMBER:
55 ? CURRENT APPLICATION DATA:
56 ? APPLICATION NUMBER: US 08/43254A
57 ? FILING DATE: 09 MAR 1996
58 ? PRIOR APPLICATION DATA:
59 ? APPLICATION NUMBER: WO 95/01370
60 ? FILING DATE: 16 FEB 1995
61 ? PRIOR APPLICATION DATA:
62 ? APPLICATION NUMBER:
63 ? FILING DATE: 16 FEB 1994
64 ? APPLICANT/AGENT INFORMATION:
65 ? NAME: Apple, Randolph L.
66 ? REGISTRATION NUMBER: 76429
67 ? REFERENCE/DOCKET NUMBER: 01-094-100-0
68 ? TITLE COMMUNICATION INFORMATION:
69 ? TELEPHONE: (415) 576-0200
70 ? TELEFAX: (415) 576 0305
71 ? INFORMATION FOR SEQ ID NO: 2:
72 ? SEQUENCE CHARACTERISTICS:
73 ? LENGTH: 8 amino acids
74 ? TYPE: amino acid
75 ? ORIGIN: 1
76 ? MEDIUM TYPE: peptide
77 US 08 717 2083

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1  STRANDEDNESS:
2  TOPLOGY: linear
3  MOLECULE TYPE: peptide
4  FEATURE:
5  NAME/KEY: peptide
6  LOCATION: 1-8
7  OTHER INFORMATION: /Notes: "Lys Calbi peak11: N-terminus"
8  US 08 693 234A 2
9
10 Query Match: 27.0%, Score 3, DB 2, Length 8;
11 Best Local Similarity: 100.0%, Pctd. No. 2.5e+05;
12 Matches: 3, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;
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14 QY 3 KPS 5
15 ID 11
16 3 KPS 5
17
18 RESULT 49
19 US 08 555 253-10
20 ? Sequence 10, Application US/08/555253
21 ? Patent No. 5866544
22 ? GENERAL INFORMATION:
23 ? APPLICANT: Goodbody, Anne
24 ? APPLICANT: Polak, Alfred
25 ? TITLE OF INVENTION: PEPTIDE-CHELATOR CONJUGATES
26 ? NUMBER OF SEQUENCES: 17
27 ? CORRESPONDENCE ADDRESS:
28 ? ADDRESSEE: Foley & Lardner
29 ? STREET: Suite 500, 4000 K Street, N.W.
30 ? CITY: Washington, D.C.
31 ? COUNTRY: USA
32 ? ZIP: 20007 5109
33 ? COMPUTER READABLE FORM:
34 ? MEDIUM TYPE: Floppy disk
35 ? COMPUTER: IBM PC compatible
36 ? OPERATING SYSTEM: PC DOS/MS-DOS
37 ? SOFTWARE: Patent In Release #1.0, Version #1.30
38 ? CURRENT APPLICATION DATA:
39 ? APPLICATION NUMBER: US/08/555,263
40 ? FILING DATE:
41 ? PRIOR APPLICATION DATA:
42 ? APPLICATION NUMBER: US 08/116,484
43 ? FILING DATE: 14 SEP 1996
44 ? APPLICATION NUMBER: US 08/202,178
45 ? FILING DATE: 25 FEB 1994
46 ? APPLICANT/AGENT INFORMATION:
47 ? NAME: Ford, Stephen A.
48 ? REGISTRATION NUMBER: 29,768
49 ? REFERENCE/DOCKET NUMBER: 01-094-290-ALLE
50 ? TELECOMMUNICATION INFORMATION:
51 ? TELEPHONE: (202) 672-5300
52 ? TELEFAX: (202) 672 5399
53 ? INDEX: 904.0f
54 ? INFORMATION FOR SEQ ID NO: 10:
55 ? SEQUENCE CHARACTERISTICS:
56 ? LENGTH: 8 amino acids
57 ? TYPE: amino acid
58 ? ORIGIN: 1
59 ? MEDIUM TYPE: peptide
60 US 08 555 253-10
61
62 Query Match: 27.0%, Score 3, DB 2, Length 8;
63 Best Local Similarity: 100.0%, Pctd. No. 2.5e+05;
64 Matches: 3, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;
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66 QY 3 KPS 5
67 ID 11
68 3 KPS 5
69
70 RESULT 51
71 US 08 104 001-10

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Sequence 45, Application US/00/496,616  
 Patent No. 5960,157  
 GENERAL INFORMATION:  
 APPLICANT: GUENTERICH, F. Peter  
 APPLICANT: GSD, Zuyi  
 APPLICANT: SANDHU, Punam  
 APPLICANT: GILLAM, Elizabeth M.  
 TITLE OF INVENTION: EXPRESSION OF A HUMAN  
 TITLE OF INVENTION: HUMAN  
 TITLE OF INVENTION: PSYCHOLOGICAL  
 NUMBER OF SEQUENCES: 08  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NEEDLE & RESINWORKS, INC.  
 STREET: Suite 1207, 127 Peachtree Street, N.E.  
 CITY: Atlanta  
 STATE: Georgia  
 COUNTRY: USA  
 ZIP: 30303 1811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 CARRIER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1 D. Version #1.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/787,443  
 FILING DATE: February 10, 1994  
 CLASSIFICATION: 455  
 AGENCY/AGENT INFORMATION:  
 NAME: Elizabeth Solby  
 REGISTRATION NUMBER: 42,206  
 REFERENCE/DECKET NUMBER: 22,000,000  
 INFORMATION INFORMATION:  
 REFERENCE: (404) 688 9770  
 REFERENCE: (404) 688 9869  
 REFERENCE: (404) 688 9869  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 % CDULT TYPE: peptide  
 HYDROPHOBICITY: N  
 FRAGMENT TYPE: N-terminal  
 US 09 194 001 43

Query Match: 27.98% Sequence: 100% (100%)  
 Best Local Similarity: 100.00% (100%)  
 Matches: 100% (100%)

Q1: 100%  
 Q2: 100%

Search completed: September 30, 2003, 11:06:49  
 Job Time: 14.937808s



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139	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	212	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
140	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	213	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
141	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	214	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
142	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	215	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
143	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	216	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
144	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	217	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
145	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	218	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
146	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	219	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
147	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	220	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
148	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	221	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
149	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	222	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
150	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	223	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
151	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	224	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
152	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	225	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
153	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	226	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
154	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	227	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
155	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	228	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
156	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	229	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
157	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	230	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
158	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	231	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
159	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	232	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
160	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	233	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl
161	3	27.3	9	9	US-09-765-386-179	Sequence 40, Appl	234	3	27.3	9	12	US-09-935-384-303	Sequence 303, Appl







1 PRIOR FILING DATE: 1998-06-30  
 2 PRIOR APPLICATION NUMBER: US 09/125,824  
 3 PRIOR FILING DATE: 1999-06-01  
 4 PRIOR APPLICATION NUMBER: US 09/455,485  
 5 PRIOR FILING DATE: 1999-12-06  
 6 PRIOR APPLICATION NUMBER: WO 99/29411  
 7 PRIOR FILING DATE: 1999-06-01  
 8 PRIOR APPLICATION NUMBER: PCT/US96/01246  
 9 PRIOR FILING DATE: 2000-12-06  
 10 NUMBER OF SEQ ID NOS: 57  
 11 SOFTWARE: FASTSEQ for Windows Version 4.0  
 12 SEQ ID NO: 22  
 13 LENGTH: 15  
 14 TYPE: FRT  
 15 ORGANISM: Homo Sapiens  
 16 US-09-787-443-12

Query Match 45.4% Score 41 DB 12 Length 15  
 Best Local Similarity 100.0% Prod. No. 22  
 Matches 5 Conservative 0 Mismatches 0 Indels 0

QY 6 MKRR 10  
 LB 11  
 5 MKRR 7

RESULT 2  
 US-09-787-443-12  
 1 Sequence ID: Application US/097866/2  
 2 Publication No. US20010147900A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: LAUB, RUTH  
 5 APPLICANT: GEMMATEX, MARY  
 6 TITLE OF INVENTION: ANTIGEN-INDUCED SUPPLEMENT  
 7 TITLE OF INVENTION: OF FACTOR VIII AND PARHENS AND/ OR  
 8 NUMBER OF SEQUENCES: 20  
 9 CORRESPONDENCE ADDRESS:  
 10 ADDRESSEE: Kuehler, Martens, 1500 S. West  
 11 STREET: 620 Newport Center Drive, Suite 101  
 12 CITY: Newport Beach  
 13 STATE: CA  
 14 COUNTRY: U.S.A.  
 15 FILING DATE: 2000  
 16 COMPUTER READABLE FORM:  
 17 MEDIUM TYPE: Diskette  
 18 SOFTWARE: IBM compatible  
 19 OPERATING SYSTEM: DOS  
 20 SOFTWARE: FASTSEQ Version 1.5  
 21 CURRENT APPLICATION DATA:  
 22 APPLICATION NUMBER: US/09/25,824  
 23 FILING DATE:  
 24 CLASSIFICATION: 424  
 25 PRIOR APPLICATION DATA:  
 26 APPLICATION NUMBER: PCT/BE96/00004  
 27 FILING DATE: 14-JUL-1995  
 28 ALTERNATIVE INFORMATION:  
 29 NAME: Altman, Daniel E.  
 30 REGISTRATION NUMBER: 34,115  
 31 REFERENCE/PATENT NUMBER: VANRA4-931,690  
 32 TECHNOMUNICAL INFORMATION:  
 33 TELEPHONE: 714-750-0454  
 34 TELEFAX: 714-760-9502  
 35 TEXT:  
 36 INFORMATION FOR SEQ ID NO: 15:  
 37 SEQUENCE CHARACTERISTICS:  
 38 LENGTH: 9 amino acids  
 39 TYPE: amino acid  
 40 STRANDEDNESS: single  
 41 TOPOLOGY: linear  
 42 FEATURE TYPE: NO. US20010147900A1  
 43 FEATURE TYPE: internal  
 44 US-09-787-443-12

Query Match 36.4% Score 41 DB 10 Length 9;  
 Best Local Similarity 100.0% Prod. No. 5005;  
 Matches 4 Conservative 0 Mismatches 0 Indels 0; Gaps 0;

QY 3 AKQR 4  
 LB 5 AKQR 8

RESULT 3  
 US-09-779-408-214  
 1 Sequence ID: Application US/09773608  
 2 Patent No. US2001015072A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Ellis  
 5 APPLICANT: Daniel E.H. Alar  
 6 APPLICANT: Elm M. Chabilla-Eld  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits  
 11 TITLE OF INVENTION: 349073 A TISSUE SPECIFIC PROTEIN  
 12 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 13 FILE REFERENCE: 129,40501  
 14 CURRENT APPLICATION NUMBER: US/09/779,308  
 15 CURRENT FILING DATE: 2001-02-08  
 16 PRIOR APPLICATION NUMBER: 60/181,020  
 17 PRIOR FILING DATE: 2000-02-08  
 18 NUMBER OF SEQ ID NOS: 718  
 19 SOFTWARE: FASTSEQ for Windows Version 4.0  
 20 SEQ ID NO: 43  
 21 LENGTH: 9  
 22 TYPE: FRT  
 23 ORGANISM: Homo Sapiens  
 24 US-09-779-408-214

Query Match 36.4% Score 41 DB 10 Length 9;  
 Best Local Similarity 100.0% Prod. No. 5005;  
 Matches 4 Conservative 0 Mismatches 0 Indels 0; Gaps 0;

QY 3 KRR 10  
 LB 5 KRR 8

RESULT 4  
 US-09-779-408-615  
 1 Sequence ID: Application US/09773608  
 2 Patent No. US2001015072A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Ellis  
 5 APPLICANT: Daniel E.H. Alar  
 6 APPLICANT: Elm M. Chabilla-Eld  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits  
 11 TITLE OF INVENTION: 349073 A TISSUE SPECIFIC PROTEIN  
 12 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 13 FILE REFERENCE: 129,40501  
 14 CURRENT APPLICATION NUMBER: US/09/779,308  
 15 CURRENT FILING DATE: 2001-02-08  
 16 PRIOR APPLICATION NUMBER: 60/181,020  
 17 PRIOR FILING DATE: 2000-02-08  
 18 NUMBER OF SEQ ID NOS: 718  
 19 SOFTWARE: FASTSEQ for Windows Version 4.0  
 20 SEQ ID NO: 615  
 21 LENGTH: 9  
 22 TYPE: FRT  
 23 ORGANISM: Homo Sapiens  
 24 US-09-779-408-615

Query Match 36.4% Score 41 DB 10 Length 9;

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Query Match          66.4%  Score 4: DB 12: Length 9:
Best Local Similarity 100.0%  Pred. No. 5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 MKPR 4
DB 1
1111
1 MKPR 4

RESULT 5
US 09 779-368 704
Sequence 703: Application US/09/27608
Publication No. US20040155972A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Altai
APPLICANT: Pia M. Chaitin-End
APPLICANT: Roger S. Robert
APPLICANT: Elana Levin
APPLICANT: Steve Chapelle Mitchell
APPLICANT: Aya Jakovlevics
TITLE OF INVENTION: 340DD7: A COMBINED SEQUENCE FOR FIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN EPIDERMAL CELLS
FILE REFERENCE: 129,405J1
CURRENT APPLICATION NUMBER: 09/27608
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 09/27608
PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 718
SOFTWARE: FASTSEQ for Windows Version 1.1
SEQ ID NO 718
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US-09 779 368-704

Query Match          66.4%  Score 4: DB 12: Length 9:
Best Local Similarity 100.0%  Pred. No. 5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 MKPR 4
DB 1
1111
1 MKPR 4

RESULT 6
US 09 779 368 704
Sequence 43: Application US/09/27608
Publication No. US20040155972A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Altai
APPLICANT: Pia M. Chaitin-End
APPLICANT: Roger S. Robert
APPLICANT: Elana Levin
APPLICANT: Steve Chapelle Mitchell
APPLICANT: Aya Jakovlevics
TITLE OF INVENTION: 340DD7: A COMBINED SEQUENCE FOR FIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN EPIDERMAL CELLS
FILE REFERENCE: 129,405J1
CURRENT APPLICATION NUMBER: 09/27608
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 09/27608
PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 718
SOFTWARE: FASTSEQ for Windows Version 1.1
SEQ ID NO 718
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US-09 779 368-704

Query Match          66.4%  Score 4: DB 12: Length 9:
Best Local Similarity 100.0%  Pred. No. 5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 MKPR 4
DB 1
1111
1 MKPR 4

RESULT 7
US 10 210 148 148
Sequence 18: Application US/10/210148
Publication No. US2004017280A1
GENERAL INFORMATION:
APPLICANT: SOGISTON, Karl Jetter
TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
FILE REFERENCE: TROM0002
CURRENT APPLICATION NUMBER: US/10/210148
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: 101/0802/24311
PRIOR FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patent Invention 1.2
SEQ ID NO 18
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US 10 210 148 148

Query Match          66.4%  Score 4: DB 12: Length 9:
Best Local Similarity 100.0%  Pred. No. 5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 MKPR 8
DB 1
1111
1 MKPR 4

RESULT 8
US 10 210 148 148
Sequence 57: Application US/10/210148
Publication No. US2004017280A1
GENERAL INFORMATION:
APPLICANT: SOGISTON, Karl Jetter
TITLE OF INVENTION: Compositions And Methods For Modulation Of Immune Response
FILE REFERENCE: TROM0002
CURRENT APPLICATION NUMBER: US/10/210148
CURRENT FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: 101/0802/24311
PRIOR FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patent Invention 1.2
SEQ ID NO 57
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapiens
US 10 210 148 148

Query Match          66.4%  Score 4: DB 12: Length 9:
Best Local Similarity 100.0%  Pred. No. 5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 MKPR 9
DB 2
1111
2 MKPR 5

RESULT 9
US 09 434 265 074
Sequence 476: Application US/09/47605
Publication No. US20040155972A1
GENERAL INFORMATION:

```

? APPLICANT: Mary Paris  
 ? APPLICANT: Pia M. Chailita-Ed  
 ? APPLICANT: Arthur B. Kaitano  
 ? APPLICANT: Steve Chappell Mitchell  
 ? APPLICANT: Daniel E.H. Atar  
 ? APPLICANT: Ava Jakobovits  
 ? TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
 ? TITLE OF INVENTION: AND DETECTION OF CANCER  
 ? FILE REFERENCE: 129.6US01  
 ? CURRENT APPLICATION NUMBER: US/09/787-4765  
 ? PRIOR FILING DATE: 2001-09-21  
 ? PRIOR APPLICATION NUMBER: 60/147,647  
 ? PRIOR FILING DATE: 2000-04-12  
 ? NUMBER OF SEQ ID NOS: 770  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 576  
 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 ? ORGANISM: Homo sapiens  
 US-09-854 765 576

Query Match 36.4%; Score 4; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 PRRS 11  
 DB 2 PRRS 5

RESULT 10  
 US-09-854 765 576  
 ? Sequence 591, Application US/09/824765  
 ? Patent No. US2002055478A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Mary Paris  
 ? APPLICANT: Pia M. Chailita-Ed  
 ? APPLICANT: Arthur B. Kaitano  
 ? APPLICANT: Steve Chappell Mitchell  
 ? APPLICANT: Daniel E.H. Atar  
 ? APPLICANT: Ava Jakobovits  
 ? TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT  
 ? TITLE OF INVENTION: AND DETECTION OF CANCER  
 ? FILE REFERENCE: 129.6US01  
 ? CURRENT APPLICATION NUMBER: US/09/824765  
 ? PRIOR FILING DATE: 2001-09-21  
 ? PRIOR APPLICATION NUMBER: 60/147,647  
 ? PRIOR FILING DATE: 2000-04-12  
 ? NUMBER OF SEQ ID NOS: 770  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 591  
 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Homo sapiens  
 ? ORGANISM: Homo sapiens  
 US-09-854 765 576

Query Match 36.4%; Score 4; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 PRRS 11  
 DB 2 PRRS 5

RESULT 11  
 US-09-779 308 130  
 ? Sequence 130, Application US/09/779308  
 ? Patent No. US20020150972A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Mary Paris  
 ? APPLICANT: Daniel E.H. Atar  
 ? APPLICANT: Pia M. Chailita-Ed

? APPLICANT: Rene S. Hubert  
 ? APPLICANT: Eiana Levin  
 ? APPLICANT: Steve Chappell Mitchell  
 ? APPLICANT: Ava Jakobovits  
 ? TITLE OF INVENTION: 34P07: A TISSUE SPECIFIC PROTEIN  
 ? TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 ? FILE REFERENCE: 129.4US01  
 ? CURRENT APPLICATION NUMBER: US/09/779,308  
 ? CURRENT FILING DATE: 2001-02-08  
 ? PRIOR APPLICATION NUMBER: 60/181,020  
 ? PRIOR FILING DATE: 2000-02-08  
 ? NUMBER OF SEQ ID NOS: 718  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 133  
 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Homo Sapiens  
 ? ORGANISM: Homo Sapiens  
 US-09-779-308-130

Query Match 36.4%; Score 4; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRR 10  
 DB 7 KPRR 10

RESULT 12  
 US-09-779-308-339  
 ? Sequence 339, Application US/09/779308  
 ? Patent No. US20020150972A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Mary Paris  
 ? APPLICANT: Daniel E.H. Atar  
 ? APPLICANT: Pia M. Chailita-Ed  
 ? APPLICANT: Rene S. Hubert  
 ? APPLICANT: Eiana Levin  
 ? APPLICANT: Steve Chappell Mitchell  
 ? APPLICANT: Ava Jakobovits  
 ? TITLE OF INVENTION: 34P07: A TISSUE SPECIFIC PROTEIN  
 ? TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 ? FILE REFERENCE: 129.4US01  
 ? CURRENT APPLICATION NUMBER: US/09/779,308  
 ? CURRENT FILING DATE: 2001-02-08  
 ? PRIOR APPLICATION NUMBER: 60/181,020  
 ? PRIOR FILING DATE: 2000-02-08  
 ? NUMBER OF SEQ ID NOS: 718  
 ? SOFTWARE: FASTSEQ for Windows Version 4.0  
 ? SEQ ID NO 339  
 ? LENGTH: 10  
 ? TYPE: PRT  
 ? ORGANISM: Homo Sapiens  
 ? ORGANISM: Homo Sapiens  
 US-09-779-308-339

Query Match 36.4%; Score 4; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 13  
 US-09-779-308-351  
 ? Sequence 351, Application US/09/779308  
 ? Patent No. US20020150972A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Mary Paris  
 ? APPLICANT: Daniel E.H. Atar  
 ? APPLICANT: Pia M. Chailita-Ed  
 ? APPLICANT: Rene S. Hubert

```

1 APPLICANT: Elana Levin
2 APPLICANT: Steve Chappell Mitchell
3 APPLICANT: Aya Jakobovits
4 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
5 FILE REFERENCE: 129.4US01
6 CURRENT APPLICATION NUMBER: US/09/779,308
7 PRIOR FILING DATE: 2001-02-08
8 PRIOR APPLICATION NUMBER: 60/181,620
9 NUMBER OF SEQ ID NOS: 718
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO: 531
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo Sapiens
15 US-09-779-408-531

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0% Pct. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

RESULT 14
US-09-779-408-531
1 Sequence 531: Application US/09779308
2 Patent No. US20020150972A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Fatis
5 APPLICANT: Daniel E.H. Atar
6 APPLICANT: Pia M. Chailita-Eid
7 APPLICANT: Rene S. Hubert
8 APPLICANT: Elana Levin
9 APPLICANT: Steve Chappell Mitchell
10 APPLICANT: Aya Jakobovits
11 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
12 FILE REFERENCE: 129.4US01
13 CURRENT APPLICATION NUMBER: US/09/779,308
14 CURRENT FILING DATE: 2001-02-08
15 PRIOR APPLICATION NUMBER: 60/181,620
16 PRIOR FILING DATE: 2000-02-08
17 NUMBER OF SEQ ID NOS: 718
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO: 531
20 LENGTH: 10
21 TYPE: PRT
22 ORGANISM: Homo Sapiens
23 US-09-779-408-531

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0% Pct. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

```

```

1 APPLICANT: Steve Chappell Mitchell
2 APPLICANT: Aya Jakobovits
3 APPLICANT: Daniel E.H. Atar
4 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
5 FILE REFERENCE: 129.4US01
6 CURRENT APPLICATION NUMBER: US/09/779,308
7 PRIOR FILING DATE: 2001-02-08
8 PRIOR APPLICATION NUMBER: 60/181,620
9 NUMBER OF SEQ ID NOS: 718
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO: 519
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo Sapiens
15 US-09-779-308-519

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0% Pct. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

RESULT 14
US-09-779-308-531
1 Sequence 531: Application US/09779308
2 Patent No. US20020150972A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Fatis
5 APPLICANT: Daniel E.H. Atar
6 APPLICANT: Pia M. Chailita-Eid
7 APPLICANT: Rene S. Hubert
8 APPLICANT: Elana Levin
9 APPLICANT: Steve Chappell Mitchell
10 APPLICANT: Aya Jakobovits
11 TITLE OF INVENTION: 34P4D7: A TISSUE SPECIFIC PROTEIN
12 FILE REFERENCE: 129.4US01
13 CURRENT APPLICATION NUMBER: US/09/779,308
14 CURRENT FILING DATE: 2001-02-08
15 PRIOR APPLICATION NUMBER: 60/181,620
16 PRIOR FILING DATE: 2000-02-08
17 NUMBER OF SEQ ID NOS: 718
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO: 531
20 LENGTH: 10
21 TYPE: PRT
22 ORGANISM: Homo Sapiens
23 US-09-779-308-531

Query Match 36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0% Pct. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10
DB 111
1 KPRR 4

RESULT 17
US-09-779-308-536
1 Sequence 536: Application US/09779308
2 Patent No. US20020150972A1
3 GENERAL INFORMATION:
4 APPLICANT: Mary Fatis
5 APPLICANT: Daniel E.H. Atar
6 APPLICANT: Pia M. Chailita-Eid
7 APPLICANT: Rene S. Hubert
8 APPLICANT: Elana Levin
9 APPLICANT: Steve Chappell Mitchell

```

1 APPLICANT: AYA JAKOBOWITS  
 2 TITLE OF INVENTION: 349307: A TISSUE SPECIFIC PROTEIN  
 3 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 4 FILE REFERENCE: 129.40501  
 5 CURRENT APPLICATION NUMBER: US/09/779,308  
 6 CURRENT FILING DATE: 2001-02-08  
 7 PRIOR APPLICATION NUMBER: 60/181,620  
 8 PRIOR FILING DATE: 2000-02-08  
 9 NUMBER OF SEQ ID NOS: 718  
 10 SOFTWARE: FASTSEQ for Windows Version 4.0  
 11 SEQ ID NO: 644  
 12 LENGTH: 10  
 13 TYPE: PRT  
 14 ORGANISM: Homo Sapiens  
 15 US-09-779,308-644

Query Match 36.4% Score 4: 19 10: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 3.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 18  
 US-09-779,308-644  
 1 Sequence 644: Application US/09/779,308  
 2 Patent No. US2002150972A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Paris  
 5 APPLICANT: Daniel E.H. Afari  
 6 APPLICANT: Pia M. Chailita-Eid  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits  
 11 TITLE OF INVENTION: 349307: A TISSUE SPECIFIC PROTEIN  
 12 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 13 FILE REFERENCE: 129.40501  
 14 CURRENT APPLICATION NUMBER: US/09/779,308  
 15 CURRENT FILING DATE: 2001-02-08  
 16 PRIOR APPLICATION NUMBER: 60/181,620  
 17 PRIOR FILING DATE: 2000-02-08  
 18 NUMBER OF SEQ ID NOS: 718  
 19 SOFTWARE: FASTSEQ for Windows Version 4.0  
 20 SEQ ID NO: 644  
 21 LENGTH: 10  
 22 TYPE: PRT  
 23 ORGANISM: Homo Sapiens  
 24 US-09-779,308-644

Query Match 36.4% Score 4: 19 10: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 3.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 19  
 US-09-779,308-644  
 1 Sequence 644: Application US/09/779,308  
 2 Patent No. US2002150972A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Paris  
 5 APPLICANT: Daniel E.H. Afari  
 6 APPLICANT: Pia M. Chailita-Eid  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits

1 TITLE OF INVENTION: 349307: A TISSUE SPECIFIC PROTEIN  
 2 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 3 FILE REFERENCE: 129.40501  
 4 CURRENT APPLICATION NUMBER: US/09/779,308  
 5 CURRENT FILING DATE: 2001-02-08  
 6 PRIOR APPLICATION NUMBER: 60/181,620  
 7 PRIOR FILING DATE: 2000-02-08  
 8 NUMBER OF SEQ ID NOS: 718  
 9 SOFTWARE: FASTSEQ for Windows Version 4.0  
 10 SEQ ID NO: 644  
 11 LENGTH: 10  
 12 TYPE: PRT  
 13 ORGANISM: Homo Sapiens  
 14 US-09-779,308-644

Query Match 36.4% Score 4: 19 10: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 3.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 3 KPRR 6

RESULT 20  
 US-09-779,308-666  
 1 Sequence 666: Application US/09/779,308  
 2 Patent No. US2002150972A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Mary Paris  
 5 APPLICANT: Daniel E.H. Afari  
 6 APPLICANT: Pia M. Chailita-Eid  
 7 APPLICANT: Rene S. Hubert  
 8 APPLICANT: Elana Levin  
 9 APPLICANT: Steve Chappell Mitchell  
 10 APPLICANT: Aya Jakobovits  
 11 TITLE OF INVENTION: 349307: A TISSUE SPECIFIC PROTEIN  
 12 TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 13 FILE REFERENCE: 129.40501  
 14 CURRENT APPLICATION NUMBER: US/09/779,308  
 15 CURRENT FILING DATE: 2001-02-08  
 16 PRIOR APPLICATION NUMBER: 60/181,620  
 17 PRIOR FILING DATE: 2000-02-08  
 18 NUMBER OF SEQ ID NOS: 718  
 19 SOFTWARE: FASTSEQ for Windows Version 4.0  
 20 SEQ ID NO: 666  
 21 LENGTH: 10  
 22 TYPE: PRT  
 23 ORGANISM: Homo Sapiens  
 24 US-09-779,308-666

Query Match 36.4% Score 4: 19 10: Length 10:  
 Best Local Similarity 100.0%: Pred. No. 3.4e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10  
 DB 5 KPRR 8

RESULT 21  
 US-09-966,422B-15  
 1 Sequence 15: Application US/09/966,422B  
 2 Publication No. US20030044892A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Bristol Myers Squibb Company  
 5 TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HSPRPMY6, EXPRESSED  
 6 FILE REFERENCE: 1004386/3553 4119C53  
 7 CURRENT APPLICATION NUMBER: US/09/966,422B  
 8 CURRENT FILING DATE: 2002-05-07  
 9 PRIOR APPLICATION NUMBER: 60/245,602  
 10 PRIOR FILING DATE: 2000-09-27

1 PRIORITY APPLICATION NUMBER: 60/400,604  
2 PRIOR FILING DATE: 2001-07-19  
3 PRIOR APPLICATION NUMBER: 60/415,412  
4 PRIOR FILING DATE: 2001-08-26  
5 NUMBER OF SEQ ID NOS: 81  
6 SOFTWARE: Patent Invention 4.0  
7 SEQ ID NO: 1  
8 TYPE: 1  
9 ORGANISM: Homo sapiens  
10 US 09-787-443-12  
11  
12 Query Match: 96.4% Score 4: 1011 Length 10;  
13 Best Local Similarity: 100.0% Prod. No. 34002;  
14 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0;  
15  
16 Q1 1 PERC 11  
17 1  
18 2 PERC 1  
19  
20 RESULT 24  
21 US 09-572-404B-2518  
22 Sequence 2518, Application US/09572404B  
23 Publication No. US2003028374A1  
24 GENERAL INFORMATION:  
25 APPLICANT: Proteom Ltd  
26 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
27 FILE REFERENCE: Human Patent US/09/572,404B  
28 CURRENT APPLICATION NUMBER: US/09/572,404B  
29 PRIOR FILING DATE: 2000-05-17  
30 NUMBER OF SEQ ID NOS: 4203  
31 SOFTWARE: Patent Invention version 1.0  
32 SEQ ID NO: 2518  
33 LENGTH: 11  
34 TYPE: PPT  
35 ORGANISM: Homo Sapiens  
36 FEATURE:  
37 OTHER INFORMATION: Sequence located in SPT at 224-233 and may interact with Sequ  
38 US 09-572-404B-2518  
39  
40 Query Match: 96.4% Score 4: 1011 Length 10;  
41 Best Local Similarity: 100.0% Prod. No. 34002;  
42 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0;  
43  
44 Q1 8 PERC 11  
45 111  
46 4 PERC 7  
47  
48 RESULT 29  
49 US 09-572-404B-263  
50 Sequence 263, Application US/09572406A  
51 Publication No. US2003028374A1  
52 GENERAL INFORMATION:  
53 APPLICANT: Proteom Ltd  
54 TITLE OF INVENTION: Complementary peptide ligands  
55 FILE REFERENCE:  
56 CURRENT APPLICATION NUMBER: US/09/572,406A  
57 PRIOR FILING DATE: 2000-05-17  
58 NUMBER OF SEQ ID NOS: 134  
59 SOFTWARE: Patent Invention version 1.0  
60 SEQ ID NO: 263  
61 LENGTH: 11  
62 TYPE: PPT  
63 ORGANISM: Arabidopsis thaliana  
64 FEATURE:  
65 OTHER INFORMATION: Sequence located in CYP8A8 or T2085 9, at 265, 264 and may  
66 US 09-572-404B-263  
67  
68 Query Match: 96.4% Score 4: 1011 Length 10;  
69 Best Local Similarity: 100.0% Prod. No. 34002;  
70 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0;  
71  
72 Q1 1 PERC 4  
73 111  
74 1 PERC 3  
75  
76 RESULT 29  
77 US 09-572-404B-266  
78 Sequence 266, Application US/09572406A  
79 Publication No. US2003028374A1  
80 GENERAL INFORMATION:  
81 APPLICANT: Proteom Ltd  
82 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
83 FILE REFERENCE: Human Patent  
84 CURRENT APPLICATION NUMBER: US/09/572,406A  
85 PRIOR FILING DATE: 2000-05-17  
86 NUMBER OF SEQ ID NOS: 4203  
87 SOFTWARE: Patent Invention version 1.0  
88 SEQ ID NO: 266  
89 LENGTH: 11  
90 TYPE: PPT  
91 ORGANISM: Homo Sapiens

1 FEATURE:  
2 OTHER INFORMATION: Sequence located in SPT at 226-235 and may interact with Sequ  
3 OTHER INFORMATION: this patent  
4 US 09-572-404B-286  
5  
6 Query Match: 96.4% Score 4: 1011 Length 10;  
7 Best Local Similarity: 100.0% Prod. No. 34002;  
8 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0;  
9  
10 Q1 1 PERC 11  
11 1  
12 2 PERC 1  
13  
14 RESULT 24  
15 US 09-572-404B-2518  
16 Sequence 2518, Application US/09572404B  
17 Publication No. US2003028374A1  
18 GENERAL INFORMATION:  
19 APPLICANT: Proteom Ltd  
20 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
21 FILE REFERENCE: Human Patent US/09/572,404B  
22 CURRENT APPLICATION NUMBER: US/09/572,404B  
23 PRIOR FILING DATE: 2000-05-17  
24 NUMBER OF SEQ ID NOS: 4203  
25 SOFTWARE: Patent Invention version 1.0  
26 SEQ ID NO: 2518  
27 LENGTH: 11  
28 TYPE: PPT  
29 ORGANISM: Homo Sapiens  
30 FEATURE:  
31 OTHER INFORMATION: Sequence located in SPT at 224-233 and may interact with Sequ  
32 US 09-572-404B-2518  
33  
34 Query Match: 96.4% Score 4: 1011 Length 10;  
35 Best Local Similarity: 100.0% Prod. No. 34002;  
36 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0;  
37  
38 Q1 8 PERC 11  
39 111  
40 4 PERC 7  
41  
42 RESULT 29  
43 US 09-572-404B-263  
44 Sequence 263, Application US/09572406A  
45 Publication No. US2003028374A1  
46 GENERAL INFORMATION:  
47 APPLICANT: Proteom Ltd  
48 TITLE OF INVENTION: Complementary peptide ligands  
49 FILE REFERENCE:  
50 CURRENT APPLICATION NUMBER: US/09/572,406A  
51 PRIOR FILING DATE: 2000-05-17  
52 NUMBER OF SEQ ID NOS: 134  
53 SOFTWARE: Patent Invention version 1.0  
54 SEQ ID NO: 263  
55 LENGTH: 11  
56 TYPE: PPT  
57 ORGANISM: Arabidopsis thaliana  
58 FEATURE:  
59 OTHER INFORMATION: Sequence located in CYP8A8 or T2085 9, at 265, 264 and may  
60 US 09-572-404B-263  
61  
62 Query Match: 96.4% Score 4: 1011 Length 10;  
63 Best Local Similarity: 100.0% Prod. No. 34002;  
64 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0;  
65  
66 Q1 1 PERC 4  
67 111  
68 1 PERC 3  
69  
70 RESULT 29  
71 US 09-572-404B-266  
72 Sequence 266, Application US/09572406A  
73 Publication No. US2003028374A1  
74 GENERAL INFORMATION:  
75 APPLICANT: Proteom Ltd  
76 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
77 FILE REFERENCE: Human Patent  
78 CURRENT APPLICATION NUMBER: US/09/572,406A  
79 PRIOR FILING DATE: 2000-05-17  
80 NUMBER OF SEQ ID NOS: 4203  
81 SOFTWARE: Patent Invention version 1.0  
82 SEQ ID NO: 266  
83 LENGTH: 11  
84 TYPE: PPT  
85 ORGANISM: Homo Sapiens

```

US 09 572 270A-231
? Sequence 231, Application US/09572270A
? Publication No. US20030148468A1
? GENERAL INFORMATION:
? APPLICANT: Proteom Ltd
? TITLE OF INVENTION: Inter-complementary peptide binding
? FILE REFERENCE:
? CURRENT APPLICATION NUMBER: US/09572270A
? CURRENT FILING DATE: 2000-05-17
? NUMBER OF SEQ ID NOS: 1144
? SOFTWARE: Protolent version 1.0
? SEQ ID NO 231
? LENGTH: 10
? TYPE: PR1
? ORGANISM: Arabidopsis thaliana
? OTHER INFORMATION: Sequence located in CYPRUS at 250,205 and may
US 09 572 270A-231

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGRK 4
   11
   3 AGRK 8
   11

RESULT 27
US 09 572 270A-231
? Sequence 231, Application US/09572270A
? Publication No. US20030148468A1
? GENERAL INFORMATION:
? APPLICANT: Proteom Ltd
? TITLE OF INVENTION: Inter-complementary peptide binding
? FILE REFERENCE:
? CURRENT APPLICATION NUMBER: US/09572270A
? CURRENT FILING DATE: 2000-05-17
? NUMBER OF SEQ ID NOS: 1144
? SOFTWARE: Protolent version 1.0
? SEQ ID NO 231
? LENGTH: 10
? TYPE: PR1
? ORGANISM: Arabidopsis thaliana
? OTHER INFORMATION: Sequence located in CYPRUS at 250,205 and may

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGRK 4
   11
   4 AGRK 7
   11

RESULT 28
US 10 190 082 352
? Sequence 352, Application US/10190082
? Publication No. US20030148264A1
? GENERAL INFORMATION:
? APPLICANT: Lasky, Lawrence A.
? APPLICANT: Sidhu, Sachdev S.
? APPLICANT: Held, Heiko A.
? TITLE OF INVENTION: PHAGE DISPLAYED PEZ DOMAIN AND PEPS
? FILE REFERENCE: P1905R1
? CURRENT APPLICATION NUMBER: US/10190082
? CURRENT FILING DATE: 2002-07-03
? PRIOR APPLICATION NUMBER: US 60/161,614
? PRIOR FILING DATE: 2001-07-06
? NUMBER OF SEQ ID NOS: 683
? SEQ ID NO 352
? LENGTH: 10
? TYPE: PR1

```

```

? ORGANISM: Artificial sequence
? FEATURE:
? OTHER INFORMATION: Synthetic
US-10-190 082 352

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKRK 5
   11
   1 AKRK 4
   11

RESULT 29
US-10-262-272A-15
? Sequence 15, Application US/10262272A
? Publication No. US20030170671A1
? GENERAL INFORMATION:
? APPLICANT: Bristol Myers Squibb Company
? TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR. HGPBMY6
? FILE REFERENCE: D0644 CIP
? CURRENT APPLICATION NUMBER: US/10/262,272A
? CURRENT FILING DATE: 2002-05-27
? PRIOR APPLICATION NUMBER: U.S. 09/965,422
? PRIOR FILING DATE: 2001-09-26
? NUMBER OF SEQ ID NOS: 91
? SOFTWARE: Patent version 4.2
? SEQ ID NO 15
? LENGTH: 10
? TYPE: PR1
? ORGANISM: Homo sapiens
US-10-262-272A-15

Query Match          36.4%  Score 4; DB 12; Length 10;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TMKP 5
   11
   5 TMKP 5
   11

RESULT 30
US-09-832-355A-B
? Sequence 8, Application US/09832355A
? Publication No. US20030027761A1
? GENERAL INFORMATION:
? APPLICANT: Kossler, Eric
? APPLICANT: Kossler, Eric
? TITLE OF INVENTION: VEGF FUSION PROTEINS
? FILE REFERENCE: 20564
? CURRENT APPLICATION NUMBER: US/09/832,355A
? CURRENT FILING DATE: 2001-04-19
? NUMBER OF SEQ ID NOS: 126
? SOFTWARE: Patent version 4.0
? SEQ ID NO 8
? LENGTH: 11
? TYPE: PR1
? ORGANISM: Homo sapiens
US 09-832-355A-B

Query Match          36.4%  Score 4; DB 11; Length 11;
Best Local Similarity 100.0%  Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KRRR 10
   11
   8 KRRR 11
   11

RESULT 31
US-10-190 972 33

```

```

3 Sequence 73: Application US/05/10145962
4 Publication No. US20030069181A1
5 GENERAL INFORMATION:
6 APPLICANT: Weiqi Almett J.
7 TITLE OF INVENTION: A method for identifying and classifying
8 FILE OF INVENTION: Basis for Multiple Invention Modification
9 FILE REFERENCE: 8921.8
10 CURRENT APPLICATION NUMBER: US/05/0962
11 PRIOR FILING DATE: 2002-05-24
12 PRIOR APPLICATION NUMBER: US 63/293,131
13 PRIOR FILING DATE: 2001-05-25
14 NUMBER OF SEQ ID NOS: 82
15 SOFTWARE: FastSeq for Windows Version 4.0
16 SEQ ID NO 93
17 LENGTH: 12
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 FEATURE:
21 OTHER INFORMATION: VEGE all spliter #1
22 US 10:54 962-74

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Query Match 36.4% Score 42 DB 12 Length 12
Best Local Similarity 100.0% Pred. No. 3 Be+02
Matches 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

QY 7 KRR 10
  111
LD 7 KRR 12

```

```

RESULT 32
3 Sequence 17: Application US/1002599
4 Publication No. US2003010422A1
5 GENERAL INFORMATION:
6 APPLICANT: Roberts, Paul D.
7 APPLICANT: M1, Zinbago
8 APPLICANT: Filazzello, Raymond
9 APPLICANT: Glattfischer, Joseph C
10 APPLICANT: Gammito, Andrea
11 TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
12 TITLE OF INVENTION: FACILITATE BREAK AND CYS PLASME AND/OR NO-TLEAS TRANSFER
13 FILE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
14 FILE REFERENCE: AP42573-A4 07496-9247
15 CURRENT APPLICATION NUMBER: US/05/0962
16 PRIOR FILING DATE: 2002-02-13
17 PRIOR APPLICATION NUMBER: 09/111966
18 PRIOR FILING DATE: 1999-09-03
19 PRIOR APPLICATION NUMBER: 07/496,924
20 PRIOR FILING DATE: 2000-09-14
21 NUMBER OF SEQ ID NOS: 90
22 SOFTWARE: FastSeq for Windows Version 4.0
23 SEQ ID NO 17
24 LENGTH: 12
25 TYPE: PRT
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: random peptide library
29 US 10:075 469-17

```

```

Query Match 36.4% Score 42 DB 12 Length 12
Best Local Similarity 100.0% Pred. No. 3 Be+02
Matches 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

QY 3 KRM 6
  111
LD 4 KRM 7

```

```

RESULT 33
3 Sequence 102: Application US/10145962
4 Publication No. US20030119021A1

```

```

5 GENERAL INFORMATION:
6 APPLICANT: Kster, Hubert
7 APPLICANT: Soddiqui, Sabir
8 APPLICANT: Little, Robert
9 TITLE OF INVENTION: Capture Experiments, Collections Thereof:
10 FILE OF INVENTION: Add Methods For Analyzing The Proteome And Complex
11 TITLE OF INVENTION: Compositions
12 FILE REFERENCE: 2474-2365
13 CURRENT APPLICATION NUMBER: US/10/197,964
14 PRIOR FILING DATE: 2002-07-16
15 PRIOR APPLICATION NUMBER: 63/036,609
16 PRIOR FILING DATE: 2001-07-16
17 PRIOR APPLICATION NUMBER: 63/014,123
18 PRIOR FILING DATE: 2001-08-21
19 PRIOR APPLICATION NUMBER: 63/063,443
20 PRIOR FILING DATE: 2002-03-11
21 NUMBER OF SEQ ID NOS: 149
22 SOFTWARE: FastSeq for Windows Version 4.0
23 SEQ ID NO 102
24 LENGTH: 12
25 TYPE: PRT
26 ORGANISM: Homo Sapiens
27 FEATURE:
28 NAME/KEY: MOD_RES
29 LOCATION: 1
30 OTHER INFORMATION: Xaa is pyroglutamic acid
31 US 10:57-954-102

```

```

Query Match 36.4% Score 42 DB 15 Length 12
Best Local Similarity 100.0% Pred. No. 3 Be+02
Matches 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

QY 7 KRR 10
  111
LD 7 KRR 7

```

```

RESULT 34
3 Sequence 27: Application US/09985672
4 Patent No. US2002155064A
5 GENERAL INFORMATION:
6 APPLICANT: Reddy, Jean Claude
7 TITLE OF INVENTION: METHOD FOR THE DETECTION AND LOCALIZATION OF
8 TITLE OF INVENTION: MALIGNANT HUMAN TUMORS
9 FILE REFERENCE: 1588-104
10 CURRENT APPLICATION NUMBER: US/09/985,672
11 PRIOR FILING DATE: 2001-07-16
12 PRIOR APPLICATION NUMBER: US/04/566,869
13 PRIOR FILING DATE: 1999-08-03
14 PRIOR APPLICATION NUMBER: 01/0598/31964
15 PRIOR FILING DATE: 1998-12-02
16 PRIOR APPLICATION NUMBER: EP 97200297.6
17 PRIOR FILING DATE: 1997-02-04
18 NUMBER OF SEQ ID NOS: 3
19 SOFTWARE: Patent ID Ver. 2.0
20 SEQ ID NO 2
21 LENGTH: 13
22 TYPE: PRT
23 ORGANISM: Homo sapiens
24 FEATURE:
25 NAME/KEY: SITE
26 LOCATION: (1)
27 OTHER INFORMATION: This site is pyroglutamate.
28 US 09-985-672-2

```

```

Query Match 36.4% Score 42 DB 10 Length 13
Best Local Similarity 100.0% Pred. No. 4 Be+02
Matches 47 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

```

QY 7 KRR 10
  111
LD 7 KRR 7

```



```

RESULT 35
US-09-988-792-4
: Sequence 4: Application US/09488792
: Publication No. US20030032599A1
: GENERAL INFORMATION:
: APPLICANT: Lukowski, Andrezej W
: APPLICANT: Gatz, Daniel B
: TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
: FILE REFERENCE: 18475-025
: CURRENT APPLICATION NUMBER: US/09488792
: PRIOR FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/252,469
: PRIOR FILING DATE: 2000-11-21
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 4
: LENGTH: 14
: TYPE: PRP
: ORGANISM: Homo sapiens
US-09-988-792-4

Query Match: 36.4%; Score 4; DB 11; Length 14;
Res. Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KMP 10
ID 1 KMP 9

RESULT 36
US-09-988-792-14
: Sequence 4: Application US/09488792
: Publication No. US20030032599A1
: GENERAL INFORMATION:
: APPLICANT: Lukowski, Andrezej W
: APPLICANT: Gatz, Daniel B
: TITLE OF INVENTION: NOVEL ANTIMICROBIAL COMPOUNDS
: FILE REFERENCE: 18475-025
: CURRENT APPLICATION NUMBER: US/09488792
: PRIOR FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/252,469
: PRIOR FILING DATE: 2000-11-21
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 14
: LENGTH: 14
: TYPE: PRP
: ORGANISM: Homo sapiens
: NAME/KEY: VARIANT
: LOCATION: (1)
: OTHER INFORMATION: wherein Xaa is ty or try
US-09-988-792-14

Query Match: 36.4%; Score 4; DB 11; Length 14;
Res. Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KMP 10
ID 6 KMP 9

RESULT 37
US-09-966-422B-35
: Sequence 35: Application US/09466422B
: Publication No. US20030044892A1
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLING RECEPTOR, EXPRESSED IN

```

```

: TITLE OF INVENTION: SMALL INTESTINE
: FILE REFERENCE: D0049NP/0053-41190S3
: CURRENT APPLICATION NUMBER: US/09/966.422B
: CURRENT FILING DATE: 2002-05-07
: PRIOR APPLICATION NUMBER: 60/235,602
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: 60/306,604
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: 60/415,412
: PRIOR FILING DATE: 2001-08-28
: NUMBER OF SEQ ID NOS: 81
: SOFTWARE: Patent In version 3.0
: SEQ ID NO 35
: LENGTH: 13
: TYPE: PRP
: ORGANISM: Homo sapiens
US-09-966-422B-35

Query Match: 36.4%; Score 4; DB 11; Length 13;
Res. Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TMKP 8
ID 6 TMKP 9

RESULT 38
US-10-169-223-25
: Sequence 25: Application US/10169223
: Publication No. US2004015946A1
: GENERAL INFORMATION:
: APPLICANT: SHIMIZU, Shigeaki
: APPLICANT: TSUCHIMOTO, Yoshinori
: TITLE OF INVENTION: BH4-Fused Polypeptides
: FILE REFERENCE: 1422-05379
: CURRENT APPLICATION NUMBER: US/10/169,223
: CURRENT FILING DATE: 2002-11-05
: PRIOR APPLICATION NUMBER: JP 11-471449
: PRIOR FILING DATE: 1999-12-27
: PRIOR APPLICATION NUMBER: PCT/JF00/09274
: PRIOR FILING DATE: 2000-12-26
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: Patent In version 3.1
: SEQ ID NO 25
: LENGTH: 13
: TYPE: PRP
: ORGANISM: Human T lymphotropic virus
US-10-169-223-25

Query Match: 36.4%; Score 4; DB 12; Length 13;
Res. Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PERS 11
ID 6 PERS 9

RESULT 39
US-10-050-200-21
: Sequence 21: Application US/10050200
: Publication No. US2003016037A1
: GENERAL INFORMATION:
: APPLICANT: Colles, Fawn
: APPLICANT: Karlsson, Lars
: TITLE OF INVENTION: Agglutininase-1 and -2 Peptide Substrates and Methods
: FILE REFERENCE: ORT-1417
: CURRENT APPLICATION NUMBER: US/10/050,200
: CURRENT FILING DATE: 2002-01-16
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: Patent In version 3.1

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SEQ ID NO: 41
LENGTH: 13
TYPE: PRI
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: peptide substitution
US-10-262-272A-35

Query Match
Best Local Similarity: 100.0%; Score 4; DB 12; Length 13;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KRR 10
LD 6 KRR 9

RESULT 41
US-10-262-272A-35
Sequence 41: Application US/10-262-272A
Publication No: US20030170671A1
GENERAL INFORMATION:
APPLICANT: Richardson, Elliott
APPLICANT: Casack, Bernadette Marie
APPLICANT: Engel, Yadan Ping
APPLICANT: Kozlowski, Bartolomae
APPLICANT: Fung, Abdul
APPLICANT: Cyber, Beth Marie
APPLICANT: Boyles, Mona
TITLE OF INVENTION: NEO-TRYPTIC PHAN
FILE REFERENCE: 27039/14/001
CURRENT APPLICATION NUMBER: US/10-265-099
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/09/755,638
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/289,434
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/092,139
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: US 60/092,195
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 60/081,456
PRIOR FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 41
LENGTH: 13
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by GeneScript Inc
US-10-265-099-1

Query Match
Best Local Similarity: 100.0%; Score 4; DB 12; Length 13;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KRR 10
LD 6 KRR 9

RESULT 41
US-10-262-272A-35
Sequence 41: Application US/10-262-272A
Publication No: US20030170671A1
GENERAL INFORMATION:
APPLICANT: Richardson, Elliott
APPLICANT: Casack, Bernadette Marie
APPLICANT: Engel, Yadan Ping
APPLICANT: Kozlowski, Bartolomae
APPLICANT: Fung, Abdul
APPLICANT: Cyber, Beth Marie
APPLICANT: Boyles, Mona
TITLE OF INVENTION: NEO-TRYPTIC PHAN
FILE REFERENCE: 27039/14/001
CURRENT APPLICATION NUMBER: US/10-265-099
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/09/755,638
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 09/289,434
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/092,139
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: US 60/092,195
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: US 60/081,456
PRIOR FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
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LENGTH: 13
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized by GeneScript Inc
US-10-265-099-1

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FILE REFERENCE: DC044-CTD
CURRENT APPLICATION NUMBER: US/10/262,272A
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 09/166,422
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In Version 4.2
SEQ ID NO: 45
LENGTH: 13
TYPE: PRI
ORGANISM: Homo Sapiens
US-10-262-272A-35

Query Match
Best Local Similarity: 100.0%; Score 4; DB 12; Length 13;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TKRP 8
LD 5 TKRP 9

RESULT 42
US-10-156-932-81
Sequence 81: Application US/10/156932
Publication No: US2003069341A1
GENERAL INFORMATION:
APPLICANT: Wong, Albert J.
TITLE OF INVENTION: Alternative Splice Forms of Proteins as
TITLE OF INVENTION: Basis for Multiple Therapeutic Modalities
FILE REFERENCE: 842-81
CURRENT APPLICATION NUMBER: US/10/156,932
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: US 60/293,797
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 81
LENGTH: 13
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: VEGF att splice #1 peptide + C
US-10-156-932-81

Query Match
Best Local Similarity: 100.0%; Score 4; DB 15; Length 13;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KRR 10
LD 9 KRR 12

RESULT 43
US-09-853-080-22
Sequence 22: Application US/09/53080
Patent No: US20020068403A1
GENERAL INFORMATION:
APPLICANT: Laub, Ralf
APPLICANT: Di Gambattista, Mario
TITLE OF INVENTION: ANTIGENIC POLYPEPTIDE SEQUENCES OF FACTOR
TITLE OF INVENTION: VIII; FRAGMENTS AND/OR EPITOPES OF THESE SEQUENCES
FILE REFERENCE: VANMA48.001CPI
CURRENT APPLICATION NUMBER: US/09/853,080
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 08/765,837
PRIOR FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: PCT/BE95/00068
PRIOR FILING DATE: 1995-07-14
PRIOR APPLICATION NUMBER: BE 9400666
PRIOR FILING DATE: 1994-07-14
NUMBER OF SEQ ID NOS: 33

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2  SEQ ID NO: 22
3  LENGTH: 15
4  TYPE: PRT
5  ORGANISM: Homo sapiens
6  FEATURES
7  OTHER INFORMATION: epitope Lys 2001 to 2007 from Lys 2 domain 1 Exon1
8  US 09-055,800 2
9
10  Query Match
11  Best Local Similarity 46.48%, Score 41, DB 91, Length 81
12  Matches 41, Conservative 0, Mismatches 0, Indels 0, Gaps 0
13
14  27 2 PRR 10
15  11
16  1 PRR 4
17
18  RESULT 47
19  US 09-055,800 4
20  Sequence 41, Application US/09072410
21  Patent No. US20020042254A1
22  GENERAL INFORMATION
23  APPLICANT: Stewart, Mary
24  APPLICANT: Kozma, Sarah
25  TITLE OF INVENTION: Dipeptidyl Peptidase Inhibitors
26  FILE REFERENCE: 4-2097/A
27  CURRENT APPLICATION NUMBER: US/09072410
28  PRIOR APPLICATION NUMBER: 2001-03-20
29  PRIOR FILING DATE: 1999-04-10
30  NUMBER OF SEQ ID NOS: 1
31  SOFTWARE: Patent In Ver. 2.0
32  SEQ ID NO: 4
33  LENGTH: 4
34  TYPE: PRT
35  ORGANISM: Homo sapiens
36  US 09-055,800 4
37
38  Query Match
39  Best Local Similarity 46.48%, Score 41, DB 91, Length 81
40  Matches 41, Conservative 0, Mismatches 0, Indels 0, Gaps 0
41
42  27 2 PRR 10
43  11
44  1 PRR 4
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46  RESULT 47
47  US 09-055,800 4
48  Sequence 41, Application US/09072410
49  Patent No. US20020042254A1
50  GENERAL INFORMATION
51  APPLICANT: Stewart, Mary
52  APPLICANT: Kozma, Sarah
53  TITLE OF INVENTION: Dipeptidyl Peptidase Inhibitors
54  FILE REFERENCE: 4-2097/A
55  CURRENT APPLICATION NUMBER: US/09072410
56  PRIOR APPLICATION NUMBER: 2001-03-20
57  PRIOR FILING DATE: 1999-04-10
58  NUMBER OF SEQ ID NOS: 1
59  SOFTWARE: Patent In Ver. 2.0
60  SEQ ID NO: 4
61  LENGTH: 4
62  TYPE: PRT
63  ORGANISM: Homo sapiens
64  US 09-055,800 4
65
66  Query Match
67  Best Local Similarity 46.48%, Score 41, DB 91, Length 81
68  Matches 41, Conservative 0, Mismatches 0, Indels 0, Gaps 0
69
70  27 2 PRR 10
71  11
72  1 PRR 4
73
74  RESULT 47
75  US 09-055,800 4
76  Sequence 41, Application US/09072410
77  Patent No. US20020042254A1
78  GENERAL INFORMATION
79  APPLICANT: Stewart, Mary
80  APPLICANT: Kozma, Sarah
81  TITLE OF INVENTION: Dipeptidyl Peptidase Inhibitors
82  FILE REFERENCE: 4-2097/A
83  CURRENT APPLICATION NUMBER: US/09072410
84  PRIOR APPLICATION NUMBER: 2001-03-20
85  PRIOR FILING DATE: 1999-04-10
86  NUMBER OF SEQ ID NOS: 1
87  SOFTWARE: Patent In Ver. 2.0
88  SEQ ID NO: 4
89  LENGTH: 4
90  TYPE: PRT
91  ORGANISM: Homo sapiens
92  US 09-055,800 4
93

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US-09-863,971A
Query Match
Best Local Similarity 27.08%, Score 41, DB 91, Length 81
Matches 0, Conservative 0, Mismatches 0, Indels 0, Gaps 0
27 0 PRR 10
18 11
2 PRR 4
RESULT 46
US 09-863,971A 8
Sequence 61, Application US/09072410
Patent No. US2002004409A1
GENERAL INFORMATION
APPLICANT: Achillea, Samuel L.
APPLICANT: Rajagopalan, Radhavan
APPLICANT: Dorshow, Richard B.
APPLICANT: Baga, Joseph E.
APPLICANT: Mallinckrodt, Inc.
TITLE OF INVENTION: Lymph-Targeted optical Contrast Agents
FILE REFERENCE: N/A-65
CURRENT APPLICATION NUMBER: US/09/863,971A
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/484,320
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES
NAME/KEY: M00 RES
LOCATION: (1) to (1)
OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is
US 09-863,971A 8
Query Match
Best Local Similarity 27.08%, Score 41, DB 91, Length 81
Matches 0, Conservative 0, Mismatches 0, Indels 0, Gaps 0
27 0 PRR 10
18 11
2 PRR 4
RESULT 47
US-09-863,971A 8
Sequence 41, Application US/09084601
Patent No. US2002004545A1
GENERAL INFORMATION
APPLICANT: Gubitz, Andrew R.
TITLE OF INVENTION: Assays for Protein Kinases Using
Fluorescent Protein Substrates
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-0834
COMPUTER READABLE FORM
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.00
COPYING: All Rights Reserved
APPLICATION NUMBER: US/09/863,971A

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1 FILING DATE: 19 Jun 2003  
 2 CLASSIFICATION: UNKNOWN  
 3 PUBLICATION DATA:  
 4 APPLICATION NUMBER: 09/09,000  
 5 FILING DATE: UNKNOWN  
 6 AGENT/AGENT INFORMATION:  
 7 NAME: STORELLO, JOHN S.  
 8 REGISTRATION NUMBER: 00041  
 9 REFERENCE/DOCKET NUMBER: 09/09,000  
 10 TELEPHONE: (415) 576-0200  
 11 TELEFAX: (415) 576-0200  
 12 INFORMATION FOR SEQ ID NO. 1:  
 13 SEQUENCE CHARACTERISTICS  
 14 LENGTH: 8 amino acids  
 15 TYPE: amino acid  
 16 STRANDEDNESS: unknown  
 17 TOPOLOGY: linear  
 18 MOLECULE TYPE: peptide  
 19 SEQUENCE DESCRIPTION: SEQ ID NO. 1:  
 20 US-09-884-443-11  
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 22 Quality Match: 27.0%, Score 4; DB 9; Length 8;  
 23 Best Local Similarity: 100.0%; Pos: 50-05;  
 24 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
 25  
 26 QY 9 RES 11  
 27 11  
 28 4 RES 5  
 29 11  
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 31 RESULT 50  
 32 US-09-884-443-11  
 33 Sequence 10; Application 09/09,000  
 34 Patent No. US2003/01142A1  
 35 GENERAL INFORMATION:  
 36 APPLICANT: Martineau, Val  
 37  
 38 FILING DATE: 27.04, Score 4; DB 9; Length 8;  
 39 Best Local Similarity: 100.0%; Pos: 50-05;  
 40 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
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 45 11  
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 48 US-09-884-443-11  
 49 Sequence 10; Application 09/09,000  
 50 Patent No. US2003/01142A1  
 51 GENERAL INFORMATION:  
 52 APPLICANT: Martineau, Val  
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 54 FILING DATE: 27.04, Score 4; DB 9; Length 8;  
 55 Best Local Similarity: 100.0%; Pos: 50-05;  
 56 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
 57  
 58 QY 9 RES 11  
 59 11  
 60 4 RES 5  
 61 11  
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 63 RESULT 48  
 64 US-09-884-443-11  
 65 Sequence 10; Application 09/09,000  
 66 Patent No. US2003/01142A1  
 67 GENERAL INFORMATION:  
 68 APPLICANT: Martineau, Val  
 69  
 70 FILING DATE: 27.04, Score 4; DB 9; Length 8;  
 71 Best Local Similarity: 100.0%; Pos: 50-05;  
 72 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
 73  
 74 QY 9 RES 11  
 75 11  
 76 4 RES 5  
 77 11  
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 79 RESULT 48  
 80 US-09-884-443-11  
 81 Sequence 10; Application 09/09,000  
 82 Patent No. US2003/01142A1  
 83 GENERAL INFORMATION:  
 84 APPLICANT: Martineau, Val  
 85  
 86 FILING DATE: 27.04, Score 4; DB 9; Length 8;  
 87 Best Local Similarity: 100.0%; Pos: 50-05;  
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 92 4 RES 5  
 93 11  
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 96 US-09-884-443-11  
 97 Sequence 10; Application 09/09,000  
 98 Patent No. US2003/01142A1  
 99 GENERAL INFORMATION:  
 100 APPLICANT: Martineau, Val

1 MOLECULE TYPE: peptide  
 2 SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
 3 US-09-884-443-12  
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 17 Patent No. US2003/01142A1  
 18 GENERAL INFORMATION:  
 19 APPLICANT: Martineau, Val  
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 33 Patent No. US2003/01142A1  
 34 GENERAL INFORMATION:  
 35 APPLICANT: Martineau, Val  
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 50 GENERAL INFORMATION:  
 51 APPLICANT: Martineau, Val  
 52  
 53 FILING DATE: 27.04, Score 4; DB 9; Length 8;  
 54 Best Local Similarity: 100.0%; Pos: 50-05;  
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 65 Patent No. US2003/01142A1  
 66 GENERAL INFORMATION:  
 67 APPLICANT: Martineau, Val  
 68  
 69 FILING DATE: 27.04, Score 4; DB 9; Length 8;  
 70 Best Local Similarity: 100.0%; Pos: 50-05;  
 71 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;  
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 73 QY 9 RES 11  
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 75 4 RES 5  
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 80 Sequence 10; Application 09/09,000  
 81 Patent No. US2003/01142A1  
 82 GENERAL INFORMATION:  
 83 APPLICANT: Martineau, Val  
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 95 US-09-884-443-12  
 96 Sequence 10; Application 09/09,000  
 97 Patent No. US2003/01142A1  
 98 GENERAL INFORMATION:  
 99 APPLICANT: Martineau, Val  
 100

1 APPLICANT: De Smet, Charles  
2 APPLICANT: Bazo-Falourd, Thierry  
3 TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEOTIDES AND USES THEREOF  
4 FIDEL REFERENCE: 10461/7054  
5 CURRENT APPLICATION NUMBER: US/09/225,834  
6 CURRENT FILING DATE: 2001-09-07  
7 PRIOR APPLICATION NUMBER: 09/185,730  
8 PRIOR FILING DATE: 2001-10-03  
9 NUMBER OF SEQ ID NOS: 43  
10 SEQ ID NO 10  
11 LENGTH: 8  
12 TYPE: PRT  
13 ORGANISM: Homo sapiens  
14 US 09/225,834, 10

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Matches: 51 Conservative 0; Mismatches: 6; Indels: 0; Gaps: 0;

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DL 5 PER 7

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GeneScan version 5.1.3  
Copyright (c) 1993-2001 Amersham Pharmacia Biotech

CM protein protein search, using sw model

Run on September 30, 2003, 10:07:34 : Search time 11.085 seconds  
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Title: US-09-787-443.12

Perfect score: 11

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Minimum DB seq length: 8

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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48	4	36.4	8	22	AA17585
49	4	36.4	8	22	AA17585
50	4	36.4	8	22	AA17585
51	4	36.4	8	22	AA17585
52	4	36.4	8	22	AA17585
53	4	36.4	8	22	AA17585
54	4	36.4	8	22	AA17585
55	4	36.4	8	22	AA17585
56	4	36.4	8	22	AA17585
57	4	36.4	8	22	AA17585
58	4	36.4	8	22	AA17585
59	4	36.4	8	22	AA17585
60	4	36.4	8	22	AA17585
61	4	36.4	8	22	AA17585
62	4	36.4	8	22	AA17585
63	4	36.4	8	22	AA17585
64	4	36.4	8	22	AA17585
65	4	36.4	8	22	AA17585
66	4	36.4	8	22	AA17585
67	4	36.4	8	22	AA17585
68	4	36.4	8	22	AA17585
69	4	36.4	8	22	AA17585
70	4	36.4	8	22	AA17585
71	4	36.4	8	22	AA17585
72	4	36.4	8	22	AA17585
73	4	36.4	8	22	AA17585
74	4	36.4	8	22	AA17585
75	4	36.4	8	22	AA17585
76	4	36.4	8	22	AA17585
77	4	36.4	8	22	AA17585
78	4	36.4	8	22	AA17585
79	4	36.4	8	22	AA17585
80	4	36.4	8	22	AA17585
81	4	36.4	8	22	AA17585
82	4	36.4	8	22	AA17585

83	4	36.4	12	15	AAR71765	Neurotensin Recept	156	3	27.3	8	4	AAP10497	Sequence of tuftsi
84	4	36.4	12	16	AAR67113	CAC Interleukine Iaa	157	3	27.3	8	4	AAP50069	Arginine vasopress
85	4	36.4	12	17	AAR74694	Amino acid sequen	158	3	27.3	8	5	AAP50071	Arginine vasopress
86	4	36.4	12	19	AAR55956	Human vascular pe	159	3	27.3	8	13	AAR24414	HCV core protein N
87	4	36.4	12	19	AAR54449	Vascular endothel	160	3	27.3	8	14	AAR40979	HCV core protein N
88	4	36.4	12	19	AAR45569	Amino acid derivat	161	3	27.3	8	14	AAR40980	HCV core protein N
89	4	36.4	12	20	AAR41444	Peptide derivatiz	162	3	27.3	8	14	AAR40981	HCV core protein N
90	4	36.4	12	20	AAR55540	Immunoglobulin Ig	163	3	27.3	8	14	AAR40981	HCV core protein N
91	4	36.4	12	20	AAR48411	Peptide tested for	164	3	27.3	8	14	AAR40989	HCV core protein N
92	4	36.4	12	21	AAR34528	Peptide #52 Chitin	165	3	27.3	8	14	AAR40991	HCV core protein N
93	4	36.4	12	21	AAR58599	Texas Red Binding	166	3	27.3	8	14	AAR40992	HCV core protein N
94	4	36.4	12	21	AAR51146	Texas Red Binding	167	3	27.3	8	14	AAR40993	HCV core protein N
95	4	36.4	12	21	AAR58149	Texas Red Binding	168	3	27.3	8	14	AAR40997	HCV core protein N
96	4	36.4	12	21	AAR55679	Human vascular end	169	3	27.3	8	14	AAR46860	Insulin-like growt
97	4	36.4	12	21	AAR50631	Vascular endotheli	170	3	27.3	8	14	AAR35958	Hepatitis C virus
98	4	36.4	12	22	AAR61022	Internalizing pep	171	3	27.3	8	14	AAR35959	Hepatitis C virus
99	4	36.4	12	22	AAR57930	Human VEGF/VEGF	172	3	27.3	8	14	AAR35960	Hepatitis C virus
100	4	36.4	12	22	AAR34574	VEGF VEGF actinatio	173	3	27.3	8	14	AAR35777	Hepatitis C virus
101	4	36.4	12	22	AAR54616	Neurotensin peptid	174	3	27.3	8	14	AAR35778	Hepatitis C virus
102	4	36.4	12	22	AAR345668	Neurotensin peptid	175	3	27.3	8	14	AAR35779	Hepatitis C virus
103	4	36.4	12	22	AAR345672	Neurotensin peptid	176	3	27.3	8	14	AAR35780	Hepatitis C virus
104	4	36.4	12	22	AAR345672	Neurotensin peptid	177	3	27.3	8	14	AAR34399	La/SSB epitope 89
105	4	36.4	12	22	AAR345672	Neurotensin peptid	178	3	27.3	8	15	AAR67846	Hepatitis C virus
106	4	36.4	12	22	AAR345672	Neurotensin peptid	179	3	27.3	8	15	AAR61370	Dynorphin-like pol
107	4	36.4	12	22	AAR24537	Neurotensin peptid	180	3	27.3	8	15	AAR61066	Dynorphin-like pol
108	4	36.4	12	23	AAR24537	Neurotensin peptid	181	3	27.3	8	15	AAR62145	HIV-1 gp120/41 pro
109	4	36.4	13	14	AAR47046	Neurotensin (Leu2)	182	3	27.3	8	15	AAR71751	Neurotensin recept
110	4	36.4	13	14	AAR47047	Neurotensin (Leu2)	183	3	27.3	8	15	AAR71752	Neurotensin recept
111	4	36.4	13	15	AAR67082	Protease inhibitor	184	3	27.3	8	16	AAR21460	Gastrin precursor
112	4	36.4	13	15	AAR71769	Neurotensin Recept	185	3	27.3	8	16	AAR21463	Gastrin precursor
113	4	36.4	13	15	AAR71773	Neurotensin Recept	186	3	27.3	8	16	AAR21335	Glucagon precursor
114	4	36.4	13	15	AAR71774	Neurotensin Recept	187	3	27.3	8	16	AAR21555	Corticotropin rele
115	4	36.4	13	17	AAR47047	Peptide fragment	188	3	27.3	8	16	AAR21556	Corticotropin rele
116	4	36.4	13	17	AAR47047	Peptide fragment	189	3	27.3	8	16	AAR21556	Corticotropin rele
117	4	36.4	13	17	AAR47047	Peptide fragment	190	3	27.3	8	16	AAR21556	Corticotropin rele
118	4	36.4	13	21	AAR16544	Non-crosslinked pe	191	3	27.3	8	16	AAR61447	HIV-1 protease inh
119	4	36.4	13	21	AAR45378	Immunogenic peptid	192	3	27.3	8	16	AAR61447	HIV-1 protease inh
120	4	36.4	13	21	AAR45378	Antic acid sequen	193	3	27.3	8	16	AAR66094	PF4-related octape
121	4	36.4	13	21	AAR45378	Antic acid sequen	194	3	27.3	8	16	AAR66094	PF4-related octape
122	4	36.4	13	22	AAR47274	Human lymphocyte	195	3	27.3	8	16	AAR64662	Myelopietic proge
123	4	36.4	13	22	AAR47274	Human lymphocyte	196	3	27.3	8	16	AAR79695	HPF3 peptide deriv
124	4	36.4	13	22	AAR47274	Neurotensin Recept	197	3	27.3	8	17	AAR604278	pp60(c-src) kinase
125	4	36.4	13	22	AAR62436	Neurotensin stat 1	198	3	27.3	8	17	AAR604278	pp60(c-src) kinase
126	4	36.4	13	22	AAR62436	Neurotensin stat 1	199	3	27.3	8	17	AAR604278	Milk derived anti-
127	4	36.4	13	22	AAR62436	Neurotensin stat 1	200	3	27.3	8	17	AAR604278	Peptide #10 from a
128	4	36.4	13	22	AAR62436	Neurotensin stat 1	201	3	27.3	8	17	AAR604278	Peptide #13 from a
129	4	36.4	13	22	AAR62436	Neurotensin stat 1	202	3	27.3	8	17	AAR604278	Anion transporter
130	4	36.4	13	22	AAR62436	Neurotensin stat 1	203	3	27.3	8	17	AAR604278	Tumour rejection a
131	4	36.4	13	22	AAR62436	Neurotensin stat 1	204	3	27.3	8	17	AAR604278	Proteinase A subst
132	4	36.4	13	22	AAR62436	Neurotensin stat 1	205	3	27.3	8	17	AAR604278	Antibody 56: displ
133	4	36.4	13	22	AAR62436	Neurotensin stat 1	206	3	27.3	8	17	AAR604278	Mouse JAK3 protein
134	4	36.4	13	22	AAR62436	Neurotensin stat 1	207	3	27.3	8	17	AAR604278	GAGE-1 protein pep
135	4	36.4	13	22	AAR62436	Neurotensin stat 1	208	3	27.3	8	17	AAR604278	Band-3 peptide SEQ
136	4	36.4	13	22	AAR62436	Neurotensin stat 1	209	3	27.3	8	17	AAR604278	Terminal peptide e
137	4	36.4	13	22	AAR62436	Neurotensin stat 1	210	3	27.3	8	17	AAR604278	Terminal peptide e
138	4	36.4	13	22	AAR62436	Neurotensin stat 1	211	3	27.3	8	17	AAR604278	Protein kinase C-b
139	4	36.4	13	22	AAR62436	Neurotensin stat 1	212	3	27.3	8	17	AAR604278	Lipolytic enzyme o
140	4	36.4	13	22	AAR62436	Neurotensin stat 1	213	3	27.3	8	17	AAR604278	Lipolytic enzyme o
141	4	36.4	13	22	AAR62436	Neurotensin stat 1	214	3	27.3	8	17	AAR604278	CD4 peptide capabl
142	4	36.4	13	22	AAR62436	Neurotensin stat 1	215	3	27.3	8	17	AAR604278	Human growth hormo
143	4	36.4	13	22	AAR62436	Neurotensin stat 1	216	3	27.3	8	17	AAR604278	Human growth hormo
144	4	36.4	13	22	AAR62436	Neurotensin stat 1	217	3	27.3	8	17	AAR604278	Human HGF-1 mutan
145	4	36.4	13	22	AAR62436	Neurotensin stat 1	218	3	27.3	8	17	AAR604278	mMCP-7 peptide sub
146	4	36.4	13	22	AAR62436	Neurotensin stat 1	219	3	27.3	8	17	AAR604278	GAGE-1 protein fra
147	4	36.4	13	22	AAR62436	Neurotensin stat 1	220	3	27.3	8	17	AAR604278	GAGE-1,2 synthetic
148	4	36.4	13	22	AAR62436	Neurotensin stat 1	221	3	27.3	8	17	AAR604278	Human GAGE peptide
149	4	36.4	13	22	AAR62436	Neurotensin stat 1	222	3	27.3	8	17	AAR604278	Mouse mast cell pr
150	4	36.4	13	22	AAR62436	Neurotensin stat 1	223	3	27.3	8	17	AAR604278	Peptide 1 from Gag
151	4	36.4	13	22	AAR62436	Neurotensin stat 1	224	3	27.3	8	17	AAR604278	Platelet factor 4
152	4	36.4	13	22	AAR62436	Neurotensin stat 1	225	3	27.3	8	17	AAR604278	Molecular mimetic
153	4	36.4	13	22	AAR62436	Neurotensin stat 1	226	3	27.3	8	17	AAR604278	Antigenic peptide
154	4	36.4	13	22	AAR62436	Neurotensin stat 1	227	3	27.3	8	17	AAR604278	Peptide common to
155	4	36.4	13	22	AAR62436	Neurotensin stat 1	228	3	27.3	8	17	AAR604278	Peptide antigenic p
156	4	36.4	13	22	AAR62436	Neurotensin stat 1	229	3	27.3	8	17	AAR604278	HIV-1 Gp41 protein







XX OS Synthetic.

XX PN WO200018801-A2.

XX FT 06-APR-2003.

XX 24-SEP-1999; 99WO-DK06500.

XX 29-SEP-1998; 98DK-0001232.

XX 29-APR-1999; 99DK-0000592.

XX (KONN/) KONN L C B.

XX (BCKE/) BCKE E.

XX (HOLM/) HOLM A.

XX (OLSE/) OLSEN M.

XX (OSTE/) OSTERGAARD S.

XX (JENS/) JENSEN P H.

XX (POLI/) POLSEN F M.

XX (SORO/) SOROKA V.

XX (RALE/) RALETS I.

XX (BERE/) BEREZIN V.

XX Rona LCB, Bock E, Holm A, Olsen M, OSTERGAARD S, Jensen PH, Polsen FM, Soroka V, Ralets I, Berezin V.

XX WPI: 2000 293111/25.

XX Compositions that bind neural cell adhesion molecules useful for treating disorders of the nervous system and muscles e.g. Alzheimer's and Parkinson's diseases.

XX Example 4: Page 25; 119pp; English.

XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule. NCAM is found in three forms, two of which are transmembrane forms, while the third is attached via a lipid anchor to the cell membrane. All three NCAM forms have an extracellular structure consisting of five immunoglobulin domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-terminal. The present sequence represents a peptide which binds to the NCAM 141/92 domain. The peptide can be used in a compound which binds to NCAM 141/92 domains, and is capable of stimulating or promoting neurite outgrowth from NCAM presenting cells, and is also capable of promoting the proliferation of NCAM presenting cells, and is also capable of promoting the treatment of normal, degenerated or damaged NCAM presenting cells. The compound may in particular be used to treat diseases of the central and peripheral nervous systems such as post-operative nerve damage, traumatic nerve damage, impaired myelination of nerve fibres, conditions resulting from a stroke, Parkinson's disease, Alzheimer's disease, dementias, sclerosis, nerve degeneration associated with diabetes, mellitus, disorders affecting the circulation, stroke or neuro-muscular transmission and schizophrenia. Conditions affecting the muscles may also be treated with the compound, such as conditions associated with impaired function of neuromuscular connections (e.g. genetic or traumatic shock or traumatic atrophic muscle disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart, liver and bowel may also be treated using the compound. The compound is used in a prosthetic nerve guide, and also to stimulate the ability to learn, and to stimulate the memory of a subject.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.4e-05;

Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQKTMKPKRS 11

DB 1 ARQKTMKPKRS 11

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RES021.4

AB069340

ID AB069340 standard; Peptide: 11 AA.

XX AC AB069340;

XX DT 21-OCT-2002 (first entry)

XX DE Human neural cell adhesion molecule (NCAM) peptide #12.

XX Human; neural cell adhesion molecule; NCAM; heart muscle cell survival; acute myocardial infarction; central nervous system disorder; stroke; peripheral nervous system disorder; postoperative nerve damage; traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia; postischaemic damage; multifarct dementia; multiple sclerosis; nerve degeneration; diabetes mellitus; neuro-muscular degeneration; Alzheimer's disease; Parkinson's disease; Huntington's disease; atrophic muscle disorder; gonad degeneration; nephrosis.

XX OS Homo sapiens.

XX PN WO200247719-A2.

XX PD 20-JUN-2002.

XX 12-DEC-2001; 2001WO-DK00822.

XX 12-DEC-2000; 2000DK-0001863.

XX (ENKA ) ENKAM PHARM AS.

XX Bock E, Berezin V, Kohler LH;

XX WPI: 2002-583473/62.

XX Use of a compound comprising a peptide of neural cell adhesion molecule, in the preparation of medicament for preventing death of cells presenting NCAM or NCAM ligand and treating central nervous system diseases.

XX Disclosure: Page 16; 57pp; English.

XX The invention relates to use of a compound (I) comprising a peptide which comprises at least 5 contiguous amino acid residues of a sequence of the neural cell adhesion molecule (NCAM), its fragment, variant or its mimic, for the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand. (I) is useful in the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand. The medicament is for the stimulation of the survival of heart muscle cells, such as survival after acute myocardial infarction. The medicament is for the treatment of diseases or conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, e.g. resulting from spinal cord injury, impaired myelination of nerve fibres, postischaemic damage, e.g. resulting from a stroke, multifarct dementia, multiple sclerosis, nerve degeneration associated with diabetes mellitus, neuro-muscular degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and Huntington's disease. The medicament is for the treatment of diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as genetic or traumatic atrophic muscle disorders, and for the treatment of diseases of conditions of various organs, such as degenerative conditions of the gonads, pancreas (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).

XX AB069329-AB069352 represent human NCAM peptides of the invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.4e-06;

Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARQKTMKPKRS 11

DB 1 ARQKTMKPKRS 11

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CC inhibitors or to target therapeutic agents to their site of action. STRAP  
 CC nucleic acids may be used for recombinant protein production, as  
 CC diagnostic and prognostic reagents, for identifying STRAP-expressing  
 CC cells for screening inhibitors of STRAP expression and for therapeutic  
 CC modulation/inhibition of STRAP expression. Since high levels of STRAP  
 CC proteins are exposed on the cell surface, they are easily targeted by  
 CC systemically administered agents, and because they are expressed mainly  
 CC on prostate epithelial cells, agents targeted to them should have  
 CC minimal side effects on other tissues.

XX Sequence 15 AA:

Query Match 45.5%, Score 5; DH 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 6 MKPRK 10  
 | | | | |  
 DQ 3 MKPRK 7

RESULT 5  
 AAP40573  
 10 AAP40573 standard; Peptide: 8 AA.

XX AAP40573:

XX 06-AUG-2001 (first entry)

DE Peptide: peptide #1 of human STEAP-1.

KW human cytosol; antiproliferative and/or anticancer therapy.

KW six transmembrane epithelial antigen of the prostate 1; STEAP-1;

KW chromosome 7p22.3; cancer; prostate; benign prostatic hyperplasia;

KW ovarian; solid; serpentine transmembrane antigen; immunogen.

XX Best subjects:

UN W20030276 AZ.

XX 07-JUN-2001

XX 01-DEC-2000; Z00000-US33040.

XX 05-JAN-1999; 99CS-0455495.

XX (X66); GENESTS INC.

XX Alan Feld, Robert RS, Kalliane AS, Sathyanarayanan V, Garg R, Faris M,

XX Jorg Lavie A.

XX WPI: 2562-97804/38.

XX New STEAP (six transmembrane epithelial antigen of the prostate)

XX proteins, expressed in human cancers, are related to cell growth and treatment

XX cancer.

XX Example 6: Page 77; 18/pp; English.

XX The present invention relates to human six transmembrane epithelial

XX antigen of the prostate (STEAP) proteins. STEAP is a member of the

XX surface serpentine transmembrane antigens. STEAP gene is used in gene

XX therapy inhibiting the development of progression of a cancer (e.g.,

XX prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP

XX or inhibiting growth or killing cells expressing STEAP in a patient,

XX comprises administering a vaccine composition to the patient. Treatment

XX of a patient with a cancer that expresses STEAP, or related gene, protein, or

XX killing cells expressing STEAP, comprises administering to the patient a

CC intracellularly. The present sequence is an immunogenic peptide of  
 CC STEAP-1. STEAP-1 gene is located on chromosome 7p22.3. This peptide is  
 CC used to immunise sheep for the generation of sheep polyclonal antibodies  
 CC towards the amino terminus of anti-STEAP-1.

XX Sequence 15 AA:

Query Match 45.5%, Score 5; DH 22; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 6 MKPRK 10  
 | | | | |  
 DQ 3 MKPRK 7

RESULT 5  
 AAP40573  
 10 AAP40573 standard; Peptide: 8 AA.

XX AAP40573:

XX 16-AUG-2002 (updated)

XX 16-FEB-1992 (first entry)

XX Sequence of cyclic analogue of neurotensin.

XX Neurotransmitter, neuromodulator; neurotensin.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified site 1

XX /Label: D Lys

XX US44 09559 A.

XX 27-MAR-1984.

XX 02-JUL-1982; E2US 0394750.

XX 02-JUL-1982; E2US 0394750.

XX (MERK) MERCK & CO INC.

XX Holly FW, Christy ME, Shepard KL, Strachan RG, Varma SL,

XX Weber LF;

XX WPI: 1984-09469/15.

XX Cyclic octapeptide analogues of neurotensin - having

XX neurotensin-like activity

XX Claim 3: Column 6; App: English.

XX The peptides of the invention have neurotensin like activity.

XX neurotensin is e.g. CNS active as a neurotransmitter or

XX neuromodulator.

XX (updated on 16-AUG-2002 to add missing GS field.)

XX Sequence 8 AA:

Query Match 36.4%, Score 4; DH 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 7 KPRK 10  
 | | | | |  
 DQ 1 KPRK 4

RESULT 7  
 AAP21985

10 AAR71745 standard; peptide: 8 AA.  
 11 AAR71745.  
 12 25-MAR-2003 (updated)  
 13 01-JAN-1995 (first entry)  
 14 Cyclic octapeptide with hypotensive activity.  
 15 Cyclic octapeptide; hypotensive ss.  
 16 Cyclic octapeptide; hypotensive ss.  
 17 Synthetic.  
 18 S01134020 A  
 19 15 JUL 1986.  
 20 13 JUL 1983; R3S0-3620434.  
 21 13 JUL 1983; R3S0-3620434.  
 22 (AAR71745) AS LATV ORGANIC SYNTHESIS INST.  
 23 Chapuis JJ. Grinshtein IV. Vequer RE;  
 24 WEI: 1387 035268/05.  
 25 Novel cyclic octapeptide with hypotensive activity has low  
 26 toxicity and is stable to carboxy peptidase  
 27 (discussed) page 1; 7pp; Russian.  
 28 The novel biologically active cyclic octapeptide which possesses  
 29 hypotensive activity is stable to carboxypeptidase activity. The  
 30 synthesis of the peptide involves acylation of the peptide chain,  
 31 using dicyclohexyl carbodiimide as the condensing agent and tert  
 32 butylhydroxy carbonyl for protecting the alpha amino groups. Final  
 33 purification is secured by paper electrophoresis. The peptide shows  
 34 a weak hypotensive activity that neurotensin by a factor of 20. The  
 35 ED50 is 9 mg/kg, eq the cellular dose is more than 10,000 fold  
 36 greater than the depressive effect dose.  
 37 (Updated on 25-MAR-2003 to correct EA field.)  
 38 Sequence: 8 AA:

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best local similarity: 100.0%; Field No. 9; 30-05;  
 Matches: 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KPER 10  
 11  
 12 1 KPER 4

RESU: 19  
 AAR71749  
 10 AAR71749 standard; peptide: 8 AA.  
 11 AAR71749.  
 12 25-MAR-2003 (updated)  
 13 15-MAY-1995 (first entry)  
 14 Neurotensin receptor fluorescent probe.  
 15 Neurotensin; NI; receptor; probe; fluorescent.  
 16 Synthetic.  
 17 Key Location/Qualifiers  
 18 Modified site 1  
 19 Note: "N-acylated with fluorescent label. See (r  
 20 below. Also this amino acid can be  
 21 substituted by Lys or Orn."

FT XX substituted by Lys or Orn."  
 11 EP606804-A2.  
 12 20-JUL-1994.  
 13 27-DEC-1993; 5451 04-0186.  
 14 00-DEC-1992; 940A 2070454.  
 15 (JYMC) UNIV MEDICAL.  
 16 Boudet A. Faute M. Gaudreau P;  
 17 WPI: 1994-226757/28.  
 18 New fluorescent markers for neurotensin receptors - useful for in  
 19 vitro labelling of neurotensin receptors on cell surface and to  
 20 isolate neurotensin-receptor expressing cells  
 21 Claim 2; Page 5; 19pp; English.  
 22 The invention concerns highly sensitive fluorescent probes which  
 23 allow for rapid and precise characterisation of neurotensin  
 24 receptor binding properties on whole cells. The probes are of  
 25 formula R1-C(=X) R in which R1 is a fluorophore chosen from  
 26 fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen  
 27 or sulphur; and R is a neurotensin-type polypeptide sequence  
 28 containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or  
 29 Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAR71745  
 30 AAR71772. The R1-CX-acyl group is linked to the peptide via the  
 31 N-terminus in position 1. The N-terminal amino acid may also be  
 32 substituted by Lys or Orn.  
 33 The present sequence represents one of the claimed peptide  
 34 sequences for R.  
 35 (Updated on 25-MAR-2003 to correct PN field.)  
 36 Sequence: 8 AA:

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best local similarity: 100.0%; Field No. 9; 30-05;  
 Matches: 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KPER 10  
 11  
 12 1 KPER 4

RESU: 19  
 AAR71750  
 10 AAR71750 standard; peptide: 8 AA.  
 11 AAR71750.  
 12 25-MAR-2003 (updated)  
 13 15-MAY-1995 (first entry)  
 14 Neurotensin receptor fluorescent probe.  
 15 Neurotensin; NI; receptor; probe; fluorescent.  
 16 Synthetic.  
 17 Key Location/Qualifiers  
 18 Modified site 1  
 19 Note: "N-acylated with fluorescent label. See (r  
 20 below. Also this amino acid can be  
 21 substituted by Lys or Orn."

FT XX substituted by Lys or Orn."  
 11 EP606804-A2.  
 12 20-JUL-1994.  
 13 27-DEC-1993; 5451 04-0186.  
 14 00-DEC-1992; 940A 2070454.  
 15 (JYMC) UNIV MEDICAL.  
 16 Boudet A. Faute M. Gaudreau P;  
 17 WPI: 1994-226757/28.  
 18 New fluorescent markers for neurotensin receptors - useful for in  
 19 vitro labelling of neurotensin receptors on cell surface and to  
 20 isolate neurotensin-receptor expressing cells  
 21 Claim 2; Page 5; 19pp; English.  
 22 The invention concerns highly sensitive fluorescent probes which  
 23 allow for rapid and precise characterisation of neurotensin  
 24 receptor binding properties on whole cells. The probes are of  
 25 formula R1-C(=X) R in which R1 is a fluorophore chosen from  
 26 fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen  
 27 or sulphur; and R is a neurotensin-type polypeptide sequence  
 28 containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or  
 29 Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAR71745  
 30 AAR71772. The R1-CX-acyl group is linked to the peptide via the  
 31 N-terminus in position 1. The N-terminal amino acid may also be  
 32 substituted by Lys or Orn.  
 33 The present sequence represents one of the claimed peptide  
 34 sequences for R.  
 35 (Updated on 25-MAR-2003 to correct PN field.)  
 36 Sequence: 8 AA:

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best local similarity: 100.0%; Field No. 9; 30-05;  
 Matches: 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KPER 10  
 11  
 12 1 KPER 4

RESU: 19  
 AAR71750  
 10 AAR71750 standard; peptide: 8 AA.  
 11 AAR71750.  
 12 25-MAR-2003 (updated)  
 13 15-MAY-1995 (first entry)  
 14 Neurotensin receptor fluorescent probe.  
 15 Neurotensin; NI; receptor; probe; fluorescent.  
 16 Synthetic.  
 17 Key Location/Qualifiers  
 18 Modified site 1  
 19 Note: "N-acylated with fluorescent label. See (r  
 20 below. Also this amino acid can be  
 21 substituted by Lys or Orn."

27 FEB 1994 95EP-0405185.  
 30 SEP 1994 92CA 2086454  
 (YK) UNIV MC21LL.  
 Bound A. Faure M. Gaudreau P.  
 WP: 1994 226757/26.  
 New fluorescent markers for neutralising receptor expressed in for in  
 vitro labelling of neutralising receptors, their surface and the  
 isolate neutralising receptor expressed in cells  
 (Page 2: Page 5: Page English  
 The convention concerns highly sensitive sources and proteins which  
 allow for rapid and precise characterization of neutralising  
 receptor binding properties in which cases the markers are of  
 low molecular weight, which allows as a consequence to choose from  
 fluorescently labelled, blue fluorescent and lysine red, X is oxygen  
 or sulphur and R is a neutralising type 1/2/3/4/5/6/7/8/9/10/11/12/13/14/15/16/17/18/19/20/21/22/23/24/25/26/27/28/29/30/31/32/33/34/35/36/37/38/39/40/41/42/43/44/45/46/47/48/49/50/51/52/53/54/55/56/57/58/59/60/61/62/63/64/65/66/67/68/69/70/71/72/73/74/75/76/77/78/79/80/81/82/83/84/85/86/87/88/89/90/91/92/93/94/95/96/97/98/99/100/101/102/103/104/105/106/107/108/109/110/111/112/113/114/115/116/117/118/119/120/121/122/123/124/125/126/127/128/129/130/131/132/133/134/135/136/137/138/139/140/141/142/143/144/145/146/147/148/149/150/151/152/153/154/155/156/157/158/159/160/161/162/163/164/165/166/167/168/169/170/171/172/173/174/175/176/177/178/179/180/181/182/183/184/185/186/187/188/189/190/191/192/193/194/195/196/197/198/199/200/201/202/203/204/205/206/207/208/209/210/211/212/213/214/215/216/217/218/219/220/221/222/223/224/225/226/227/228/229/230/231/232/233/234/235/236/237/238/239/240/241/242/243/244/245/246/247/248/249/250/251/252/253/254/255/256/257/258/259/260/261/262/263/264/265/266/267/268/269/270/271/272/273/274/275/276/277/278/279/280/281/282/283/284/285/286/287/288/289/290/291/292/293/294/295/296/297/298/299/300/301/302/303/304/305/306/307/308/309/310/311/312/313/314/315/316/317/318/319/320/321/322/323/324/325/326/327/328/329/330/331/332/333/334/335/336/337/338/339/340/341/342/343/344/345/346/347/348/349/350/351/352/353/354/355/356/357/358/359/360/361/362/363/364/365/366/367/368/369/370/371/372/373/374/375/376/377/378/379/380/381/382/383/384/385/386/387/388/389/390/391/392/393/394/395/396/397/398/399/400/401/402/403/404/405/406/407/408/409/410/411/412/413/414/415/416/417/418/419/420/421/422/423/424/425/426/427/428/429/430/431/432/433/434/435/436/437/438/439/440/441/442/443/444/445/446/447/448/449/450/451/452/453/454/455/456/457/458/459/460/461/462/463/464/465/466/467/468/469/470/471/472/473/474/475/476/477/478/479/480/481/482/483/484/485/486/487/488/489/490/491/492/493/494/495/496/497/498/499/500/501/502/503/504/505/506/507/508/509/510/511/512/513/514/515/516/517/518/519/520/521/522/523/524/525/526/527/528/529/530/531/532/533/534/535/536/537/538/539/540/541/542/543/544/545/546/547/548/549/550/551/552/553/554/555/556/557/558/559/560/561/562/563/564/565/566/567/568/569/570/571/572/573/574/575/576/577/578/579/580/581/582/583/584/585/586/587/588/589/590/591/592/593/594/595/596/597/598/599/600/601/602/603/604/605/606/607/608/609/610/611/612/613/614/615/616/617/618/619/620/621/622/623/624/625/626/627/628/629/630/631/632/633/634/635/636/637/638/639/640/641/642/643/644/645/646/647/648/649/650/651/652/653/654/655/656/657/658/659/660/661/662/663/664/665/666/667/668/669/670/671/672/673/674/675/676/677/678/679/680/681/682/683/684/685/686/687/688/689/690/691/692/693/694/695/696/697/698/699/700/701/702/703/704/705/706/707/708/709/710/711/712/713/714/715/716/717/718/719/720/721/722/723/724/725/726/727/728/729/730/731/732/733/734/735/736/737/738/739/740/741/742/743/744/745/746/747/748/749/750/751/752/753/754/755/756/757/758/759/760/761/762/763/764/765/766/767/768/769/770/771/772/773/774/775/776/777/778/779/780/781/782/783/784/785/786/787/788/789/790/791/792/793/794/795/796/797/798/799/800/801/802/803/804/805/806/807/808/809/810/811/812/813/814/815/816/817/818/819/820/821/822/823/824/825/826/827/828/829/830/831/832/833/834/835/836/837/838/839/840/841/842/843/844/845/846/847/848/849/850/851/852/853/854/855/856/857/858/859/860/861/862/863/864/865/866/867/868/869/870/871/872/873/874/875/876/877/878/879/880/881/882/883/884/885/886/887/888/889/890/891/892/893/894/895/896/897/898/899/900/901/902/903/904/905/906/907/908/909/910/911/912/913/914/915/916/917/918/919/920/921/922/923/924/925/926/927/928/929/930/931/932/933/934/935/936/937/938/939/940/941/942/943/944/945/946/947/948/949/950/951/952/953/954/955/956/957/958/959/960/961/962/963/964/965/966/967/968/969/970/971/972/973/974/975/976/977/978/979/980/981/982/983/984/985/986/987/988/989/990/991/992/993/994/995/996/997/998/999/1000/1001/1002/1003/1004/1005/1006/1007/1008/1009/1010/1011/1012/1013/1014/1015/1016/1017/1018/1019/1020/1021/1022/1023/1024/1025/1026/1027/1028/1029/1030/1031/1032/1033/1034/1035/1036/1037/1038/1039/1040/1041/1042/1043/1044/1045/1046/1047/1048/1049/1050/1051/1052/1053/1054/1055/1056/1057/1058/1059/1060/1061/1062/1063/1064/1065/1066/1067/1068/1069/1070/1071/1072/1073/1074/1075/1076/1077/1078/1079/1080/1081/1082/1083/1084/1085/1086/1087/1088/1089/1090/1091/1092/1093/1094/1095/1096/1097/1098/1099/1100/1101/1102/1103/1104/1105/1106/1107/1108/1109/1110/1111/1112/1113/1114/1115/1116/1117/1118/1119/1120/1121/1122/1123/1124/1125/1126/1127/1128/1129/1130/1131/1132/1133/1134/1135/1136/1137/1138/1139/1140/1141/1142/1143/1144/1145/1146/1147/1148/1149/1150/1151/1152/1153/1154/1155/1156/1157/1158/1159/1160/1161/1162/1163/1164/1165/1166/1167/1168/1169/1170/1171/1172/1173/1174/1175/1176/1177/1178/1179/1180/1181/1182/1183/1184/1185/1186/1187/1188/1189/1190/1191/1192/1193/1194/1195/1196/1197/1198/1199/1200/1201/1202/1203/1204/1205/1206/1207/1208/1209/1210/1211/1212/1213/1214/1215/1216/1217/1218/1219/1220/1221/12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XX angiodysplasia, peptic ulcers, inflammatory skin conditions.

XX **Sequence** 8 AA:

Query Match 36.4% Score 41 DB 22 Length 8;  
Best Local Similarity 100.0% Pred. No. 9, 4e+05;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 KRR 5  
II  
RR 3 KRR 6

# RESULT 12

AA007125  
ID AA007125 standard; Peptide: 8 AA.

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CC ordered hydrophobic interactions and have multiple attachment sites near  
 CC to the dye chromophore for ease of forming linearized polymers. The  
 CC presence of rigid and extended chromophore backbones enhances their  
 CC fluorescence quantum yield and extends their maximum absorption beyond  
 CC 400 nm. Conjugation of biomolecules is readily achievable. The present  
 CC sequence represents the amino acid sequence of neurotensin analogue, used  
 CC in the method of the invention.

XX  
 XX  
 XX Sequence 8 AA:  
 Query Match 46.4%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10  
 I I I  
 Db 1 KPRR 4

RESULT 14  
 AAB73426  
 ID AAB73426 standard: peptide; 8 AA.  
 XX  
 XX AAB73426

XX 25-JUN-2001 (first entry)  
 XX  
 XX Neurotensin analogue peptide; SEQ ID NO:7.

XX Neurotensin analogue; bioconjugate; bis-indocyanine dye;  
 KW hydrophilic; optical diagnostic imaging; tumour detection; cancer;  
 KW endoscopy; coronary angiography; atherosclerotic plaque; blood clot.  
 XX  
 XX Synthetic.

XX  
 XX Key Location/Qualifiers  
 FI Misc difference 1 /note= "D form residue"

XX US6190641-B1.  
 XX DE-FEB-2001

XX JP-JAN-2000 2000US 0484322  
 XX JP-JAN-2000 2000US 0484322

XX (M/W) MALLINCKRODT INC.  
 XX Achilleto S. Rajagopalan R. Borshaw RB, Bagaj JE;  
 XX WPI: 2001-26428/29.

XX Composition containing bis-indocyanine dye and carrier, useful in  
 FI diagnosis and therapy, e.g. of tumours, with the dye resistant to  
 FI aqueous solution.

XX Example 9, Column 13; 15pp; English.

XX The invention relates to compositions comprising a hydrophilic  
 CC bis-indocyanine dye with a heterocyclic group in the polymethine chain,  
 CC and a pharmaceutically acceptable carrier or excipient. The invention  
 CC also relates to diagnostic and therapeutic methods that involve  
 CC administering the bis-indocyanine dye compositions to a human; and  
 CC a method for making compositions of the invention by conjugating dyes  
 CC to peptides or biomolecules by solid phase synthesis. The bis-indocyanine  
 CC dye compositions are useful for optical tomographic imaging of organs;  
 CC monitoring organ function; coronary angiography; fluorescent endoscopy;  
 CC detection, imaging and therapy (photodynamic or localised) of tumours;  
 CC laser-guided surgery (particularly for detecting microvascularities during  
 CC laparoscopy); and photocoagulation and solid tumour metastases during  
 CC partial application in diagnosis of atherosclerotic plaques and blood  
 CC clots. Also, measuring the pattern of blood clearance of a conjugate

CC of the invention can be used for diagnosis of tumours and other diseases.  
 CC The bis-indocyanine dyes are designed not to aggregate in solution  
 CC (by preventing intra- and inter-molecular hydrophobic interactions);  
 CC to have many attachment sites near to the chromophore for formation of  
 CC a dendrimer; to allow easy conjugation to biomolecules; and to have a  
 CC rigid and extended chromophore backbone that enhances the fluorescent  
 CC quantum yield and extends the absorbance maximum to beyond 600 nm.  
 CC Sequences AAB73426 represent synthetic peptide used in an  
 CC exemplification to illustrate the use of bis-indocyanine dyes of the  
 CC invention to prepare bioconjugates. The present sequence represents a  
 CC neurotensin analogue peptide.

XX Sequence 8 AA:  
 Query Match 46.4%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. NO. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPRR 10  
 I I I  
 Db 1 KPRR 4

RESULT 15  
 AAB73426  
 ID AAB73426 standard: peptide; 8 AA.  
 XX  
 XX AAB73426

XX 25-JUN-2001 (first entry)  
 XX  
 XX Neurotensin analogue peptide; SEQ ID NO:7.

XX Neurotensin analogue; bioconjugate; bis-indocyanine dye;  
 KW hydrophilic; optical diagnostic imaging; tumour detection; cancer;  
 KW endoscopy; coronary angiography; atherosclerotic plaque; blood clot.  
 XX  
 XX Synthetic.

XX  
 XX Key Location/Qualifiers  
 FI Misc difference 1 /note= "D form residue"

XX US6190641-B1.  
 XX DE-FEB-2001

XX JP-JAN-2000 2000US 0484322  
 XX JP-JAN-2000 2000US 0484322

XX (M/W) MALLINCKRODT INC.  
 XX Achilleto S. Rajagopalan R. Borshaw RB, Bagaj JE;  
 XX WPI: 2001-26428/29.

XX Novel indocyanine dyes that absorb and emit light in near infrared  
 FI region of electromagnetic spectrum, useful for imaging, diagnosis and  
 FI therapy of various diseased states -

XX Example 9; Column 14; 15pp; English.

XX The invention relates to compositions comprising a hydrophilic  
 CC bis-indocyanine dye with a heterocyclic group in the polymethine chain,  
 CC and a pharmaceutically acceptable carrier or excipient. The invention  
 CC also relates to diagnostic and therapeutic methods that involve  
 CC administering the bis-indocyanine dye compositions to a human; and  
 CC a method for making compositions of the invention by conjugating dyes  
 CC to peptides or biomolecules by solid phase synthesis. The bis-indocyanine  
 CC dye compositions are useful for optical tomographic imaging of organs;  
 CC monitoring organ function; coronary angiography; fluorescent endoscopy;  
 CC detection, imaging and therapy (photodynamic or localised) of tumours;



laser assisted surgery (particularly for detecting micrometastases during laparoscopy); and photoacoustic and sonotomographic methods. A particular application is diagnosis of atherosclerotic plaques and blood clots. Also, measuring the pattern of blood circulation of a composition of the invention can be used for diagnosis of tumours and other diseases. The bis-indocyanine dyes are designed not to aggregate in solution (by preventing intra- and inter-molecular hydrophobic interactions) to have many attachment sites available to the dye, thereby for formation of a dendrimer; to allow easy conjugation to an antibody, cell, and to become rigid and extended chromophore backbone that enhances the fluorescence quantum yield and extends the absorption maximum to beyond 800 nm. Sequences AA97427-AA97442 represent synthetic peptides used in an extension to illustrate the use of bis and tetra-cyanine dyes of the invention to prepare bioconjugates; the present sequence represents a neurotensin analogue peptide.

Query Match: 36.4% Score 4: DB 22; Length 8;  
 Best Local Similarity: 100.0%; Prod. No. 9.3e+05;  
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 7 KPRR 10  
 II  
 DL 1 KPRR 4

RESIDUE 12  
 AA97427 standard: peptide: 8 AA.  
 XX  
 AC AA97437;  
 XX  
 ZF APR 2001 (first entry)  
 XX  
 DE Neurotensin analogue peptide SEQ ID NO:7.  
 XX  
 KW Optical Modality: cyanine dye; imaging; diagnosis; detection; tumour;  
 KW optical diagnostic imaging; therapy; cytostatic; blood clot;  
 KW atherosclerotic plaque; photodynamic therapy; LACS; micrometastasis;  
 KW laser assisted guided surgery.  
 XX  
 CS Synthesis.  
 XX  
 FH Key location/qualifiers  
 FI Miss difference 1 /note "1-form residue"  
 FT  
 XX US6180095-B1.  
 XX  
 PD 10 JAN 2001.  
 XX  
 PF 18 JAN 2001; 2000US-0484418.  
 XX  
 PK 18 JAN 2001; 2000US-0484418.  
 XX  
 PA (PLCW ) MALLINCKRODT INC.  
 XX  
 PI Achileto S. Rajadopalai R. Borskow RB. Bugaj JE;  
 XX WPL: 2001 20.699/20.  
 XX  
 PT Composition useful for imaging, diagnosis and therapy of various  
 PT diseased states comprises cyanine dyes that absorb and emit light in  
 PI near infrared region of electromagnetic spectrum  
 XX  
 PS Example 9: Column 14: 15pp; English.  
 XX  
 CS The present invention describes a composition which comprises cyanine  
 CS dyes (I). (i) has cytostatic activity. (i) is useful for performing a  
 CS diagnostic or therapeutic procedure, e.g. for diagnosing atherosclerotic  
 CS plaques and blood clots, and for localised therapy, photodynamic therapy  
 CS and laser assisted guided surgery (LACS) for the detection of  
 CS micrometastases. (i) are also useful for imaging, diagnosis and therapy  
 CS of various diseased states, for optical diagnostic imaging and therapy,  
 CS in endoscopic applications for the detection of tumours and other  
 CS abnormalities, for photoacoustic tumour imaging, detection and therapy  
 CS and for sonotomographic tumour imaging, detection and therapy. (i)  
 CS prevent dye aggregation in solution predisposed to form dendrimers,  
 CS capable of absorbing or emitting beyond 800 nm, have good photophysical  
 CS properties, and have tissue-specific targeting capability. The present  
 CS sequence represents a peptide which is used in an example from the  
 CS present invention.  
 XX  
 SQ Sequence: 8 AA;  
 Query Match: 36.4% Score 4: DB 22; Length 8;  
 Best Local Similarity: 100.0%; Prod. No. 9.3e+05;  
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 7 KPRR 10  
 II  
 DL 1 KPRR 4



XX 7. Vasoactive intestinal peptide (VIP) fluorescence detection in human adenoma, esophagus,  
 KW gastrointestinal tract; bronchial tract; bladder; cervix; breast;  
 KW optical tomography; optical tomography  
 XX  
 XX Unidentified.  
 XX  
 XX BEL9917713-ALI.  
 XX  
 XX 19-06-2000.  
 XX  
 XX 09 APR-1999; 99E-101713.  
 XX  
 XX 09 APR-1999; 99E-101713.  
 XX  
 XX 09 APR-1999; 99E-101713.  
 XX  
 XX (DIAG ) INST DIAGNOSTIKFORSCHUNG GMBH.  
 XX  
 XX Göttsch K., Becker A., Schmidt W., Wiedenmann B., Hensenius C.,  
 XX Volker E., Endert K., Schneider-Mergener J.  
 XX WP1: 2001-000423/01.  
 XX  
 XX New conjugates of vasoactive intestinal peptide, somatostatin or  
 XX neurotensin peptides and polymethine dyes are used for e.g. in-vivo  
 XX fluorescence diagnosis of tumors and other diseased tissues.  
 XX  
 XX Claim 17: Page 17; 32pp; German.  
 XX  
 XX This invention describes novel conjugates (1) of vasoactive intestinal  
 XX peptide (VIP), somatostatin or neurotensin peptides and polymethine dyes.  
 XX The products of the invention can also be used for a diagnostic method  
 XX comprising administering (1) to a patient, either intravenously or to the  
 XX bronchi by inhalation or to the gastrointestinal tract, esophagus or  
 XX bladder by spraying and then washing out excess (1), and then performing  
 XX an endoscopic investigation by local excitation of fluorescence at an  
 XX excitation wavelength of 350-1200 nm and site-specific detection of the  
 XX fluorescence emitted by the dye. (1) are useful for in-vivo diagnosis of  
 XX tumors, other diseased tissues or adenomas by means of optical detection  
 XX procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or  
 XX inflammatory tissues by means of endoscopic procedures in the  
 XX gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or  
 XX means of optical fluorescence and/or absorption diagnosis of breast tumors by  
 XX the breast). The peptide component provides receptor-specific binding to  
 XX target tissues and the polymethine dye provides a fluorescence signal  
 XX that is detectable with high sensitivity.  
 XX  
 XX Sequence: 8 AA:  
 XX  
 XX Query Match: 46.4%; Score 4; Dh 22; Length: 8;  
 XX Best Local Similarity: 100.0%; Pred. No. 9; 30-05;  
 XX Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 XX  
 XX 09 7 KPRK 10  
 XX 111  
 XX 5 KPRK 8  
 XX  
 XX RESULT 21  
 XX AAB45683  
 XX ID: AAB45683 standard; Peptide: 8 AA.  
 XX  
 XX AAB45683:  
 XX  
 XX 09-MAR-2001 (first entry)  
 XX  
 XX Neurotensin peptide analog #17.  
 XX  
 XX Vasoactive intestinal peptide; somatostatin; neurotensin; diagnosis;  
 KW polymethine dye; fluorescence; detection; tumor; adenoma; esophagus;  
 KW gastrointestinal tract; bronchial tract; bladder; cervix; breast;  
 KW optical tomography; optical tomography  
 XX  
 XX Unidentified.  
 XX  
 XX BEL9917713-ALI.  
 XX  
 XX 19-06-2000.  
 XX

XX  
 XX BEL9917713-ALI.  
 XX  
 XX 19-06-2000.  
 XX  
 XX 09 APR-1999; 99E-101713.  
 XX  
 XX 09 APR-1999; 99E-101713.  
 XX  
 XX (DIAG ) INST DIAGNOSTIKFORSCHUNG GMBH.  
 XX  
 XX Göttsch K., Becker A., Schmidt W., Wiedenmann B., Hensenius C.,  
 XX Volker E., Endert K., Schneider-Mergener J.  
 XX WP1: 2001-000423/01.  
 XX  
 XX New conjugates of vasoactive intestinal peptide, somatostatin or  
 XX neurotensin peptides and polymethine dyes are used for e.g. in-vivo  
 XX fluorescence diagnosis of tumors and other diseased tissues.  
 XX  
 XX Claim 17: Page 17; 32pp; German.  
 XX  
 XX This invention describes novel conjugates (1) of vasoactive intestinal  
 XX peptide (VIP), somatostatin or neurotensin peptides and polymethine dyes.  
 XX The products of the invention can also be used for a diagnostic method  
 XX comprising administering (1) to a patient, either intravenously or to the  
 XX bronchi by inhalation or to the gastrointestinal tract, esophagus or  
 XX bladder by spraying and then washing out excess (1), and then performing  
 XX an endoscopic investigation by local excitation of fluorescence at an  
 XX excitation wavelength of 350-1200 nm and site-specific detection of the  
 XX fluorescence emitted by the dye. (1) are useful for in-vivo diagnosis of  
 XX tumors, other diseased tissues or adenomas by means of optical detection  
 XX procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or  
 XX inflammatory tissues by means of endoscopic procedures in the  
 XX gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or  
 XX means of optical fluorescence and/or absorption diagnosis of breast tumors by  
 XX the breast). The peptide component provides receptor-specific binding to  
 XX target tissues and the polymethine dye provides a fluorescence signal  
 XX that is detectable with high sensitivity.  
 XX  
 XX Sequence: 8 AA:  
 XX  
 XX Query Match: 46.4%; Score 4; Dh 22; Length: 8;  
 XX Best Local Similarity: 100.0%; Pred. No. 9; 30-05;  
 XX Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 XX  
 XX 09 7 KPRK 10  
 XX 111  
 XX 5 KPRK 4  
 XX  
 XX RESULT 22  
 XX AAB45684  
 XX ID: AAB45684 standard; Peptide: 8 AA.  
 XX  
 XX AAB45684:  
 XX  
 XX 09-MAR-2001 (first entry)  
 XX  
 XX Neurotensin peptide analog #17.  
 XX  
 XX Vasoactive intestinal peptide; somatostatin; neurotensin; diagnosis;  
 KW polymethine dye; fluorescence; detection; tumor; adenoma; esophagus;  
 KW gastrointestinal tract; bronchial tract; bladder; cervix; breast;  
 KW optical tomography; optical tomography  
 XX  
 XX Unidentified.  
 XX  
 XX BEL9917713-ALI.  
 XX  
 XX 19-06-2000.  
 XX

PF 09 Ark 1999, 99DE-101771.  
 PF 09 Ark 1999, 99DE-101771.  
 XX (GIAJ-) INST DIAGNOSTIKFORSCHUNG GMBH  
 XX  
 PF Licha K, Becker A, Sommer W, Wiedenmann B, Hensenius G,  
 PF Wolker-Engert R, Schneider-Mergener J  
 XX  
 PF WPI: 2001 000424/01.  
 XX  
 PF New conjugates of vasoactive intestinal peptide, somatostatin or  
 PF neurotensin peptides and polymethine dyes are used for e.g. in-vivo  
 PF fluorescence diagnosis of tumors and other diseased tissues.  
 XX  
 PF Claim 17, Page 17; 32pp; German.  
 XX  
 CC This invention describes novel conjugates (1) of vasoactive intestinal  
 CC peptide (VIP), somatostatin or neurotensin peptides and polymethine dyes.  
 CC The products of the invention can also be used for a diagnostic method  
 CC comprising administering (1) to a patient, either intravenously or to the  
 CC bronchi by inhalation or to the gastrointestinal tract, esophagus or  
 CC bladder by spraying and then washing out excess (1), and then performing  
 CC an endoscopic investigation by local excitation of fluorescence at an  
 CC excitation wavelength of 350-1200 nm and site-specific detection of the  
 CC fluorescence emitted by the dye. (1) are useful for in-vivo diagnosis of  
 CC tumors, other diseased tissues or adenomas by means of optical detection  
 CC procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or  
 CC inflammatory tissues by means of endoscopic procedures in the  
 CC gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or  
 CC for in-vivo fluorescence and/or absorption diagnosis of breast tumors by  
 CC means of optical mammography (transillumination or optical tomography of  
 CC the breast). The peptide component provides receptor-specific binding to  
 CC target tissues and the polymethine dye provides a fluorescence signal  
 CC that is detectable with high sensitivity.  
 XX  
 SQ Sequence: 8 AA:  
 Query Match: 36.4%; Score 4; PP 22; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9; 3e-05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KRRR 10  
 LD 1  
 1 KRRR 4  
 RESULT 24  
 AAR47067  
 CC AAR47066 standard; Peptide: 8 AA.  
 XX  
 AC AAR47067  
 XX  
 PF 09 Ark 2001 (first entry)  
 XX  
 CC Neurotensin; peptide analog #14.  
 XX  
 KW Vasoactive intestinal peptide; somatostatin; neurotensin; trans-Sar  
 KW polymethine dye; fluorescence; detection; in-vivo; endosomal; esophagus;  
 KW gastrointestinal tract; bronchial tract; bladder; cervix; breast;  
 KW optical mammography; optical tomography  
 XX  
 CS Randomized.  
 XX  
 PF LE1067713 A1.  
 XX  
 PF 09 Ark 1999, 99DE-101771.  
 XX  
 PF 09 Ark 1999, 99DE-101771.  
 XX  
 PF (GIAJ-) INST DIAGNOSTIKFORSCHUNG GMBH

XX  
 PF Licha K, Becker A, Sommer W, Wiedenmann B, Hensenius G,  
 PF Wolker-Engert R, Schneider-Mergener J  
 XX  
 PF WPI: 2001 000424/01.  
 XX  
 PF New conjugates of vasoactive intestinal peptide, somatostatin or  
 PF neurotensin peptides and polymethine dyes are used for e.g. in-vivo  
 PF fluorescence diagnosis of tumors and other diseased tissues.  
 XX  
 PF Claim 17, Page 17; 32pp; German.  
 XX  
 CC This invention describes novel conjugates (1) of vasoactive intestinal  
 CC peptide (VIP), somatostatin or neurotensin peptides and polymethine dyes.  
 CC The products of the invention can also be used for a diagnostic method  
 CC comprising administering (1) to a patient, either intravenously or to the  
 CC bronchi by inhalation or to the gastrointestinal tract, esophagus or  
 CC bladder by spraying and then washing out excess (1), and then performing  
 CC an endoscopic investigation by local excitation of fluorescence at an  
 CC excitation wavelength of 350-1200 nm and site-specific detection of the  
 CC fluorescence emitted by the dye. (1) are useful for in-vivo diagnosis of  
 CC tumors, other diseased tissues or adenomas by means of optical detection  
 CC procedures, in-vivo fluorescence diagnosis of tumors, tumor cells and/or  
 CC inflammatory tissues by means of endoscopic procedures in the  
 CC gastrointestinal tract, esophagus, bronchial tract, bladder or cervix or  
 CC for in-vivo fluorescence and/or absorption diagnosis of breast tumors by  
 CC means of optical mammography (transillumination or optical tomography of  
 CC the breast). The peptide component provides receptor-specific binding to  
 CC target tissues and the polymethine dye provides a fluorescence signal  
 CC that is detectable with high sensitivity.  
 XX  
 SQ Sequence: 8 AA:  
 Query Match: 36.4%; Score 4; DB 22; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9; 3e-05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KRRR 10  
 LD 1  
 1 KRRR 4  
 RESULT 24  
 AAR47067  
 CC AAR47066 standard; Peptide: 8 AA.  
 XX  
 AC AAR47067  
 XX  
 PF 09 Ark 2001 (first entry)  
 XX  
 CC Neurotensin; peptide sequence.  
 XX  
 KW Fluorescent; biocompatible; indocyanine; dye; therapy; endoscopic;  
 KW optical diagnosis; imaging; tumor; photoacoustic tumor imaging;  
 KW sonofluorescence; gastroscopy; neurotensin.  
 XX  
 CS Synthetic.  
 XX  
 PF Key: position/positions  
 PF Misc difference: 1  
 PF Note: "50-term res.dat"  
 XX  
 PF 156254319-B1.  
 XX  
 PF 24 030, 2001.  
 XX  
 PF 10 AAK 2000; 200005 0000170  
 XX  
 PF 10 AAK 2000; 200005 0001420  
 XX  
 PF 09 Ark 1999, 99DE-101771.  
 XX  
 PF (GIAJ-) INST DIAGNOSTIKFORSCHUNG GMBH

XX WH: 2001-056565/62.

XX In vivo or in vitro fluorescence is tested and by adding dye conjugates.

PT organic solvents to new indocyanine dye conjugates.

XX Example 7, Column 14: 14pp: endlish.

XX The invention relates to restoration of in vivo or in vitro fluorescence that involves adding biocompatible organic solvents to conjugates of indocyanine dyes. The dyes are of specific formula indicated in the specification. The method is useful for treating, diagnosing and therapy of various disease (particularly for of liver, hepatocellular carcinoma and therapy, in endoscopic applications for the detection of tumors and other abnormalities, for localized therapy, for endoscopic imaging, detection and therapy, and somifluorescence detection of tumors and other abnormalities, for localized therapy, photodynamic tumor imaging, detection and therapy, and somifluorescence tumor imaging, detection and therapy). The present sequence represents a neuropeptide analogue, which may be conjugated to dyes of the invention.

XX Sequence 8 AA:

Query Match 36.4% Score 4: DB 22: Length 8:

Best Local Similarity 100.0% Pred. No. 9.3e+05:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10

DE 1 KPRR 4

RESULT 25

AA097459

TO AA097459 standard; peptide: 8 AA

XX AA097459

XX AA097459

XX 18 AUG 2002 (first entry)

XX Synthesis: neuropeptide analogue peptide.

XX Cysteine dye bioconjugates; optical tomography; fluorescence endoscopy; atherosclerotic plaque; blood clot; laser assisted guided surgery; glioblastoma; starburst dendrites; tissue-specific; light emission; peptide-dye conjugate; light absorption; near infrared region; neuropeptide.

XX Synthetic.

XX Key Location/Qualifiers

FF Misc difference 1 /note: "D form residue"

XX US2002044909-A1

XX 18 APR 2002.

XX 23 MAY 2001: 2001US-069977.

XX 18 JAN 2000: 2000US 0484320.

XX (MOLW ) MAIL:KKR03 INC.

XX Achilleto SL, Rajagopalan R, Darshaw RB, Bugaj JE;

XX WPI: 2002-434599/46.

XX New cyanine dye bioconjugates, useful in performing diagnostic and therapeutic procedures including optical tomography and fluorescence endoscopy.

XX Example 9: Page 8: 11pp: Endlish.

XX The present invention relates to new cyanine dye bioconjugates. The bioconjugates of the invention are useful in performing diagnostic and therapeutic procedures including optical tomography and fluorescence endoscopy. The method is capable of diagnosing atherosclerotic plaques and blood clots and is useful in laser assisted guided surgery for the detection of microtumors. The molecules of the invention preserve the

XX or in vitro fluorescence. The method involves adding biocompatible organic solvents to conjugates of indocyanine dyes. The dyes are of a formula given in the specification. The dyes prevent aggregation in solution, are predisposed to form dendrites, absorb or emit beyond 600 nm, possess desirable photophysical properties, and show tissue specific targeting capabilities. The method is used for imaging, diagnosis and therapy of various disease (particularly for liver, hepatocellular carcinoma and therapy, in endoscopic applications for the detection of tumors and other abnormalities, for localized therapy, photodynamic tumor imaging, detection and therapy, and somifluorescence tumor imaging, detection and therapy). The present sequence represents a neuropeptide analogue, which may be conjugated to dyes of the invention.

XX Sequence 8 AA:

Query Match 36.4% Score 4: DB 22: Length 8:

Best Local Similarity 100.0% Pred. No. 9.3e+05:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 KPRR 10

DE 1 KPRR 4

RESULT 26

AA097459

TO AA097459 standard; peptide: 8 AA

XX AA097459

XX AA097459

XX 18 AUG 2002 (first entry)

XX Synthesis: neuropeptide analogue peptide.

XX Cysteine dye bioconjugates; optical tomography; fluorescence endoscopy; atherosclerotic plaque; blood clot; laser assisted guided surgery; glioblastoma; starburst dendrites; tissue-specific; light emission; peptide-dye conjugate; light absorption; near infrared region; neuropeptide.

XX Synthetic.

XX Key Location/Qualifiers

FF Misc difference 1 /note: "D form residue"

XX US2002044909-A1

XX 18 APR 2002.

XX 23 MAY 2001: 2001US-069977.

XX 18 JAN 2000: 2000US 0484320.

XX (MOLW ) MAIL:KKR03 INC.

XX Achilleto SL, Rajagopalan R, Darshaw RB, Bugaj JE;

XX WPI: 2002-434599/46.

XX New cyanine dye bioconjugates, useful in performing diagnostic and therapeutic procedures including optical tomography and fluorescence endoscopy.

XX Example 9: Page 8: 11pp: Endlish.

XX The present invention relates to new cyanine dye bioconjugates. The bioconjugates of the invention are useful in performing diagnostic and therapeutic procedures including optical tomography and fluorescence endoscopy. The method is capable of diagnosing atherosclerotic plaques and blood clots and is useful in laser assisted guided surgery for the detection of microtumors. The molecules of the invention preserve the

XX fluorescence efficiency of the dye molecules, do not associate in  
 CC solution, form starburst dendrimers, are capable of absorbing or emitting  
 CC light in the near infrared region and can be rendered tissue specific.  
 CC The present amino acid sequence represents a synthetic neurotensin and the  
 CC peptide that was used in the methods of the invention for synthesis of  
 CC peptide-dye conjugates.

SC Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRP 10

DB 11

SC 1 KPRP 4

RESULT 27

AAK71754

ID AAK71754 standard; peptide: 9 AA.

XX AC AAK71754

XX AC AAK71754

XX 25-MAR-2003 (updated)

XX 15-MAY-1995 (first entry)

XX NE

XX Neurotensin receptor fluorescent probe.

XX Neurotensin N1 receptor; probe: fluorescent.

XX SC

XX Synthetic.

XX FH

XX Key Location/Qualifiers

XX Mod:filled site

XX Note "N-acylated with fluorescent label. See CC  
 CC below. Also this amino acid can be  
 CC substituted by Lys or Orn."

XX XX

XX E666664 A2.

XX 20-JUL-1994.

XX 27-DEC-1993 94EP-0403185.

XX 30-DEC-1992 92CA-2066453.

XX (UVM) UNIV MICHIGAN.

XX Beaudet A. Faure M. Gaudreau P.

XX WPL 1994-224757/28.

XX New fluorescent markers for neurotensin receptors - useful for in

XX vitro labelling of neurotensin receptors on cell surface and to

XX isolate neurotensin-receptor expressing cells

XX Claim 2; Page 5; 19pp; English.

XX The invention concerns highly sensitive fluorescent probes which

XX allow for rapid and precise characterisation of neurotensin

XX receptor binding properties on whole cells. The probes are of

XX formula R1-C(-X)-R in which R1 is a fluorophore chosen from

XX fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen

XX or sulphur; and R is a neurotensin-type polypeptide sequence

XX containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or

XX Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745

XX AAK71772. The R1-CX-acyl group is linked to the peptide via the

XX N-terminus in position 1. The N-terminal amino acid may also be

XX subd. by Lys or Orn.

XX The present sequence represents one of the claimed peptide

XX sequences for R.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SC Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRP 10

DB 11

SC 1 KPRP 4

RESULT 27

AAK71754

ID AAK71754 standard; peptide: 9 AA.

XX SC Sequence 9 AA:

Query Match 36.4% Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRP 10

DB 11

SC 2 KPRP 5

RESULT 28

AAK71754

ID AAK71754 standard; peptide: 9 AA.

XX AC AAK71754

XX AC AAK71754

XX 25-MAR-2003 (updated)

XX 15-MAY-1995 (first entry)

XX NE

XX Neurotensin receptor fluorescent probe.

XX Neurotensin N1 receptor; probe: fluorescent.

XX SC

XX Synthetic.

XX FH

XX Key Location/Qualifiers

XX Mod:filled site

XX Note "N-acylated with fluorescent label. See CC  
 CC below. Also this amino acid can be  
 CC substituted by Lys or Orn."

XX XX

XX E666664 A2.

XX 20-JUL-1994.

XX 27-DEC-1993 94EP-0403185.

XX 30-DEC-1992 92CA-2066453.

XX (UVM) UNIV MICHIGAN.

XX Beaudet A. Faure M. Gaudreau P.

XX WPL 1994-224757/28.

XX New fluorescent markers for neurotensin receptors - useful for in

XX vitro labelling of neurotensin receptors on cell surface and to

XX isolate neurotensin-receptor expressing cells

XX Claim 2; Page 5; 19pp; English.

XX The invention concerns highly sensitive fluorescent probes which

XX allow for rapid and precise characterisation of neurotensin

XX receptor binding properties on whole cells. The probes are of

XX formula R1-C(-X)-R in which R1 is a fluorophore chosen from

XX fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen

XX or sulphur; and R is a neurotensin-type polypeptide sequence

XX containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or

XX Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745

XX AAK71772. The R1-CX-acyl group is linked to the peptide via the

XX N-terminus in position 1. The N-terminal amino acid may also be

XX subd. by Lys or Orn.

XX The present sequence represents one of the claimed peptide

XX sequences for R.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SC Sequence 9 AA:

Query Match 36.4% Score 4; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRP 10

DB 11

SC 2 KPRP 5

RESULT 28

AAK71754

ID AAK71754 standard; peptide: 9 AA.

XX AC AAK71754

XX AC AAK71754

XX 25-MAR-2003 (updated)

XX 15-MAY-1995 (first entry)

XX NE

XX SC Sequence 9 AA:

Query Match 36.4% Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRP 10

DB 11

SC 2 KPRP 5

RESULT 28

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XX AC AAK71754

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XX Neurotensin N1 receptor; probe: fluorescent.

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XX Synthetic.

XX FH

XX Key Location/Qualifiers

XX Mod:filled site

XX Note "N-acylated with fluorescent label. See CC  
 CC below. Also this amino acid can be  
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XX E666664 A2.

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XX 27-DEC-1993 94EP-0403185.

XX 30-DEC-1992 92CA-2066453.

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XX Claim 2; Page 5; 19pp; English.

XX The invention concerns highly sensitive fluorescent probes which

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XX receptor binding properties on whole cells. The probes are of

XX formula R1-C(-X)-R in which R1 is a fluorophore chosen from

XX fluorescein, rhodamine, blue fluorescent and Texas red; X is oxygen

XX or sulphur; and R is a neurotensin-type polypeptide sequence

XX containing the core sequence Arg-Arg-Pro-Tyr-Ile-Leu or

XX Arg-Arg-Pro-Tyr-Ile-Leu. Specific sequences are given in AAK71745

XX AAK71772. The R1-CX-acyl group is linked to the peptide via the

XX N-terminus in position 1. The N-terminal amino acid may also be

XX subd. by Lys or Orn.

XX The present sequence represents one of the claimed peptide

XX sequences for R.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SC Sequence 9 AA:

Query Match 36.4% Score 4; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 KPRP 10

DB 11

SC 2 KPRP 5

RESULT 28

AAK71754

ID AAK71754 standard; peptide: 9 AA.

XX AC AAK71754

XX AC AAK71754

XX 25-MAR-2003 (updated)

XX 15-MAY-1995 (first entry)

XX NE

QY 2 KRR 12  
 DE 111  
 2 KRR 5

REF: 11 29  
 AAB39962  
 ID AAB39962 standard; peptide; 9 AA.  
 XX  
 AC AAB39962  
 XX  
 DE 25 MAR 2003 (updated)  
 DE 09 SEP 1996 (first entry)

XX Factor VIII antigenic peptide (residue 1052-185-Pae2094,  
 XX Factor VIII modification inhibitor; activity, blood clot; antibody;  
 KW von Willebrand factor; immune disorder;  
 XX Synthesis.  
 XX  
 XX W0960252-A2.  
 XX  
 DE 01 FEB 1996.  
 DE 14 JUL 1995 95WO-HR00048.  
 XX  
 DE 14 JUL 1994 94BS-0303566.  
 XX  
 DE (Title) The EX-ROCKE BR161,006  
 XX  
 DE In combination with M, Leach M;  
 DE W01, 1996-1-5861/11.  
 XX  
 DE Factor VIII antigenic polypeptide (fragments and epitopes) also  
 DE inhibitors of factor VIII and antibodies; useful for e.g.  
 DE preventing and treating immune disorders involving inhibition of  
 DE factor VIII binding  
 XX  
 DE Claim 14, Page 34; 4pp; French.  
 XX  
 DE Proposes AAB39962 are derived from the factor VIII protein, residue 1200  
 DE a modified Factor VIII in which residues 1222-1223 are replaced by AVAL607  
 DE Lys-Asp-Ileu-Val and Asp214 by Tyr-Val and Leu215 by Arg-methylated factor  
 DE VIII and derived peptides can be used to block or inhibit activity of  
 DE inhibitors of factor VIII binding to factor VIII and antibodies  
 DE antibodies, thus preventing or treating immune disorders  
 DE (Updated on 25-MAR-2003 to reflect AAB39962)  
 XX  
 DE Sequence 9 AA.  
 DE  
 DE Query Match 46.4%; Score 4; DB 22; Length 9;  
 DE Best Local Similarity 100.0%; Pred. NO 9.3e-05;  
 DE Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 DE  
 DE QY 1 AROK 4  
 DE 111  
 DE 5 AROK 8

REF: 11 4  
 AAB39924  
 ID AAB39924 standard; peptide; 9 AA.  
 XX  
 AC AAB39924  
 XX  
 DE 24 JAN 2002 (first entry)

DE Human peptide #1489 encoded by a SNP in human gene  
 XX immunosuppressive, immunostimulatory, anti-inflammatory, apoptosis

KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiogenesis; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; cytokine; interferon;  
 KW interleukin; G-protein; coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.  
 XX  
 XX Homo sapiens.  
 XX  
 XX W0200147944 A2.  
 XX  
 DE 05-JUL-2001.  
 XX  
 DE 28-DEC-2000; 2000WO-0535498.  
 XX  
 DE 28-DEC-1999; 94ES-0174419.  
 PR 27-DEC-2000; 2000US 0174419.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 XX Shimkels EA, Leach M;  
 XX W01, 2001-465215/50.  
 XX  
 DE Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 DE oncogenes and histones, useful for diagnosing and treating, e.g.  
 DE cancer, autoimmune diseases and infections.  
 XX  
 DE (Title) Page 3994; 4.4pp; English.  
 XX  
 DE The present invention relates to oligonucleotides (see AAL2679; AAL34659)  
 DE encoding polymorphic variants of proteins related to amylases, amyloid  
 DE proteins, angiogenic, apoptosis related proteins, cadherin, cyclin,  
 DE polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 DE complement related proteins, cytochromes, cytokines, cytokines,  
 DE interferons, interleukins, G-protein coupled receptors and thioesterases.  
 DE The present sequence is a peptide encoded by one such oligonucleotide.  
 DE The oligonucleotides and the peptides encoded by them may be used in the  
 DE prevention, diagnosis and treatment of diseases associated with  
 DE inappropriate expression of the proteins listed above. Disorders that may  
 DE be prevented, diagnosed and/or treated include multifactorial diseases  
 DE with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 DE arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 DE and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 DE brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 DE system and an infection of pathogenic organisms.  
 XX  
 DE Sequence 9 AA.  
 DE  
 DE Query Match 46.4%; Score 4; DB 22; Length 9;  
 DE Best Local Similarity 100.0%; Pred. NO 9.3e-05;  
 DE Matches 4; Conservative 0; Mismatches 0;  
 DE  
 DE QY 6 PRAS 11  
 DE 11  
 DE 1 PRAS 4

REF: 11  
 AAB45674  
 ID AAB45674 standard; peptide; 9 AA.  
 XX  
 AC AAB45674  
 XX  
 DE 09-MAR-2001 (first entry)

DE Neurotensin peptide analog #7.  
 XX  
 DE Vasoactive intestinal peptide; somatostatin; neurotensin; diagnosis;  
 KW polychelone dye; fluorescence; detection; tumor; adenoma; esophagus;  
 KW gastrointestinal tract; bronchial tract; bladder; cervix; breast;  
 KW optical mammography; optical tomography.











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ID      1111
        6 RQT 5

RESULT 4:
ABR26636
ID      ABR26636 Standard; Peptide: 9 AA.
AC      ABR26636;
XX
XX
XX      19 MAY-2003 (first entry)
XX
XX      Human cancer-related protein 186PIH9 HLA peptide #1077.
XX
XX      Human; cytostatic; vaccine; cancer; immune response; HLA;
XX      human leukocyte antigen.
XX
XX      Homo sapiens.
XX
XX      W020283921 A2.
XX
XX      24 OCT-2002.
XX
XX      10-APR-2002; 2002W0-US11654.
XX
XX      10-APR-2001; 2001US-28273P.
XX
XX      10-APR-2001; 2001US-283112P.
XX
XX      25-APR-2001; 2001US-28653CP.
XX
XX      (AGEN-) AGENSYS INC.
XX
XX      Jakobovits A., Chailita-Eid PM, Paris M, Ge W, Hubert RS;
XX      Morrison K., Morrison RK., Raitano AB;
XX
XX      WPI; 2003-075555/07.
XX
XX      New composition comprising a substance that modulates the structure of
XX      proteins and polynucleotides, useful for therapeutic, prognostic and
XX      diagnostic reagents for eliciting cellular or humoral immune response
XX      in cancer patients.
XX
XX      Claim 13; Page 397; 1021pp; English.
XX
XX      The present invention relates to novel human cancer-related genes and
XX      proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX      proteins are useful for eliciting a humoral or cellular immune response.
XX      The genes are useful as probes and primers for the amplification and/or
XX      detection of genes, mRNAs or their fragments, as reagents for the
XX      diagnosis and/or prognosis of cancer, as coding sequences capable of
XX      directing the expression of the protein, as tools for modulation or
XX      inhibiting the expression of genes and/or translation of transcripts, and
XX      as therapeutic agents. The proteins and peptides are useful as
XX      therapeutic, prognostic and diagnostic reagents for cancer. The present
XX      sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX      from the invention.
XX
XX      Sequence 9 AA:
XX
XX      Query Match 36.4%; Score 4; DB 24; Length 9;
XX      Best Local Similarity 100.0%; Pred. No. 9, 3e-05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      2 RQT 5
XX      111
XX      2 RQT 5
XX
XX
XX
XX
XX      RESULT 42
XX      ABR26636
XX      ID      ABR26636 standard; Peptide: 9 AA.
XX
XX      AC      ABR26636;
XX
XX      19 MAY-2003 (first entry)
XX
XX      Human cancer-related protein 186PIH9 HLA peptide #1095.
XX
XX      Human; cytostatic; vaccine; cancer; immune response; HLA;
XX      human leukocyte antigen.
XX
XX      Homo sapiens.
XX
XX      W020283921 A2.
XX
XX
XX
XX
XX      RESULT 4:
XX      ABR26636
XX      ID      ABR26636 Standard; Peptide: 9 AA.
XX
XX      AC      ABR26636;
XX
XX
XX
XX
XX      1111
XX      6 RQT 5

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XX 24 OCT-2002;
XX
XX 10 APR-2001; 2002W0-US11654
XX
XX 10 APR-2001; 2001US-282749F
XX
XX 10 APR-2001; 2001US-283112F
XX
XX 25 APR-2001; 2001US-285540F
XX
XX (ADEN-) AGENSYS INC.
XX
XX Jakubovits A., Challinor RD PM, Paris M, Ge W, Hubert RS,
XX Morrison K., Morrison RK., Kaitano AB;
XX WPI: 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients
XX
XX Claim 1: Page 397; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABZ78175-ABZ78181). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulation or
XX inhibiting the expression of the protein, as tools for modulation or
XX as therapeutic agents; the proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
XX Query Match 46.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.36+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 ROKT 5
XX 1 1
XX 1 ROKT 4
XX
XX RESULT 44
XX AAR71757
XX ID AAR71757 standard; peptide: 10 AA.
XX
XX AC AAR71757;
XX
XX DT 25-MAR-2003 (updated)
XX
XX ET 15-MAY-1995 (first entry)
XX
XX LE Neofolium receptor fluorescent probe.
XX
XX KW Neofolium; NP; receptor; probe; fluorescent.
XX
XX OS Synthetic.
XX
XX FH Key location/Qualifiers
XX FT Modified-site ;
XX F1 /note "N-acetylated with fluorescent label. See CC
XX FT below. Also this amino acid can be
XX FT substituted by lys or orn."
XX
XX PN EP56804-A2
XX
XX PD 20-JUL-1994.
XX
XX PF 27-DEC-1993; 93EP 0403185.
XX
XX PR 30-DEC-1992; 92CA 2086453.
XX
XX PA (UYMC-) UNIV MGNILL.
XX
XX PL Beaudet A., Faure M., Gaudreau P;
XX
XX WPI: 1994-22757/28.
XX
XX New 11 different markers for angiotensin receptors - useful for in

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XX
XX 24 OCT-2002;
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XX 10 APR-2001; 2002W0-US11654
XX
XX 10 APR-2001; 2001US-282749F
XX
XX 10 APR-2001; 2001US-283112F
XX
XX 25 APR-2001; 2001US-285540F
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XX Morrison K., Morrison RK., Kaitano AB;
XX WPI: 2003-075555/07.
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XX diagnostic reagents for eliciting cellular or humoral immune response
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XX proteins (ABZ78120-ABZ78168 and ABZ78175-ABZ78181). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulation or
XX inhibiting the expression of the protein, as tools for modulation or
XX as therapeutic agents; the proteins and peptides are useful as
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XX from the invention.
XX
XX Query Match 46.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.36+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 ROKT 5
XX 1 1
XX 1 ROKT 4
XX
XX RESULT 44
XX AAR71757
XX ID AAR71757 standard; peptide: 10 AA.
XX
XX AC AAR71757;
XX
XX DT 25-MAR-2003 (updated)
XX
XX ET 15-MAY-1995 (first entry)
XX
XX LE Neofolium receptor fluorescent probe.
XX
XX KW Neofolium; NP; receptor; probe; fluorescent.
XX
XX OS Synthetic.
XX
XX FH Key location/Qualifiers
XX FT Modified-site ;
XX F1 /note "N-acetylated with fluorescent label. See CC
XX FT below. Also this amino acid can be
XX FT substituted by lys or orn."
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XX PF 27-DEC-1993; 93EP 0403185.
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XX PR 30-DEC-1992; 92CA 2086453.
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XX PA (UYMC-) UNIV MGNILL.
XX
XX PL Beaudet A., Faure M., Gaudreau P;
XX
XX WPI: 1994-22757/28.
XX
XX New 11 different markers for angiotensin receptors - useful for in

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specific complementary peptides to proteins encoded by genes of plant genomes. The present sequence is the 5th peptide from Arabidopsis thaliana. The peptides of the present invention are used in an assay to identify a peptide, especially a peptide, peptide or heptapeptide. The peptides are also useful for tools for agricultural research and development.

Supply: 10 A;

Query Match	Score	Length
Consistent Similarity	100.0%	Prod No. 40000
Patterns	41	Conservative for Molecular modeling

1 APR 4  
111  
2 APR 8

15

PA: 3545

Dr. J. Edgar Hoover

1. ☒ 2. ☒ 3. ☒ 4. ☒ 5. ☒ 6. ☒ 7. ☒ 8. ☒ 9. ☒ 10. ☒ 11. ☒ 12. ☒ 13. ☒ 14. ☒ 15. ☒ 16. ☒ 17. ☒ 18. ☒ 19. ☒ 20. ☒ 21. ☒ 22. ☒ 23. ☒ 24. ☒ 25. ☒ 26. ☒ 27. ☒ 28. ☒ 29. ☒ 30. ☒ 31. ☒ 32. ☒ 33. ☒ 34. ☒ 35. ☒ 36. ☒ 37. ☒ 38. ☒ 39. ☒ 40. ☒ 41. ☒ 42. ☒ 43. ☒ 44. ☒ 45. ☒ 46. ☒ 47. ☒ 48. ☒ 49. ☒ 50. ☒ 51. ☒ 52. ☒ 53. ☒ 54. ☒ 55. ☒ 56. ☒ 57. ☒ 58. ☒ 59. ☒ 60. ☒ 61. ☒ 62. ☒ 63. ☒ 64. ☒ 65. ☒ 66. ☒ 67. ☒ 68. ☒ 69. ☒ 70. ☒ 71. ☒ 72. ☒ 73. ☒ 74. ☒ 75. ☒ 76. ☒ 77. ☒ 78. ☒ 79. ☒ 80. ☒ 81. ☒ 82. ☒ 83. ☒ 84. ☒ 85. ☒ 86. ☒ 87. ☒ 88. ☒ 89. ☒ 90. ☒ 91. ☒ 92. ☒ 93. ☒ 94. ☒ 95. ☒ 96. ☒ 97. ☒ 98. ☒ 99. ☒ 100. ☒

Admission






































3154-4511 (test entry)

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Adaptation to the environment is a key factor in the survival of a species. The ability of a species to adapt to its environment is a key factor in the survival of a species. The ability of a species to adapt to its environment is a key factor in the survival of a species.

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**THE UNIVERSITY OF CHICAGO**

2017-2018

**A**

### Summary

$$M^2 = \frac{1}{2} \left( \frac{1}{\lambda^2} + \frac{1}{\mu^2} \right) = \frac{1}{2} \left( \frac{1}{\lambda^2} + \frac{1}{\mu^2} \right) = \frac{1}{2} \left( \frac{1}{\lambda^2} + \frac{1}{\mu^2} \right)$$

2017年12月

EX-111-2001

2000

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EF 1A-48S 2016 209090-0001; 78.

THE UNIVERSITY OF CHICAGO

$$131.41 = 19.46 + 99.93 = (11) \cdot 9.0849$$

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**THE UNIVERSITY OF CHICAGO**

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$$x = 1$$
[illegible]

2000

P1 A set of peptide standards for amino acid analysis, independent of  
P2 chromatographic results compared with those reported by others.  
P3 Chromatographic results compared with those reported by others.  
P4 Encoded TV codes of plant species.

Figure 2: Example of a 2D plot of the function  $f(x, y)$  and its level sets.

xx The present invention relates to a set of peptide fragments consisting of specific complementary peptides to proteins encoded by genes of plant genomes. The present sequence is one of the peptides of the Arabidopsis thaliana. The peptides of the present invention are useful in at least one of the following applications: (a) to identify a peptide, especially a peptide peptide, or a polypeptide, the peptides are also useful for tools for identifying a resistant and the development.

Suppose  $\mathbf{A} \in \mathbb{A}^n$

Query Match: 36.48; Score 4; 100.00; 100.00  
 Best local Similarity 100.00; Pred No. 4; 0.00  
 Matches 4; Conservative 0; Mismatch % 0; Pctags 0; 0.00

$$A^2 - A = A(A - I)$$

Survey completed: September 10, 2004 (10/10/04)  
 Date: 4/7/1997



OK protein - protein search, using sw model  
Run on: September 30, 2003, 11:02:01, Search time 41.08s, Sequences (without duplicates) 42,479 Million cells up data s/sec  
Title: US-09-787-443-14  
Perfect score: 11 AAKTKKSKL-11  
Scoring table: 0.1150 gapop 60.0 / gapext 45.0  
Searched: 1197863 seqs, 16972673 residues  
Word size: 9  
Total number of hits satisfying chosen parameters: 273822  
Minimum hit seq length: 8  
Maximum hit seq length: 15  
Post processing: Listed first 500 similarities  
Database: A\_Geneseq\_29Jun03:•  
1: /SIDSI/qcdata/qcseq/qcseqemb/emb/AA1946.EAT:•  
2: /SIDSI/qcdata/qcseq/qcseqemb/emb/AA1981.EAT:•  
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4: /SIDSI/qcdata/qcseq/qcseqemb/emb/AA1983.EAT:•  
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6: /SIDSI/qcdata/qcseq/qcseqemb/emb/AA1985.EAT:•  
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23: /SIDSI/qcdata/qcseq/qcseqemb/emb/AA2002.EAT:•  
24: /SIDSI/qcdata/qcseq/qcseqemb/emb/AA2003.EAT:•  
SUMMARIES  
Prod. No. is the number of results predicted by chance to have a score greater than or equal to the start of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	length	db hit	Description
1	11	100.0	11	21	AAV85542 NCAM Ig1 binding p
2	11	100.0	11	23	AB069342 Human neural cell
3	5	45.5	8	20	AAV39614 CTLA-4 VLD CDR1 re
4	5	45.5	9	23	AAV44825 Human B43 associat
5	5	45.5	9	23	ABV74702 Transcription fact
6	5	45.5	10	22	AAV594020 Human complementat
7	5	45.5	10	24	AAV54022 Human complementat
8	5	45.5	10	24	AAV54322 Human novel protei
9	4	36.4	8	13	AAV228* Exchange imp. for 1,

10	4	35.4	8	14	AAV43246 Cytotoxic T lympho
11	4	35.4	8	16	AAV78841 P. falciparum circ
12	4	35.4	8	17	AAV89040 Linker sequence in
13	4	35.4	8	17	AAV91036 Single chain monoc
14	4	35.4	8	18	AAV32246 Linker peptide 5 o
15	4	35.4	8	18	AAV41565 Linker sequence 4
16	4	35.4	8	19	AAV4273 mPCP-7 peptide sub
17	4	35.4	8	19	AAV4664 Reptide from P.fal
18	4	35.4	8	19	AAV56994 Enzyme inhibitor p
19	4	35.4	8	21	AAV24656 Cytotoxic T lympho
20	4	35.4	8	21	AAV78489 SSX-5 derived pept
21	4	35.4	8	21	AAV74697 SSX-4 derived pept
22	4	35.4	8	21	AAV73724 SSX-2 derived pept
23	4	35.4	8	21	AAV79744 SSX-2 derived pept
24	4	35.4	8	21	AAV76732 SSX-2 HLA binding
25	4	35.4	8	21	AAV76744 SSX-1 HLA binding
26	4	35.4	8	23	AAV74688 Transcription fact
27	4	35.4	8	24	AAV64629 Motif-specific and
28	4	35.4	9	16	AAV21554 Corticotropin rele
29	4	35.4	9	18	AAV0450 Melanoma antigen H
30	4	35.4	9	19	AAV41588 Melanoma antigen H
31	4	35.4	9	21	AAV78491 SSX-5 derived pept
32	4	35.4	9	21	AAV79701 SSX-4 derived pept
33	4	35.4	9	21	AAV79708 SSX-2 derived pept
34	4	35.4	9	21	AAV79727 SSX-2 derived pept
35	4	35.4	9	21	AAV79745 SSX-1 derived pept
36	4	35.4	9	21	AAV76726 SSX-2 HLA binding
37	4	35.4	9	21	AAV76735 SSX-2 HLA binding
38	4	35.4	9	21	AAV76745 SSX-1 HLA binding
39	4	35.4	9	22	AAV94092 Vaccine related MH
40	4	35.4	9	23	AAV65757 Plant ICK protein
41	4	35.4	9	23	AAV54513 CTL epitope HLA pe
42	4	35.4	9	23	AAV94682 CTL epitope HLA pe
43	4	35.4	9	23	AAV94793 CTL epitope HLA pe
44	4	35.4	9	23	AAV94797 CTL epitope HLA pe
45	4	35.4	9	23	AAV94887 CTL epitope HLA pe
46	4	35.4	9	23	AAV94998 CTL epitope HLA pe
47	4	35.4	9	23	AAV95081 CTL epitope HLA pe
48	4	35.4	9	24	AAV16032 Human cancer-relat
49	4	35.4	9	24	AAV15053 Human cancer-relat
50	4	35.4	9	24	AAV16209 Human cancer-relat
51	4	35.4	9	24	AAV16237 Human cancer-relat
52	4	35.4	9	24	AAV16244 Human cancer-relat
53	4	35.4	9	24	AAV16369 Human cancer-relat
54	4	35.4	9	24	AAV15398 Human cancer-relat
55	4	35.4	9	24	AAV15580 Human cancer-relat
56	4	35.4	9	24	AAV15596 Human cancer-relat
57	4	35.4	9	24	AAV15767 Human cancer-relat
58	4	35.4	9	24	AAV16791 Human cancer-relat
59	4	35.4	9	24	AAV16973 Human cancer-relat
60	4	35.4	9	24	AAV17008 Human cancer-relat
61	4	35.4	9	24	AAV17185 Human cancer-relat
62	4	35.4	9	24	AAV17603 Human cancer-relat
63	4	35.4	9	24	AAV17981 Human cancer-relat
64	4	35.4	9	24	AAV18040 Human cancer-relat
65	4	35.4	9	24	AAV18242 Human cancer-relat
66	4	35.4	9	24	AAV18461 Human cancer-relat
67	4	35.4	9	24	AAV18644 Human cancer-relat
68	4	35.4	10	15	AAV58621 GP2b residues 148-
69	4	35.4	10	19	AAV40420 Nitric oxide synth
70	4	35.4	10	20	AAV30682 Apo-B100 derived p
71	4	35.4	10	20	AAV97977 Human synaptonemal
72	4	35.4	10	20	AAV97977 NMD somatostatin-2
73	4	35.4	10	21	AAV78309 SCP-1 HLA binding
74	4	35.4	10	22	AAV13158 Human SCR-1 protei
75	4	35.4	10	22	AAV84014 Arabidopsis thalia
76	4	35.4	10	22	AAV87924 Saccharomyces cere
77	4	35.4	10	22	AAV93333 Granulocyte-colony
78	4	35.4	10	23	AAV93536 Human novel protei
79	4	35.4	10	23	AAV94797 Human novel protei
80	4	35.4	10	23	AAV95333 Human novel protei
81	4	35.4	10	23	AAV95333 Human novel protei
82	4	35.4	10	23	AAV94568 CTL epitope HLA pe

87	4	36.4	10	24	AAH92452	CTL epitope HLA pe	156	4	36.4	15	5	AAH60754	Sequence of a port
88	4	36.4	10	24	AAH92456	CTL epitope HLA pe	157	4	36.4	15	21	AAH63143	Human secreted pr
89	4	36.4	10	24	AAH94943	CTL epitope HLA pe	158	4	36.4	15	21	AAH65529	Oestrogen receptor
90	4	36.4	10	24	AAH94967	CTL epitope HLA pe	159	4	36.4	15	22	AAH99027	Human calcium ion
91	4	36.4	10	24	AAH95564	CTL epitope HLA pe	160	4	36.4	15	22	AAH964081	Alkylation-DNA-pro
92	4	36.4	10	24	AAH95813	CTL epitope HLA pe	161	4	36.4	15	23	AAH49391	Human phosphatid
93	4	36.4	10	24	AAH97447	CTL epitope HLA pe	162	4	36.4	15	23	AAH15038	Human H1G protein
94	4	36.4	10	24	AAH11175	Human cancer relat	163	4	36.4	15	23	AAH49276	Human cell signal/
95	4	36.4	10	24	AAH11114	Human cancer relat	164	4	36.4	15	23	AAH49276	Oestrogen receptor
96	4	36.4	10	24	AAH11227	Human cancer relat	165	4	36.4	15	23	AAH49276	Human cancer relat
97	4	36.4	10	24	AAH11230	Human cancer relat	166	4	36.4	15	24	AAH34297	Human cancer relat
98	4	36.4	10	24	AAH11490	Human cancer relat	167	4	36.4	15	24	AAH34329	Human cancer relat
99	4	36.4	10	24	AAH11490	Human cancer relat	168	4	36.4	15	24	AAH34413	Human cancer relat
100	4	36.4	10	24	AAH11492	Human cancer relat	169	4	36.4	15	24	AAH34512	Human cancer relat
101	4	36.4	10	24	AAH11523	Human cancer relat	170	4	36.4	15	24	AAH34549	Synthetic subst
102	4	36.4	10	24	AAH11545	Human cancer relat	171	4	36.4	15	24	AAH34549	Linkage peptide fo
103	4	36.4	10	24	AAH11689	Human cancer relat	172	4	36.4	15	24	AAH34549	Linkage peptide fo
104	4	36.4	10	24	AAH11705	Human cancer relat	173	4	36.4	15	24	AAH34549	Hypotensive peptid
105	4	36.4	10	24	AAH11715	Human cancer relat	174	4	36.4	15	24	AAH34549	GMP-140 MAB CDR2L
106	4	36.4	10	24	AAH11715	Human cancer relat	175	4	36.4	15	24	AAH34549	La/SSA epitope 330
107	4	36.4	10	24	AAH11715	Human cancer relat	176	4	36.4	15	24	AAH34549	Ro/SSA epitope 263
108	4	36.4	10	24	AAH11715	Human cancer relat	177	4	36.4	15	24	AAH34549	Ro/SSA epitope 264
109	4	36.4	10	24	AAH11715	Human cancer relat	178	4	36.4	15	24	AAH34549	Hepatitis C Virus
110	4	36.4	10	24	AAH11715	Human cancer relat	179	4	36.4	15	24	AAH34549	Hepatitis C Virus
111	4	36.4	10	24	AAH11715	Human cancer relat	180	4	36.4	15	24	AAH34549	Hepatitis C Virus
112	4	36.4	10	24	AAH11715	Human cancer relat	181	4	36.4	15	24	AAH34549	Hepatitis C Virus
113	4	36.4	10	24	AAH11715	Human cancer relat	182	4	36.4	15	24	AAH34549	Hepatitis C Virus
114	4	36.4	10	24	AAH11715	Human cancer relat	183	4	36.4	15	24	AAH34549	Hepatitis C Virus
115	4	36.4	10	24	AAH11715	Human cancer relat	184	4	36.4	15	24	AAH34549	Hepatitis C Virus
116	4	36.4	10	24	AAH11715	Human cancer relat	185	4	36.4	15	24	AAH34549	Hepatitis C Virus
117	4	36.4	10	24	AAH11715	Human cancer relat	186	4	36.4	15	24	AAH34549	Hepatitis C Virus
118	4	36.4	10	24	AAH11715	Human cancer relat	187	4	36.4	15	24	AAH34549	Hepatitis C Virus
119	4	36.4	10	24	AAH11715	Human cancer relat	188	4	36.4	15	24	AAH34549	Hepatitis C Virus
120	4	36.4	10	24	AAH11715	Human cancer relat	189	4	36.4	15	24	AAH34549	Hepatitis C Virus
121	4	36.4	10	24	AAH11715	Human cancer relat	190	4	36.4	15	24	AAH34549	Hepatitis C Virus
122	4	36.4	10	24	AAH11715	Human cancer relat	191	4	36.4	15	24	AAH34549	Hepatitis C Virus
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124	4	36.4	10	24	AAH11715	Human cancer relat	193	4	36.4	15	24	AAH34549	Hepatitis C Virus
125	4	36.4	10	24	AAH11715	Human cancer relat	194	4	36.4	15	24	AAH34549	Hepatitis C Virus
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128	4	36.4	10	24	AAH11715	Human cancer relat	197	4	36.4	15	24	AAH34549	Hepatitis C Virus
129	4	36.4	10	24	AAH11715	Human cancer relat	198	4	36.4	15	24	AAH34549	Hepatitis C Virus
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131	4	36.4	10	24	AAH11715	Human cancer relat	200	4	36.4	15	24	AAH34549	Hepatitis C Virus
132	4	36.4	10	24	AAH11715	Human cancer relat	201	4	36.4	15	24	AAH34549	Hepatitis C Virus
133	4	36.4	10	24	AAH11715	Human cancer relat	202	4	36.4	15	24	AAH34549	Hepatitis C Virus
134	4	36.4	10	24	AAH11715	Human cancer relat	203	4	36.4	15	24	AAH34549	Hepatitis C Virus
135	4	36.4	10	24	AAH11715	Human cancer relat	204	4	36.4	15	24	AAH34549	Hepatitis C Virus
136	4	36.4	10	24	AAH11715	Human cancer relat	205	4	36.4	15	24	AAH34549	Hepatitis C Virus
137	4	36.4	10	24	AAH11715	Human cancer relat	206	4	36.4	15	24	AAH34549	Hepatitis C Virus
138	4	36.4	10	24	AAH11715	Human cancer relat	207	4	36.4	15	24	AAH34549	Hepatitis C Virus
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143	4	36.4	10	24	AAH11715	Human cancer relat	212	4	36.4	15	24	AAH34549	Hepatitis C Virus
144	4	36.4	10	24	AAH11715	Human cancer relat	213	4	36.4	15	24	AAH34549	Hepatitis C Virus
145	4	36.4	10	24	AAH11715	Human cancer relat	214	4	36.4	15	24	AAH34549	Hepatitis C Virus
146	4	36.4	10	24	AAH11715	Human cancer relat	215	4	36.4	15	24	AAH34549	Hepatitis C Virus
147	4	36.4	10	24	AAH11715	Human cancer relat	216	4	36.4	15	24	AAH34549	Hepatitis C Virus
148	4	36.4	10	24	AAH11715	Human cancer relat	217	4	36.4	15	24	AAH34549	Hepatitis C Virus
149	4	36.4	10	24	AAH11715	Human cancer relat	218	4	36.4	15	24	AAH34549	Hepatitis C Virus
150	4	36.4	10	24	AAH11715	Human cancer relat	219	4	36.4	15	24	AAH34549	Hepatitis C Virus
151	4	36.4	10	24	AAH11715	Human cancer relat	220	4	36.4	15	24	AAH34549	Hepatitis C Virus
152	4	36.4	10	24	AAH11715	Human cancer relat	221	4	36.4	15	24	AAH34549	Hepatitis C Virus
153	4	36.4	10	24	AAH11715	Human cancer relat	222	4	36.4	15	24	AAH34549	Hepatitis C Virus
154	4	36.4	10	24	AAH11715	Human cancer relat	223	4	36.4	15	24	AAH34549	Hepatitis C Virus
155	4	36.4	10	24	AAH11715	Human cancer relat	224	4	36.4	15	24	AAH34549	Hepatitis C Virus

203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human	Human</																																																																																																																																																																																																																																																																																																																																																																																																																																																	

436	3	27.3	9	17	AAW43418	Human leucocyte an	446	3	27.3	9	42	ABP16002	HIV A24 super moti
437	3	27.3	9	17	AAW43527	Human leucocyte an	449	3	27.3	9	42	ABP16400	HIV A24 super moti
438	3	27.3	9	17	AAW43559	Human leucocyte an	450	3	27.3	9	22	ABP17496	HIV B27 super moti
439	3	27.3	9	17	AAW43479	Human leucocyte an	451	3	27.3	9	22	ABP18774	HIV B58 super moti
440	3	27.3	9	17	AAW43432	Human leucocyte an	452	3	27.3	9	22	ABP20498	HIV A03 moti1; gag
441	3	27.3	9	17	AAW43524	Human leucocyte an	453	3	27.3	9	22	ABP20861	HIV A03 moti1; ref
442	3	27.3	9	17	AAW12509	SH2-1, cyto1,2, pep1,0	454	3	27.3	9	22	ABP21503	HIV A03 moti1; pol
443	3	27.3	9	17	AAW43502	A1, cyto1,2, moti1,1,1	455	3	27.3	9	22	ABP21889	HIV A03 moti1; rev
444	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	456	3	27.3	9	22	ABP221891	HIV A03 moti1; rev
445	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	457	3	27.3	9	22	ABP22259	HIV A03 moti1; vpu
446	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	458	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
447	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	459	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
448	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	460	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
449	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	461	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
450	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	462	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
451	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	463	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
452	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	464	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
453	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	465	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
454	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	466	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
455	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	467	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
456	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	468	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
457	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	469	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
458	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	470	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
459	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	471	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
460	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	472	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
461	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	473	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
462	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	474	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
463	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	475	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
464	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	476	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
465	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	477	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
466	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	478	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
467	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	479	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
468	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	480	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
469	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	481	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
470	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	482	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
471	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	483	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
472	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	484	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
473	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	485	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
474	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	486	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
475	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	487	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
476	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	488	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
477	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	489	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
478	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	490	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
479	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	491	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
480	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	492	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
481	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	493	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
482	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	494	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
483	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	495	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
484	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	496	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
485	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	497	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
486	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	498	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
487	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	499	3	27.3	9	22	ABP22268	HIV A03 moti1; vpu
488	3	27.3	9	17	AAW43492	SH2-1, cyto1,2, pep1,0	500	3	27.3	9	24	ABP11119	House dust mite de

## ALIGNMENTS

## RESULT 1

AAW88542  
 ID AAW88542 standard; peptide: 11 AA.

XX  
 AA

XX  
 AA

XX  
 37-AM2200 (first entry)

XX  
 NCAM lql binding peptide #14.

XX  
 NCAM: neural cell adhesion molecule; lql: immunoglobulin domain 1;  
 neurite outgrowth; promoter; proliferation; nerve damage; sclerosis;  
 XX  
 impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;  
 XX  
 Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;  
 XX  
 treatment: prosthetic nerve guide; treatment: nervous system.







XX Sequence: 10 AA:  
SQ  
Query Match 45.5% Score 5; DB 23; Length 10;  
Best Local Similarity 100.0% (Ident. No. 96)  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 RRSK 7  
DE 1 11  
DE 6 RRSK 10  
RESIDUE 8  
AAP9228  
10 AAP9228 standard; Peptide: 10 AA  
XX AAP9228  
XX 02 JUN 2002 (first entry)  
XX Human bowel protein GalP2H3; HLA binding peptide #1005.  
XX Human human leukocyte antigen HLA polymorphic region GalP2H3  
KW GalP2H3 Transport protein; cancer; breast; prostate; prostate  
KW chromosome 1q44; chromosome 2q24; 11p11.1; 11p15.5  
XX  
XX Home sapiens  
XX  
XX W209214361A2  
XX 21 FEB 2002  
XX 07 AUG 2001; 2001W09US25782  
XX 07 AUG 2001; 2001US 246329  
XX (ADEX) ALEXSYS INC.  
XX  
XX Kaitum Ave., Chualar, CA 95521-1001, Alameda Co., Calif 94501.  
XX Robert E. Hubert RS, Jr. W. J. Hubert's Ave.  
XX WJH 2001 269174/51.  
XX Recombinant 83p2H3 gene products for use in the treatment of cancer  
XX in a solid tumor, comprising a heterodimeric protein consisting of a heavy chain  
XX in a dimeric sample from the end of the chain and a light chain, and a heavy chain  
XX  
XX Example 11, Page 247; 270pp; English  
XX The invention relates to methods for the treatment of cancer, and to a heavy chain  
XX protein whose gene is located on the chromosome 11p11.1, and to a light chain  
XX biological sample from a patient who has been subjected to having  
XX cancer (especially prostate cancer), comprising a heterodimeric protein  
XX consisting of a heavy chain and a light chain, and a heavy chain  
XX an individual and (b) comparing the status of the status of a heavy chain  
XX products in a normal sample. Also included are methods of identifying  
XX function or status, generating an antibody, and a heavy chain and light chain  
XX 83p2H3 (or related protein GalP2H3), whose gene is located on the chromosome  
XX 12q24.1) using identified HLA (human leukocyte antigen) binding  
XX peptides derived from the protein, delivered to a cytotoxic agent to  
XX a cell expressing 83p2H3 by comparing the status of the status of a heavy chain  
XX antibody, a recombinant protein consisting of a heavy chain and a light chain  
XX the antibody, a non-human transmembrane protein that reduces the recombinant  
XX protein, a hybridoma that produces the recombinant protein, a single  
XX chain monoclonal antibody that comprises the variable domains of the  
XX heavy and light chains of the antibody, a hybridoma that produces the antibody,  
XX polypeptide that encodes the monoclonal antibody and antibody that  
XX immune response to a 83p2H3 protein, by providing a heavy chain related  
XX protein that comprises a heavy chain of a heavy chain and a light chain  
XX epitope that comprises a heavy chain of a heavy chain and a light chain  
XX useful for monitoring 83p2H3 gene expression in a cell, and a method  
XX for monitoring the presence of cancer in an individual, the method is

CC useful for inhibiting the growth of cancer cells that express 83p2H3, for  
CC treating cancer and the vector is useful for treating a patient with a  
CC cancer that expresses 83p2H3. The immunological methods are useful for  
CC generating an immune response against 83p2H3, and for detecting the  
CC presence of 83p2H3-related protein or polypeptide in a biological  
CC sample from a patient who has or who is suspected of having cancer. The  
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging,  
CC methodologies and treatment, to detect and quantify 83p2H3 and mutant  
CC 83p2H3-related proteins, for purifying a 83p2H3-related protein, for  
CC isolating 83p2H3 homologues/related molecules, and for generating anti-  
CC antibody antibodies that mimic the 83p2H3 protein. The present sequence  
CC is an HLA binding peptide motif from 83p2H3 or its related protein  
CC GalP2H3.  
XX  
XX Sequence: 10 AA:  
SQ  
Query Match 45.5% Score 5; DB 23; Length 10;  
Best Local Similarity 100.0% (Ident. No. 96)  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 RRSK 11  
DE 1 11  
DE 6 RRSK 7  
RESIDUE 8  
AAP9228  
10 AAP9228 standard; Peptide: 10 AA  
XX AAP9228  
XX 27 JUN 1996 (first entry)  
XX Linkage peptide for subunits I and II of single chain fused monellin  
XX analogues.  
XX Monellin: fusion peptide; Sweetener; linkage peptide.  
XX Synthesis.  
XX W0816271 A  
XX 27 JUN 1996  
XX 27 JUN 1996; 54W US 2,114  
XX 27 JUN 1997; 57US 0,644,443  
XX (USP) DEXY Biotek Corp KAITUM  
XX Kim SH, Cho JM  
XX WJH 1999 028222/03.  
XX Sweetener pumpkin, natural single chain monellin analogue  
XX having the two subunits covalently bonded via peptide link.  
XX Claim 13; Page 18; 24pp; English.  
XX A fusion protein was produced by synthesizing 14 oligomers and ligating  
XX them to produce a ds DNA mol. encoding the amino acid sequence. The new  
XX gene was cloned and used to transform E.coli JM101 to express the  
XX protein. The linkage peptide, which joins the two subunits of monellin, is  
XX one of twelve claimed.  
XX The new peptide is a sweetener and can be used in carbonated drinks and  
XX various food products including gum, meat products, instant soups, yogurt,  
XX desserts, and cereal, in animal feeds, in dental hygiene products, such as  
XX toothpaste, mouthwash and pharmaceuticals. It can also be expressed  
XX in yeasts or plants to increase sweetness of fruit and vegetables.  
XX See also: AAP92289 92, and W0816271 A and W081627 A.  
XX  
XX Sequence: 9 AA:  
SQ



Query Match 36.4% Score 41 DP 100.0% Gap 0  
 Best Local Similarity 100.0% Pct. No. 9.3e+05  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 KSKD 6  
 LB 1 KSKD 5

RESULT 10  
 AAR43246  
 ID AAR43246 standard; peptide; # AA  
 AC AAR43246  
 DT 25-MAR-2003 (updated)  
 DT 24-MAR-1994 (first entry)  
 XX Cytotoxic T lymphocyte recognition/induction peptide  
 XX CD4 vaccines: malaria; specific antigen derived  
 XX Synthesie  
 XX W0426101-A2  
 XX 14 Oct 1993  
 XX 25 APR 1993; 91WO 0809711  
 XX 23 APR 1993; 92GB 0008604  
 XX 20-AUG 1993; 92GB-0017704  
 XX (USIS) USIS INNOVATION 110  
 XX Elvin L. Gorbach EM, Bl. L AV. Remington AA; Warfield G  
 XX WP1: 1993 46833/42  
 XX peptide(s) recognising or inducing cytotoxic T lymphocytes  
 XX useful in vaccines against malaria or HIV so derived from  
 XX specific antigen and human leukocyte antigen class I  
 XX restricted epitope  
 XX Claim 6: Page 63; 35pp; English  
 XX The sequence is that of peptide which is derived from T cell  
 XX induced cytotoxic T lymphocytes. It is derived from the consensus antigen  
 XX motif  
 XX (Updated on 25-MAR-2003 to correct P1 field.)  
 XX Sequence # AA:  
 Query Match 36.4% Score 41 DP 100.0% Gap 0  
 Best Local Similarity 100.0% Pct. No. 9.3e+05  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 KSKD 11  
 LB 1 KSKD 4

RESULT 11  
 AAR78841  
 ID AAR78841 standard; peptide; # AA  
 AC AAR78841  
 DT 25-MAR-2003 (updated)  
 DT 27-MAR-1995 (first entry)  
 XX F. talcipharm circus.sp. 368 475 cytol. x100 lymphocyte epitope  
 XX

KW Circus.sp. 368 475 cytol. x100; CTL; epitope; helper T; HTL; cell;  
 KW lymphocyte; viruses; parasites; tumours; antigens; treatment;  
 KW disease prevention;  
 XX Plasmidium falciparum  
 XX W 9522317 A1  
 XX 24-AUG-1995  
 XX 16-FEB-1995; 95WO 0502121  
 XX 15-FEB-1994; 94US 197484  
 XX (CYT) CYTEL Corp.  
 XX Vitellio MA, Chestnut RW, Sette AB, Celis E, Grey H;  
 XX WP1: 1995-302545/39  
 XX Campen. inducing cytotoxic T lymphocyte response to prot. viral,  
 PT bacterial, parasitic or tumour antigens useful in the treatment  
 PT and prevention of diseases associated with the antigen e.g.  
 PT hepatitis B  
 XX Disclosure: Page 12; 109pp; English  
 XX A compo. which induces a cytotoxic T lymphocyte (CTL) response to  
 XX an antigen (Ag) in a mammal comprises: a CTL Ag response inducing  
 XX peptide (i.e. AAR78841) and a lipid conjugated helper T cell  
 XX inducing peptide. The compo. induces a CTL response to bacterial,  
 XX viral or tumour Ags, and is therefore useful in the treatment and  
 XX prevention of diseases associated with the Ag.  
 XX (Updated on 25-MAR-2003 to correct P1 field.)  
 XX Sequence # AA:  
 Query Match 36.4% Score 41 DP 16; Length 8;  
 Best Local Similarity 100.0% Pct. No. 9.3e+05  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 KSKD 11  
 LB 1 KSKD 4

RESULT 12  
 AAR88040  
 ID AAR88040 standard; peptide; # AA  
 AC AAR88040  
 DT 25-MAR-2003 (updated)  
 DT 10-JUL-1995 (first entry)  
 XX linker sequence in lamellin single chain form analogue.  
 XX monellin; analogue; Serendipity Berry; Dioscoreophyllum cominitii;  
 KW sweetener; food; beverage; single chain form.  
 XX Synthetic  
 XX DS5478923-A  
 XX 21-DEC-1995  
 XX 25-MAR-1994; 94US-0218264  
 XX 30-MAR-1995; 94US-0502257  
 XX 19-JUN-1987; 87US-0064341  
 XX 04-NOV-1987; 87US-017124  
 XX 18-JAN-1993; 93US-046585  
 XX 25-MAR-1994; 94US-0218264



CC substitution. The B chain and the A chain are linked by a covalent bond  
CC or a hydrophilic, physiologically acceptable linker capable of  
CC providing a spacing length equivalent to a peptide of 1-10 amino acids.  
CC This linker peptide is selected so as to reside on the external portion  
CC of the molecule and not to disturb the native conformation. This protein  
CC can be used for sweetening foods and beverages. The monellin analogues  
CC are thermostable and retain high intensity sweetening power even after  
CC heating to 100 degree. C at acidic pH.  
XX  
SQ Sequence 8 AA:  
Query Match 36.4% Score 4: DB 14: Length 8:  
Best Local Similarity 100.0% Pred. No. 9.3e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 3 KTRF 5  
DB 2 KTRF 5  
11  
RESULT 16  
AAW41565  
ID AAW41565 standard; Protein: 8 AA  
XX  
AC AAW41565:  
XX  
DI 18 FEB 1998 (first entry)  
XX  
DE Linker sequence 4 of single-chain protein sweetener monellin.  
XX  
KW single chain protein; sweetener; emulsifier; heat stability; adjuvant;  
KW beverage; pharmaceutical; toothpaste; general hygiene; antibody;  
KW purification; sucrose.  
XX  
CS Synthetic.  
XX  
FN US5670339 A.  
XX  
PE 24 SEP 1997.  
XX  
PR 06 JUN 1995: 950S-0650945.  
XX  
PR 09 MAR 1997: 960S-062257.  
PR 19 JUN 1987: 870S-066434.  
PR 19 JUN 1987: 870S-066434.  
PR 24 NOV 1987: 870S-0317124.  
PR 18 JAN 1990: 900S-0405525.  
PR 02 NOV 1993: 930S-0336326.  
PR 06 JUN 1995: 950S-0650945.  
XX  
LA (LICK ) LICKY SWEETER CORP.  
LA (R032 ) UNIV CALIFORNIA.  
XX  
LC Chao JM, Kim S:  
XX  
DB WI 1997 479455/44.  
XX  
PT New DNA encoding a single chain form of the sweetener monellin  
PT that is stable to heating at acidic pH, useful as additive for  
PT foods, beverages, pharmaceuticals, toothpaste etc.  
XX  
PS Example 5, Column 12; 10pp; English.  
XX  
CC This linker sequence is used to prepare a recombinant single-chain form  
CC of the protein sweetener monellin. The recombinant protein has the  
CC formula B-A where B and A represent peptide portions of the B chain and  
CC A chain respectively of the native monellin and A is a linker between the  
CC B and A chains. The linker sequence A can be a covalent bond or can  
CC consist of a peptide of 1-10 gene encoded amino acids, with sufficient  
CC hydrophilicity and length to reside on the outside of the molecule  
CC without distortion of the native conformation. This peptide-glycyl  
CC oligomers can also be used as linkers. The single-chain protein sweetener  
CC retains the sweetness properties of the double chain native monellin, but

CC are stable under conditions where the native protein is denatured. This  
CC protein sweetener is many times sweeter than sucrose, and can be used as  
CC a substitute for sugar in foods and beverages (juices, hot drinks or  
CC carbonated beverages), chewing gum, toothpastes, mouthwashes, dental  
CC hygiene products and pharmaceuticals. They can also be used to generate  
CC specific antibodies for their purification.  
XX  
SQ Sequence 8 AA:  
Query Match 46.4% Score 4: DB 18: Length 8:  
Best Local Similarity 100.0% Pred. No. 9.3e+05:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
QY 3 KTRF 5  
DB 2 KTRF 5  
11  
RESULT 16  
AAW64273  
ID AAW64273 standard; Peptide: 8 AA  
XX  
AC AAW64273:  
XX  
DI 24 NOV 1996 (first entry)  
XX  
DE mMCP-7 peptide substrate.  
XX  
KW MCP-7; mouse; mast cell; protease 7; trypsinase-7; blood clot;  
KW anticoagulant; myocardial infarction; reocclusion; thromboembolism;  
KW cerebral embolism; thrombosis; therapy.  
XX  
CS Synthetic.  
XX  
FN WO9824886-A1.  
XX  
PD 11 JUN 1998.  
XX  
PE 25 NOV 1997: 97WO US21620.  
XX  
PR 04 DEC 1996: 960S-0032354.  
XX  
PR (EGHM ) BRIGHAM & WOMENS HOSPITAL.  
XX  
XX Stevens KL:  
XX  
PR WPI: 1998 4335CH/29.  
XX  
PT New compositions containing trypsinase-7, e.g. mouse mast cell  
PT protease-7 - are used to treat clot formation in e.g. myocardial  
PT infarction; reocclusion following angioplasty or pulmonary  
PT thromboembolism  
XX  
PS Example: Page 45; 92pp; English.  
XX  
CC This is a substrate peptide of mouse mast cell protease 7 (mMCP-7,  
CC see AAW64273). It is one of 21 peptides (see AAW64270-90) obtained by  
CC incubating a phage display peptide library 2 times with a  
CC recombinant FLAG-tagged mMCP 7 polypeptide, isolating clones, and  
CC deducing the amino acid sequence of the protease susceptible  
CC domains in the ph11 fusion proteins. Only one peptide (see AAW64270)  
CC was obtained after 4 rounds of screening. mMCP-7 has been  
CC characterised as having fibrinogen as its physiological substrate.  
CC It can be used to prevent or treat fibrin clot formation in vitro  
CC and in vivo. Trypsinase-7 proteases of the invention, including  
CC mMCP-7 and its homologues, can be used to treat disorders that are  
CC mediated by irreversibly thrombus clot formation, such as myocardial  
CC infarct and reocclusion following angioplasty, and are also useful  
CC for surgical procedures that require that blood does not clot.  
XX  
SQ Sequence 8 AA:  
Query Match 46.4% Score 4: DB 19: Length 8:

Best Local Similarity 100.0%; Seed No. 9; 4005;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 RKSK 10  
DB 111  
5 RKSK 8

RESULT 19  
AAW56994  
ID AAW56994 standard; peptide: 8 AA  
XX AAW56994  
XX AAW56994  
XX 25 SEP 1998 (first entry)  
XX Peptide from P. talpae (CSP 48 378)  
XX Mannose; antigen; antigen-presenting complex; mannose-epitope peptide; T cell  
XX vaccine; treatment  
XX Synthetic  
XX W0981478 A1  
XX 02 APR 1998  
XX 25 SEP 1997 9780-NL05011  
XX 24 SEP 1996 96EP-0202701  
XX (CYLC) ELKSONIV LELLEN  
XX Enrichment; DM; Koning F;  
XX WPI: 1998 240611/20  
XX Inducible uptake and presentation of antigen(s) by adding mannose  
XX residue(s) to antigen for induction of T cell response; useful in  
XX v.a. vaccines against viral infections(s)  
XX Disclosure: Page 29; 47pp; English  
XX The peptides AAW54559 W54609 are examples of peptides to which at least  
XX 1 (preferably 2) mannose can be attached to increase their uptake as  
XX antigens by antigen-presenting cells. Uptake of antigen-mannosylated  
XX peptides will increase the T cell response. Peptides which uptake of antigenic  
XX peptides blocks the T cell response. Peptides which uptake of antigenic  
XX antigens can be used in treatment of type 1 diabetes, rheumatoid  
XX arthritis, graft rejection, etc. Peptides which are used to  
XX prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths  
XX and parasites.  
XX Sequence 8 AA;  
SQ

Query Match 36.4%; Score 4; DB 19; Length 8;  
Best Local Similarity 100.0%; Seed No. 9; 38-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 RKSK 11  
DB 111  
1 RKSK 4

RESULT 18  
AAW56994  
ID AAW56994 standard; peptide: 8 AA  
XX AAW56994  
XX AAW56994  
XX 25 JUL 1998 (first entry)  
XX cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:8.  
XX

DE Enzyme inhibitor; peptide SEQ ID NO:195.  
XX  
KW Enzyme inhibitor: t-PA; a PA; chymotrypsin; serine protease; active;  
KW latent; substrate subtraction phage display peptide library;  
KW identification; kinase; phosphatase; serpin.  
XX  
XX Basic suppins.  
XX W09747314-A1  
XX 18 DEC 1997  
XX 10 JUN 1997 97W-0509761  
XX 10 JUN 1996 96US 0019495  
XX (SCRI) SCHIFFS RES INST  
XX Ke S. Madison EL  
XX WPI: 1998-062746/6  
XX Substrate subtraction phage display peptide libraries - used to  
XX distinguish between active and latent forms of enzyme, e.g. serine  
XX protease  
XX Claim 25, Page 106; 18pp; English  
XX The present sequence represents an enzyme inhibitor peptide used in  
XX the method of the invention to distinguish between t-PA and u-PA. The  
XX present invention describes a substrate subtraction library for the  
XX identification of peptide substrates selective between a first enzyme  
XX (E1) and a second enzyme (E2), comprising a collection of different  
XX peptides, substantially lacking peptides that are effective substrates  
XX for E1. Also described are: (1) a method (M1) for identifying peptide  
XX substrates selective between a first enzyme (E1) and a second enzyme  
XX (E2); (2) a compound comprising the amino acid sequence of a peptide  
XX identified by M1; (3) a polypeptide for use as an enzyme inhibitor  
XX comprising one of 237 amino acid sequences (see AAW56801 to AAW56947,  
XX and AAW56949 to AAW57038); (4) a recombinant DNA vector comprising DNA  
XX (1) encoding a protease inhibitor including the sequence identified by  
XX the M1; (5) a prokaryotic or eukaryotic cell containing the vector of  
XX (4); (6) an antibody (Ab) immunoreactive with at least one of the  
XX peptides identified by M1; and (7) a diagnostic assay for distinguishing  
XX between active and latent forms of protease inhibitors, that uses (Ab).  
XX The library and method are used for distinguishing between active and  
XX latent forms of enzyme inhibitors, e.g. proteases, kinases and  
XX phosphatases. (Ab) are used for affinity purification of recombinant  
XX peptides and in the identification of naturally occurring protease  
XX inhibitors. Enzyme-inhibiting peptides identified can be used to treat a  
XX serpin deficiency or a disorder of serine proteases.  
XX Sequence 8 AA;  
SQ

Query Match 36.4%; Score 4; DB 19; Length 8;  
Best Local Similarity 100.0%; Seed No. 9; 38-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 RKSK 10  
DB 111  
3 RKSK 6

RESULT 19  
AAW56994  
ID AAW56994 standard; peptide: 8 AA  
XX AAW56994  
XX AAW56994  
XX 05 JAN 2001 (first entry)  
XX cytotoxic T lymphocyte (CTL) epitope SEQ ID NO:8.  
XX

KW A1Pase; Hsp70; heat shock proteins; cytot. xpr. 1; lymphocyte; CTLs  
 KW immune response; infectious disease; inducible; cytotoxic; T cell;  
 KW cytostatic; immunostimulant; cellular immune response inhibitor;  
 KW proteoglycan; leukaemia; cancer

XX Homo sapiens.

XX W0200149041 A1.

XX 24-AUG-2001.

XX 18-FEB-2002; 2000KW-JP00941.

XX 19-FEB-1999; 99JF-0041515.

XX (SAME) SSK1P09 ELECTRIC INS. etc.

XX Shinkura N., Udono H., Yui K.

XX WPI: 2000-04-044749.

XX Fused protein capable of inducing cellular immune response, used in as  
 PT active ingredient for drug compositions in prevention and/or treatment  
 PT infectious diseases such as malignant cancer.

XX Claim 5; Page 52; 72pp; Japanese.

XX The present invention describes a fused protein (1) prepared from a  
 CC peptide containing a CIL (cytotoxic T lymphocyte) epitope recognized by  
 CC cytotoxic T cells and a protein containing the A1Pase domain of a heat  
 CC shock protein. Also described are: (2) a drug composition containing (1)  
 CC as active ingredient; (3) a DNA encoding (1); (4) an expression vector  
 CC containing the DNA of (2); and (5) a first time point which can retain the  
 CC expression vector of (3). (1) has cytostatic, immunostimulant and  
 CC proteoglycan activities, and can be used as a cellular immune response  
 CC inducer. The protein is used, as an active ingredient for drug  
 CC compositions in preventing and/or treating infectious diseases such as  
 CC malaria or cancer e.g. to provide systemic immunity against leishmania.  
 CC The present sequence represents a specifically claimed CIL epitope  
 CC for use in a fused protein of the present invention.

XX Sequence: 8 AA:

Query Match: 90.4%, Score 41, Length 40;  
 Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KSKD 11  
 DL 111  
 10 1 KSKD 4

RESULT 20  
 AAY76449  
 ID AAY76449 standard; Peptide: 8 AA.

XX AAY76449.

XX 10-MAY-2000 (first entry)

XX SSK 5 derived peptide #14.

XX Cancer: SSK family; SSK-1; SSK-2; SSK-3; SSK-4; SSK-5; NY-ESO-1;  
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CIL;  
 KW cytostatic; melanoma; synovial sarcoma.

XX Homo sapiens.

XX W0200000824 A1.

XX 16-JAN-2000.

XX 25-JUN-1999; 99W0 US14493.

XX 25-JUN-1999; 99W0 US14493.

XX 25-JUN-1999; 99W0 US14493.

XX 25-JUN-1999; 99W0 US14493.

XX 26-JUN-1998; 98US-0105699.  
 XX (LUDW) LUDWIG INST CANCER RES.  
 XX Tatesi O., Schin B., Pirouzdschah M., Rammensee G., Stevanovic S;  
 PI Chen Y., Gure A., Gid J.;  
 XX WPI: 2000-170334/15.  
 XX Determining the possible presence of breast, endometrial, colorectal,  
 PI lung, bladder or head-neck cancer.  
 XX Example 13; Page 21; 40pp; English.

XX A method has been developed for determining the possible presence of a  
 CC cancer, which is not melanoma or synovial sarcoma. The method comprises  
 CC assaying a sample taken from the subject to determine the expression of  
 CC an SSK gene, and determining the expression as a determination of the  
 CC possible presence of cancer. Expression of SSK1 gene indicates possible  
 CC presence of breast, endometrial, colorectal, lung, bladder or head-neck  
 CC cancer. These cancers are also detected by SSK2 and SSK4 gene  
 CC expression. SSK2 gene expression additionally indicates possible presence  
 CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression  
 CC of SSK4 gene also indicates possible presence of ovarian or stomach  
 CC cancer. SSK5 gene expression indicates the same cancers as SSK1, except  
 CC breast cancer. Determining expression of SSK gene can be used to monitor  
 CC progress of melanoma or synovial sarcoma, which is not cancer. The  
 CC SSK-derived peptide complex stimulates proliferation of cytolytic T  
 CC cells. This is useful for treating cancer, especially melanoma. AAY76464  
 CC to AAY78464 represent specifically claimed HLA binding peptides for use  
 CC in the method of the invention. AA288452 to AA288465 represent PCR  
 CC primers used in the isolation of SSK genes in the exemplification of the  
 CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762  
 CC represent peptides derived from SSK proteins or NY-ESO-1, which are used  
 CC in the exemplification of the present invention.

XX Sequence: 8 AA:

Query Match: 90.4%, Score 41, Length 40;  
 Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PERK 8  
 DL 111  
 5 PERK 5

RESULT 21  
 AAY79697  
 ID AAY79697 standard; Peptide: 8 AA.

XX AAY79697.

XX 10-MAY-2000 (first entry)

XX SSK 4 derived peptide #21.

XX Cancer: SSK family; SSK-1; SSK-2; SSK-3; SSK-4; SSK-5; NY-ESO-1;  
 KW HLA binding; human leukocyte antigen; cytolytic T cell; CIL;  
 KW cytostatic; melanoma; synovial sarcoma.

XX Homo sapiens.

XX W0200000824 A1.

XX 06-JAN-2000.

XX 25-JUN-1999; 99W0 US14493.

XX 26-JUN-1998; 98US-0105699.

XX (LUDW) LUDWIG INST CANCER RES.



XX Example 14: Page 26: 44pp: English.

PS A method has been developed for determining the possible presence of a

XX cancer, which is not melanoma or synovial sarcoma. The method comprises

XX assaying a sample taken from the subject to determine the expression of

XX an SSX gene, and determining the expression as a determination of the

XX possible presence of cancer. Expression of SSX1 gene indicates possible

XX presence of breast, endometrial, sarcomatous, lung, bladder or head neck

XX cancer. These cancers are also detected by SSX2 and SSX4 gene

XX expression. SSX2 gene expression additionally indicates possible presence

XX of lymphatic renal cell cancer, thymic and pancreatic cancer. Expression

XX of SSX5 gene also indicates possible presence of cancer or sarcoma.

XX cancer, SSX5 gene expression and, thus, the same cancers as SSX1, except

XX breast cancer. Determining expression of SSX gene can be used to monitor

XX progress of melanoma or synovial sarcoma, which is not cancer. The

XX SSX-derived peptide complex stimulates proliferation of cytotoxic T

XX cells. This is useful for treating cancer, especially melanoma. AAY78464

XX to AAY78468 represent specifically claimed HLA binding peptides for use

XX in the method of the invention. AAY8462 to AAY8465 represent PCR

XX primers used in the isolation of SSX genes in the exemplification of the

XX present invention. AAY78469 to AAY7860, and AAY7966 to AAY7972

XX represent peptides derived from SSX proteins of NY-ESO-1, which are used

XX in the exemplification of the present invention.

XX Sequence: 8 AA:

Query Match 4446, Score 4, DB 21, Length 8,  
Best Local Similarity 100.0%, Prod. No. 9, 3e-05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PERK R  
L I I  
D L 5 PERK R

RESLI 25  
AAY78744  
ID AAY78744 standard: peptide: 8 AA.  
XX  
AC AAY78744;  
XX  
XX 13-APR 2002 (first entry)  
XX  
DE SSX-1 HLA binding motif: #2.  
XX  
KW SSX-2: SSX1 gene; breast cancer; melanoma; NY ESO-1; SYP 1; MAGE-3;  
KW diagnosis; detection; tumour rejection antigen precursor; PCR primers;  
KW HLA binding motif.  
XX  
CS Homo sapiens.  
XX  
FN W220600642-A1.  
XX  
ED 06-JAN-2000.  
XX  
FF 03-JUN-1999; 99W0-081229.  
XX  
FR 26-JUN-1998; 98US-0105967.  
XX  
FA (CDSW) L2EWI3 INST CANCER RES.  
XX  
FI Sahlin O, Tureci O, Chen Y, Gell JO, Pfreundschuh M;  
XX  
XX WPL: 2000-137070/12.  
XX  
XX Detecting breast cancer and melanoma used for diagnosis and in  
XX development of targeted therapy .  
XX  
XX Example 2: Page 14: 24pp: English.

PS This sequence represents a HLA binding motif from the SSX-1 protein.

XX The invention relates to a method for determining breast cancer or

XX melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and

XX SCP-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGE-3 for melanoma, the

XX expression of at least one is an indicator of possible breast cancer, and

XX the expression of at least two is an indicator of possible melanoma. The

XX method is used to diagnose breast cancer and melanoma, and to develop

XX therapies, e.g., a mixture of peptides, derived from longer antigens and

XX known to associate with major histocompatibility complex to promote

XX cytolytic T cell proliferation, can be prepared based on the determined

XX pattern of antigen expression in a particular sample. Detecting two or

XX more of the specified tumour rejection antigen precursors improves the

XX accuracy of the assay.

XX Sequence: 8 AA:

XX melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and

XX SCP-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGE-3 for melanoma, the

XX expression of at least one is an indicator of possible breast cancer, and

XX the expression of at least two is an indicator of possible melanoma. The

XX method is used to diagnose breast cancer and melanoma, and to develop

XX therapies, e.g., a mixture of peptides, derived from longer antigens and

XX known to associate with major histocompatibility complex to promote

XX cytolytic T cell proliferation, can be prepared based on the determined

XX pattern of antigen expression in a particular sample. Detecting two or

XX more of the specified tumour rejection antigen precursors improves the

XX accuracy of the assay.

XX Sequence: 8 AA:

Query Match 4446, Score 4, DB 21, Length 8,  
Best Local Similarity 100.0%, Prod. No. 9, 3e-05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PERK R  
L I I  
D L 5 PERK R

RESLI 25  
AAY78744  
ID AAY78744 standard: peptide: 8 AA.  
XX  
AC AAY78744;  
XX  
XX 13-APR 2002 (first entry)  
XX  
DE SSX-1 HLA binding motif: #2.  
XX  
KW SSX-2: SSX1 gene; breast cancer; melanoma; NY ESO-1; SYP 1; MAGE-3;  
KW diagnosis; detection; tumour rejection antigen precursor; PCR primers;  
KW HLA binding motif.  
XX  
CS Homo sapiens.  
XX  
FN W220600642-A1.  
XX  
ED 06-JAN-2000.  
XX  
FF 03-JUN-1999; 99W0-081229.  
XX  
FR 26-JUN-1998; 98US-0105967.  
XX  
FA (CDSW) L2EWI3 INST CANCER RES.  
XX  
FI Sahlin O, Tureci O, Chen Y, Gell JO, Pfreundschuh M;  
XX  
XX WPL: 2000-137070/12.  
XX  
XX Detecting breast cancer and melanoma used for diagnosis and in  
XX development of targeted therapy .  
XX  
XX Example 2: Page 14: 24pp: English.

PS This sequence represents a HLA binding motif from the SSX-1 protein.

XX The invention relates to a method for determining breast cancer or

XX melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and

XX SCP-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGE-3 for melanoma, the

XX expression of at least one is an indicator of possible breast cancer, and

XX the expression of at least two is an indicator of possible melanoma. The

XX method is used to diagnose breast cancer and melanoma, and to develop

XX therapies, e.g., a mixture of peptides, derived from longer antigens and

XX known to associate with major histocompatibility complex to promote

XX cytolytic T cell proliferation, can be prepared based on the determined

XX pattern of antigen expression in a particular sample. Detecting two or

XX more of the specified tumour rejection antigen precursors improves the

XX accuracy of the assay.

XX Sequence: 8 AA:





SQ Sequence 5 AA: Query Match 36.4%; Score 4; DB 24; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9; ver 2.5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REKK 8  
 DB 1 REKK 4

RESULT 28  
 AAW21554  
 ID AAW21554 standard; Peptide: 9 AA.  
 XX AC AAW21554;  
 XX DT 05-JUN-1997 (first entry)  
 XX DE Corticotropin releasing factor binding protein signal oligopeptide-46.  
 XX KW Hydrophilic; signal oligopeptide; hydrophobicity; maximal; vaccine; SIV;  
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;  
 KW charge; polarity; farcetyl synthetase; plasminogen activator inhibitor 1;  
 KW hydroxyoctylglutaryl coenzyme A reductase; alcohol precursor; thesaur;  
 KW gonadotropin precursor; plasminogen activator; inhibitor 2; proteolysis;  
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;  
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVS;  
 KW herpes virus 2 glycoprotein B; HSV2; celladhesin; apolipoprotein A;  
 KW Tropicoma pallidum membrane protein (MPA); asial arylolol polypeptide;  
 KW fibrinolytic MMP1; schistosoma elastase precursor; schistosomiasis;  
 KW hepatitis delta antigen; rev protein; HIV; VIV; androstenedione;  
 XX OS Homo sapiens.  
 XX W 0915566 AL.  
 XX EN 20 JUL 1995.  
 XX ID 12-JAN-1996; 95W0-US00575  
 XX PF 14-JAN-1994; 94US-0182248.  
 XX PA (RACH/) KATH M.  
 XX PI RACH M.  
 XX UR KPL 1995-260954/44.  
 XX PT Identifying signal oligopeptides; 6 proteins (5 peptides); shows as  
 XX between protein(s)  
 XX PS Claim 5; Page 81; 88pp; English.  
 XX CC The sequences given in AAW21554 represent hydrophilic signal oligo-  
 CC peptides. These signal oligopeptides are recognised on the surface  
 CC of the protein and are represented by the hydrophobicity maxima of  
 CC the protein. These peptides are enriched in charged amino acids  
 CC arranged with neutral spacer amino acids. The specific signal  
 CC character of these oligopeptides is determined by a characteristic  
 CC combination of conformation and charge within the signal sequence.  
 CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action or interaction of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by omitting one or more amino acids at  
 CC the N- and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with similar charge and/or  
 CC polarity, by omitting one or more amino acids or a combination of these.

SQ Sequence 9 AA: Query Match 36.4%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; ver 2.5;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TRER 7  
 DB 6 TRER 9

RESULT 29  
 AAW09450  
 ID AAW09450 standard; Peptide: 9 AA.  
 XX AC AAW09450;  
 XX DT 05-JUN-1997 (first entry)  
 XX DE Melanoma antigen; HOM MEL 40 HLA-A2-1 binding nonapeptide.  
 XX KW Melanoma; tumour antigen; HOM-MEL 40; serological fishing;  
 KW vaccine; HLA-A2-1; cytotoxic T lymphocyte.  
 XX OS Homo sapiens.  
 XX W 09440209 AL.  
 XX EN 19-DEC-1996.  
 XX PF 07-JUN-1996; 96W0-US09726.  
 XX PR 10-MAY-1996; 96US-0644116.  
 XX PR 07-JUN-1996; 96US-0479428.  
 XX PR 03-JAN-1996; 96US-0580380.  
 XX PA (LUDW-) LUDWIG INST CANCER RES.  
 XX PI Pfreundschuh M, Kammensee H;  
 XX DR WPI: 1997-051896/05.  
 XX PT Novel method of serological fishing - allows isolation of molecules  
 XX (resp. antigens) associated with pathological conditions, e.g.  
 XX Hodgkin's disease, cancer or autoimmune disease  
 XX PS Claim 2; Page 24; 44pp; English.  
 XX CC 3 Nonapeptides (AAW09449) were detected in the deduced amino acid  
 CC sequence for the novel melanoma cell antigen HOM-MEL 40 (see also  
 CC AAT47748) following a screening for sequences that might act as  
 CC HLA-A2.1 binders/cytotoxic T lymphocyte (CTL) stimulators.  
 CC Peptides that bind to HLA-A2.1 have the consensus sequence given in  
 CC AAW09452 or AAW09455. Experimental evidence indicated that HLA-A2  
 CC positive tumour cells present a nonamer derived from HOM-MEL 40,  
 CC suggesting that HOM-MEL 40-specific vaccines, useful in inducing  
 CC CTL, are possible.

QY 5 REKK 8  
 DB 3 REKK 6

RESULT 30  
 AAW41588  
 ID AAW41588 standard; Peptide: 9 AA.  
 XX



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XX 24 JUN 1998: 98US 0105809.
XX (1 ROW) 1 DWTG INST: CANCER RES.
XX Parvez G., Sahin U., Pritumatschuh M., Kammensee G., Stevanovic S.
XX Chao Y., Gure A., Old LJ.
XX WPI: 2003-176934/15.
XX Determining the possible presence of breast, endometrial, colorectal,
XX lung, bladder or head-neck cancer.
XX Example 13: Page 24: 40pp: English.
XX A method has been developed for determining the possible presence of a
XX cancer, which is not melanoma or synovial sarcoma. The method comprises
XX assaying a sample taken from the subject to determine the expression of
XX an SSX gene, and determining the suppression as a determination of the
XX possible presence of cancer. Expression of SSX1 gene indicates possible
XX presence of breast, endometrial, colorectal, lung, bladder or head-neck
XX cancer. These cancers are also detected by SSX2 and SSX4 gene
XX expression. SSX2 gene expression additionally indicates possible presence
XX of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
XX of SSX4 gene also indicates possible presence of ovarian or stomach
XX cancer. SSX5 gene expression indicates the same cancers as SSX1, except
XX breast cancer. Determining expression of SSX gene can be used to monitor
XX progress of melanoma or synovial sarcoma, which is not cancer. The
XX SSX derived peptide complex stimulates proliferation of cytolytic T
XX cells. This is useful for treating cancer, especially melanoma. AAY78464
XX to AAY78468 represent specifically claimed HLA binding peptides for use
XX in the method of the invention. AAY8452 to AAY8465 represent PCR
XX primers used in the isolation of SSX genes in the exemplification of the
XX present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762
XX represent peptides derived from SSX proteins or NY ES0 1, which are used
XX in the exemplification of the present invention.
XX Sequence: 9 AA.
XX Query Match: 36.4%, Score 41, DB 21, Length 9.
XX Post-Score Similarity: 100.0%, Pred. No. 9, 9e+05.
XX Mismatches: 4, Conservations: 0, Mismatches: 0, Indels: 0, Gaps: 0.
XX
XX QY 1 REPR B
XX 1 1
XX 1 REPR 4
XX
XX SLIP...
XX AAY78464
XX 1 1
XX 1 REPR 4
XX
XX 1 MAY 2000 (First entry)
XX SSX 2 derived peptide #23.
XX
XX Cancer: SSX family: SSX 1, SSX 2, SSX 3, SSX 4, SSX 5, NY ES-0.
XX HLA binding: human leukocyte antigen, cytolytic T cell, C1.1.
XX Cytostatic melanoma: synovial sarcoma.
XX Homo Sapiens.
XX W0220000924 A1.
XX 06 JAN 2000.
XX 25 JUN 1999. 99W 021449.
XX 26 JUN 1999. 99US 0105809.
XX (1 ROW) 1 DWTG INST: CANCER RES.
XX 25 JUN 1999. 99US 0105809.
XX (1 ROW) 1 DWTG INST: CANCER RES.
XX 25 JUN 1999. 99US 0105809.
XX (1 ROW) 1 DWTG INST: CANCER RES.

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XX Parvez G., Sahin U., Pritumatschuh M., Kammensee G., Stevanovic S.
XX Chao Y., Gure A., Old LJ.
XX WPI: 2003-176934/15.
XX Determining the possible presence of breast, endometrial, colorectal,
XX lung, bladder or head-neck cancer.
XX Example 13: Page 24: 40pp: English.
XX A method has been developed for determining the possible presence of a
XX cancer, which is not melanoma or synovial sarcoma. The method comprises
XX assaying a sample taken from the subject to determine the expression of
XX an SSX gene, and determining the suppression as a determination of the
XX possible presence of cancer. Expression of SSX1 gene indicates possible
XX presence of breast, endometrial, colorectal, lung, bladder or head-neck
XX cancer. These cancers are also detected by SSX2 and SSX4 gene
XX expression. SSX2 gene expression additionally indicates possible presence
XX of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
XX of SSX4 gene also indicates possible presence of ovarian or stomach
XX cancer. SSX5 gene expression indicates the same cancers as SSX1, except
XX breast cancer. Determining expression of SSX gene can be used to monitor
XX progress of melanoma or synovial sarcoma, which is not cancer. The
XX SSX derived peptide complex stimulates proliferation of cytolytic T
XX cells. This is useful for treating cancer, especially melanoma. AAY78464
XX to AAY78468 represent specifically claimed HLA binding peptides for use
XX in the method of the invention. AAY8452 to AAY8465 represent PCR
XX primers used in the isolation of SSX genes in the exemplification of the
XX present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762
XX represent peptides derived from SSX proteins or NY ES0 1, which are used
XX in the exemplification of the present invention.
XX Sequence: 9 AA.
XX Query Match: 36.4%, Score 41, DB 21, Length 9.
XX Post-Score Similarity: 100.0%, Pred. No. 9, 9e+05.
XX Mismatches: 4, Conservations: 0, Mismatches: 0, Indels: 0, Gaps: 0.
XX
XX QY 1 REPR B
XX 1 1
XX 1 REPR 4
XX
XX SLIP...
XX AAY78464
XX 1 1
XX 1 REPR 4
XX
XX 1 MAY 2000 (First entry)
XX SSX 2 derived peptide #23.
XX
XX Cancer: SSX family: SSX 1, SSX 2, SSX 3, SSX 4, SSX 5, NY ES-0.
XX HLA binding: human leukocyte antigen, cytolytic T cell, C1.1.
XX Cytostatic melanoma: synovial sarcoma.
XX Homo Sapiens.
XX W0220000924 A1.
XX 06 JAN 2000.
XX 25 JUN 1999. 99W 021449.
XX 26 JUN 1999. 99US 0105809.
XX (1 ROW) 1 DWTG INST: CANCER RES.
XX 25 JUN 1999. 99US 0105809.
XX (1 ROW) 1 DWTG INST: CANCER RES.
XX 25 JUN 1999. 99US 0105809.
XX (1 ROW) 1 DWTG INST: CANCER RES.

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LR WPI: 2000 170933/15.  
XX  
PI determining the possible presence of breast and/or head-neck cancer.  
XX Lung, bladder or head-neck cancer.  
XX Example 13: Page 25; 4pp; English.  
XX  
XX A method has been developed for detecting the possible presence of a  
XX cancer, which is not melanoma or synovial sarcoma. The method comprises  
XX assaying a sample taken from the subject to determine the expression of  
XX an SSX gene, and determining the expression as a determination of the  
XX possible presence of cancer. Expression of SSX1 gene indicates possible  
XX presence of breast, endometrial, cervical, lung, bladder or head-neck  
XX cancer. These cancers are also detected by SSX2 and SSX4 gene  
XX expression. SSX2 gene expression additionally indicates possible presence  
XX of lymphoma, renal cell cancer, glioma and prostate cancer. Expression  
XX of SSX4 gene also indicates possible presence of ovarian or stomach  
XX cancer. SSX5 gene expression indicates the same cancers as SSX1, except  
XX breast cancer. Determined expression of SSX gene can be used to monitor  
XX progress of melanoma or synovial sarcoma, which is not cancer. The  
XX SSX derived peptide complex stimulates proliferation of cytolytic T  
XX cells. This is useful for treating cancer, especially melanoma. AAY78464  
XX to AAY78468 represent specifically claimed HLA binding peptides for use  
XX in the method of the invention. AAY78469 to AAY78762 represent PCR  
XX primers used in the isolation of SSX genes in the exemplification of the  
XX present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762  
XX represent peptides derived from SSX proteins or NY-ESO-1, which are used  
XX in the exemplification of the present invention.  
XX  
XX Sequence: 9 AA:  
XX  
XX Query Match: 36.4%, Score 13; Db 21; Length 9;  
XX Best local Similarity: 100.0%; Prod. No. 9.3e-05;  
XX Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
XX  
XX  
XX 5 REEK 8  
XX 11  
XX 1 REEK 4  
XX  
XX  
XX RES11 46  
XX AAY78464  
XX ID AAY78465 Standard: Peptide: 9 AA.  
XX  
XX AAY78465  
XX  
XX 10 MAY 2000 (first entry)  
XX  
XX SSX 1 derived peptide #1.  
XX  
XX Cancer, SSX family; SSX 1; SSX 2; NY-ESO-1; NY-ESO-2; NY-ESO-3;  
XX HLA binding; human leukocyte antigen; protein; gene; cell; tissue;  
XX cytostatic; melanoma; synovial sarcoma  
XX  
XX Bone sapiens  
XX  
XX W 20000042 AL  
XX  
XX 06 JAN 2000  
XX  
XX 03 JUN 1999 96W0-0512295  
XX  
XX 26 JUN 1998 96US-0105007  
XX  
XX (LHW) LEWIS INST CANCER RES  
XX  
XX Sahli U, Tureci O, Chen Y, Old LJ, Pfreundschuh M;  
XX  
XX WPI: 2000 170933/12  
XX  
XX Detecting breast cancer and melanoma used for diagnosis and in  
XX development of targeted therapy  
XX  
XX Example 2: Page 12; 24pp; English.  
XX  
XX This sequence represents a HLA binding motif from the SSX-2 protein.  
XX The invention relates to a method for determining breast cancer or  
XX lung, bladder or head-neck cancer.

XX  
XX Example 13: Page 25; 4pp; English.  
XX  
XX A method has been developed for determining the possible presence of a  
XX cancer, which is not melanoma or synovial sarcoma. The method comprises  
XX assaying a sample taken from the subject to determine the expression of  
XX an SSX gene, and determining the expression as a determination of the  
XX possible presence of cancer. Expression of SSX1 gene indicates possible  
XX presence of breast, endometrial, cervical, lung, bladder or head-neck  
XX cancer. These cancers are also detected by SSX2 and SSX4 gene  
XX expression. SSX2 gene expression additionally indicates possible presence  
XX of lymphoma, renal cell cancer, glioma and prostate cancer. Expression  
XX of SSX4 gene also indicates possible presence of ovarian or stomach  
XX cancer. SSX5 gene expression indicates the same cancers as SSX1, except  
XX breast cancer. Determined expression of SSX gene can be used to monitor  
XX progress of melanoma or synovial sarcoma, which is not cancer. The  
XX SSX derived peptide complex stimulates proliferation of cytolytic T  
XX cells. This is useful for treating cancer, especially melanoma. AAY78464  
XX to AAY78468 represent specifically claimed HLA binding peptides for use  
XX in the method of the invention. AAY78469 to AAY78762 represent PCR  
XX primers used in the isolation of SSX genes in the exemplification of the  
XX present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762  
XX represent peptides derived from SSX proteins or NY-ESO-1, which are used  
XX in the exemplification of the present invention.  
XX  
XX Sequence: 9 AA:  
XX  
XX Query Match: 36.4%, Score 13; Db 21; Length 9;  
XX Best local Similarity: 100.0%; Prod. No. 9.3e-05;  
XX Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
XX  
XX  
XX 5 REEK 8  
XX 11  
XX 1 REEK 4  
XX  
XX  
XX RES11 46  
XX AAY78464  
XX ID AAY78465 Standard: Peptide: 9 AA.  
XX  
XX AAY78465  
XX  
XX 10 MAY 2000 (first entry)  
XX  
XX SSX 2 HLA binding motif #2.  
XX  
XX SSX 2; SSX 1; SSX 2; NY-ESO-1; NY-ESO-2; NY-ESO-3;  
XX HLA binding; human leukocyte antigen; protein; gene; cell; tissue;  
XX cytostatic; melanoma; synovial sarcoma  
XX  
XX Bone sapiens  
XX  
XX W 20000042 AL  
XX  
XX 06 JAN 2000  
XX  
XX 03 JUN 1999 96W0-0512295  
XX  
XX 26 JUN 1998 96US-0105007  
XX  
XX (LHW) LEWIS INST CANCER RES  
XX  
XX Sahli U, Tureci O, Chen Y, Old LJ, Pfreundschuh M;  
XX  
XX WPI: 2000 170933/12  
XX  
XX Detecting breast cancer and melanoma used for diagnosis and in  
XX development of targeted therapy  
XX  
XX Example 2: Page 12; 24pp; English.  
XX  
XX This sequence represents a HLA binding motif from the SSX-2 protein.  
XX The invention relates to a method for determining breast cancer or  
XX lung, bladder or head-neck cancer.

melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and SSCP-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGP-3 for melanoma. The expression of at least one is an indicator of possible breast cancer, and the expression of at least two is an indicator of possible melanoma. The method is used to diagnose breast cancer and melanoma, and to develop therapies, e.g., a mixture of peptides, derived from longer antigens and known to associate with major histocompatibility complex to promote cytolytic T cell proliferation, can be prepared based on the determined pattern of antigen expression in a particular sample. Detecting two or more of the specified tumour rejection antigen precursors improves the accuracy of the assay.

XX Sequence: 9 AA;

Query Match: 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8

DB 3 REK 6

RESULT 47

AAV76745

ID: AAV76745 standard; Peptide: 9 AA;

AC AAV76745;

DC 13-APR-2000 (first entry)

XX SSX-2 HLA binding motif #14.

XX SSX-2; SSX1 gene; breast cancer; melanoma; NY-ESO-1; SSCP-1; MAGP-3;

KW diagnosis; detection; tumour rejection antigen precursor; PCR primer;

KW HLA binding motif;

XX Homo sapiens;

XX W020000642-A1;

XX 06-JAN-2000;

XX 03-JUN-1999; 99WD-US12293;

XX 26-JUN-1998; 98US-0105907;

XX (LUDW) LODWIG INST CANCER RES;

XX Salim U, Tureci O, Chen Y, Old LJ, Pfreundschuh M;

XX W01-2000-14703/12;

XX Detecting breast cancer and melanoma used for diagnosis and in

XX development of targeted therapy.

XX Example 2; Page 12; 24pp; English.

XX This sequence represents a HLA binding motif from the SSX-2 protein. The invention relates to a method for determining breast cancer or melanoma in a sample by assaying for expression of NY-ESO-1, SSX-2 and SSCP-1 for breast cancer, or NY-ESO-1, SSX-2 and MAGP-3 for melanoma. The expression of at least one is an indicator of possible breast cancer, and the expression of at least two is an indicator of possible melanoma. The method is used to diagnose breast cancer and melanoma, and to develop therapies, e.g., a mixture of peptides, derived from longer antigens and known to associate with major histocompatibility complex to promote cytolytic T cell proliferation, can be prepared based on the determined pattern of antigen expression in a particular sample. Detecting two or more of the specified tumour rejection antigen precursors improves the accuracy of the assay.

XX Sequence: 9 AA;

Query Match: 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8

DB 3 REK 6

RESULT 49

AAV99002

ID: AAV99002 standard; Peptide: 9 AA;

XX Sequence: 9 AA;

Query Match: 36.4%; Score 4; DB 21; Length 9;  
Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8

DB 3 REK 6

XX AAN94012;  
 XX AC  
 XX DT C7 DEC 2001 (first entry)  
 XX DE Vaccine related MHC ligand peptide SEQ ID No:196;  
 XX EE  
 XX KW glutamic acid; glutamine; valine; arginine; histidine; aspartic acid; asparagine;  
 KW MHC; immunomodulator; antitumor; endotoxin; isopentenyl;  
 KW virulence; bactericidal; antiparasitic; endocytosis; crystallin;  
 KW medicine; pharmacological; immune system; tumor; immunodeficiency;  
 KW autoimmune; hypersensitivity; allergy; graft rejection; infection;  
 KW hormonal disorder; central nervous system disease; cancer; melanoma;  
 XX anti-melanoma vaccine; human immunodeficiency virus;  
 XX OS Influenza virus;  
 XX PK W:200170772 A2;  
 XX PP 27 SEP 2001;  
 XX EE 22 MAR 2001; Z001W0-PR00872;  
 XX FR 23 MAR 2001; Z000PR-0003711;  
 XX IA (FABR ) FABRE MEDICAMENT SA PIERRE;  
 XX EE KLINIQUE BARON C. CORVAIA N. BUCK A. GATSOULIS;  
 XX EE WP1: 2001-611475/70;  
 XX EE  
 XX PT Stabilized pharmaceutical containing N-terminal glutamic acid or  
 XX PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt  
 XX PT with strong acid;  
 XX PS Claim 9; Page 64; 149pp; French;  
 XX CC The present invention describes a pharmaceutical compound (i) that  
 CC contains an N terminal glutamic acid (Glu) or glutamine (Gln) residue  
 CC in the form of an addition salt with a strong, physiologically  
 CC acceptable acid (11). Also described are: (a) a pharmaceutical  
 CC composition containing at least one (i); (b) a vaccine containing at  
 CC least one (i) where this is a major immunomodulatory complex (IMP)  
 CC (claim 1a); (c) a method for in vitro diagnosis of diseases associated  
 CC with the presence of (1a); (d) a kit for action (c) that includes a (1a);  
 CC and (e) a process for preparing (1); (f) has immunomodulatory, preventive  
 CC antitumor, antiparasitic, antitubercular, bactericidal, antiparasitic,  
 CC immunological and cytostatic activities. Also described is human (i)  
 CC veterinary medicine; in pharmaceutical compositions for treatment of  
 CC disorders, e.g. immune deficiency, infectious diseases, opportunistic  
 CC allergy, graft rejection, infection, cancer, tumor and central  
 CC nervous system diseases); also, where (i) is a viral agent (1a), the  
 CC vaccines for treatment or prevention of (c); (ii) a bacterial parasite  
 CC or fungal infection; or (11) of cancer. A particular application is in  
 CC anti-melanoma vaccines; (1) are also useful for in vitro diagnosis of  
 CC diseases associated with interactions between IMP and (1); e.g. melanoma  
 CC and human immunodeficiency virus infection. *RAY9408 to AAN94012*  
 CC represent peptides which can be used in pharmaceutical compositions from  
 CC the present invention.  
 XX SC Sequence 9 AA;  
 XX Query Match 46.4% Score 4; Db 22; Length 9;  
 XX Best Local Similarity 100.0% Id. No. 9; 3e-05;  
 XX Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 XX QY 2 RKTR 5  
 XX Eb 6 RKTR 9  
 XX  
 XX RESULT 40  
 XX AAG55757  
 XX ID AAG55757 standard; Peptide: 9 AA;  
 XX AC AAG55757;  
 XX DT 27 AUG 2002 (first entry)  
 XX DE Plant ICK protein conserved motif : #65  
 XX EE  
 XX KW Plant; inhibitor of cyclin dependent kinase; ICK.  
 XX OS Arabidopsis thaliana;  
 XX XX W0200228893-A2;  
 XX PP 11-AIR 2002;  
 XX EE 29-JUN-2001; Z001W0-1601492;  
 XX PR 14-JUL 2002; Z000US-218471P;  
 XX PR 13-OCT 2000; Z000US-241219P;  
 XX XX (CRGP-) CRGPDESIGN NV;  
 XX PA Frankard VMS, Petes Bota AM, Droual A, Mironov V, Inze D;  
 XX PI Metzfeld Y;  
 XX DE WP1: 2002-471311/50;  
 XX EE  
 XX PT Novel plant ICK (inhibitors of Cyclin Dependent Kinases) polypeptide  
 XX PT used to screen substrates, drugs or compounds which modulate ICK  
 XX PT activity and treat disorders characterised by an insufficient or  
 XX PT excessive production of ICK inhibitors -  
 XX PS Disclosure; Page 14; 141pp; English;  
 XX CC this invention relates to the DNA and protein sequences of novel  
 CC isolated ICK (inhibitors of Cyclin dependent kinases) proteins.  
 CC the sequences of the invention may be used for treating disorders  
 CC characterised by insufficient or excessive production of an ICK  
 CC inhibitor. The protein of the invention may also be used to screen  
 CC for naturally-occurring ICK substrates, drugs or compounds which  
 CC modulate ICK activity, as well as to treat disorders characterised by  
 CC insufficient or excessive production of ICK protein, forms which have  
 CC decreased or aberrant activity compared to ICK wild type protein.  
 CC the present sequence represents an inhibitor of cyclin dependent  
 CC kinase (ICK) protein of the invention.  
 XX SC Sequence 9 AA;  
 XX Query Match 46.4% Score 4; Db 23; Length 9;  
 XX Best Local Similarity 100.0% Id. No. 9; 3e-05;  
 XX Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 XX QY 7 RKSR 10  
 XX Eb 6 RKSR 9  
 XX  
 XX RESULT 41  
 XX ABB94513  
 XX ID ABB94513 standard; Peptide: 9 AA;  
 XX AC ABB94513;  
 XX DT 17-JUN-2002 (first entry)  
 XX EE CTL epitope HLA peptide SEQ ID No:42;  
 XX KW Human; 158p114; chromosome 8q22q23; 158p114; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL;  
 XX CS Homo sapiens

XX ID AAG55757 standard; Peptide: 9 AA;  
 XX AC AAG55757;  
 XX DT 27 AUG 2002 (first entry)  
 XX DE Plant ICK protein conserved motif : #65  
 XX EE  
 XX KW Plant; inhibitor of cyclin dependent kinase; ICK.  
 XX OS Arabidopsis thaliana;  
 XX XX W0200228893-A2;  
 XX PP 11-AIR 2002;  
 XX EE 29-JUN-2001; Z001W0-1601492;  
 XX PR 14-JUL 2002; Z000US-218471P;  
 XX PR 13-OCT 2000; Z000US-241219P;  
 XX XX (CRGP-) CRGPDESIGN NV;  
 XX PA Frankard VMS, Petes Bota AM, Droual A, Mironov V, Inze D;  
 XX PI Metzfeld Y;  
 XX DE WP1: 2002-471311/50;  
 XX EE  
 XX PT Novel plant ICK (inhibitors of Cyclin Dependent Kinases) polypeptide  
 XX PT used to screen substrates, drugs or compounds which modulate ICK  
 XX PT activity and treat disorders characterised by an insufficient or  
 XX PT excessive production of ICK inhibitors -  
 XX PS Disclosure; Page 14; 141pp; English;  
 XX CC this invention relates to the DNA and protein sequences of novel  
 CC isolated ICK (inhibitors of Cyclin dependent kinases) proteins.  
 CC the sequences of the invention may be used for treating disorders  
 CC characterised by insufficient or excessive production of an ICK  
 CC inhibitor. The protein of the invention may also be used to screen  
 CC for naturally-occurring ICK substrates, drugs or compounds which  
 CC modulate ICK activity, as well as to treat disorders characterised by  
 CC insufficient or excessive production of ICK protein, forms which have  
 CC decreased or aberrant activity compared to ICK wild type protein.  
 CC the present sequence represents an inhibitor of cyclin dependent  
 CC kinase (ICK) protein of the invention.  
 XX SC Sequence 9 AA;  
 XX Query Match 46.4% Score 4; Db 23; Length 9;  
 XX Best Local Similarity 100.0% Id. No. 9; 3e-05;  
 XX Matches 4; Conservative 0; Mismatches 0; Gaps 0;  
 XX QY 7 RKSR 10  
 XX Eb 6 RKSR 9  
 XX  
 XX RESULT 41  
 XX ABB94513  
 XX ID ABB94513 standard; Peptide: 9 AA;  
 XX AC ABB94513;  
 XX DT 17-JUN-2002 (first entry)  
 XX EE CTL epitope HLA peptide SEQ ID No:42;  
 XX KW Human; 158p114; chromosome 8q22q23; 158p114; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CTL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL;  
 XX CS Homo sapiens

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XX Synthetic.
XX W0200216596 A2.
XX
XX 26 FEB 2002.
XX
XX 22 AUG 2001: 2001W0216596A2.1.
XX
XX 22 AUG 2001: 2000US-227-98P.
XX
XX 10 APR 2001: 2001US-262739P.
XX
XX (AGEN) AGENSYS INC.
XX
XX Chailita-Eid IM, Robert KS, Kaitano AH, Afar DEH, Levin E;
XX Paris M, Ge W, Jakubovits A;
XX WPI: 2002-265957/1.
XX
XX Monitoring 158P1H4 gene products in biological sample from patient who
XX has or is suspected of having cancer, useful for treating cancer.
XX comprises identifying presence of aberrant 158P1H4 gene products in
XX biological sample.
XX
XX Claim 64: Page 143, 209pp; English.
XX
XX The present invention describes a method for monitoring 158P1H4 gene
XX products in a biological sample from a patient who has or is suspected
XX of having cancer. The method comprises determining the status of 158P1H4
XX gene products in a tissue sample from an individual, comparing the
XX status to the status of 158P1H4 gene products in a normal sample, and
XX identifying the presence of aberrant 158P1H4 gene products in the sample.
XX 158P1H4 sequences have cytostatic activity and can be used in vaccine
XX production. 158P1H4 polynucleotides may be used in monitoring genetic
XX abnormalities. The 158P1H4 proteins may be used in assessing the status
XX of 158P1H4 gene products in normal versus cancerous tissues and so
XX elucidating the malignant phenotype, in generating and characterizing
XX domain specific antibodies, for identifying agents or cellular factors
XX that bind to 158P1H4 or its particular domain, and for generating
XX cancer vaccines. Antibodies against 158P1H4 are useful in diagnostic
XX and prognostic assays, in treating patients with cancer, in generating
XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,
XX and as immunological reagents for detecting 158P1H4 expressing cells.
XX The antibodies are particularly useful in bladder cancer diagnosis and
XX prognostic assays, and imaging methodologies. The 158P1H4 gene has been
XX located to chromosome 8q22-q23, and the 158P1H4 gene also described in
XX the present invention has been located to chromosome 8q23. ABL50400 to
XX ABL50429 and ABB94468 to ABB94468 represent sequences used in the
XX exemplification of the present invention.
XX
XX Sequence: 9 AA:
XX
XX Query Match: 36.4%, Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%, Pref. No. 9, 3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 RKSK 10
XX (11)
XX 4 RKSK 9
XX
XX RESULTS: A2
XX ABB94468
XX
XX ABB94468: standard; Peptide: 9 AA.
XX
XX ABB94468:
XX
XX 17-JUN-2002 (first entry)
XX
XX CTL epitope HLA peptide SEQ ID NO:122.
XX
XX Human, 158P1H4: chromosome 8q22-q23, 158P1H4, chromosome 8q23; cancer;
XX bladder cancer; immune response; cytotoxic T lymphocyte (CTL); HLA;
XX human leukocyte antigen; helper T lymphocyte, HTL.

```

```

XX Homo sapiens.
XX Synthetic.
XX
XX W0200216596 A2.
XX
XX 26 FEB 2002.
XX
XX 22 AUG 2001: 2001W0216596A2.1.
XX
XX 22 AUG 2001: 2000US-227-98P.
XX
XX 10 APR 2001: 2001US-262739P.
XX
XX (AGEN) AGENSYS INC.
XX
XX Chailita-Eid IM, Robert KS, Kaitano AH, Afar DEH, Levin E;
XX Paris M, Ge W, Jakubovits A;
XX WPI: 2002-265957/1.
XX
XX Monitoring 158P1H4 gene products in biological sample from patient who
XX has or is suspected of having cancer, useful for treating cancer.
XX comprises identifying presence of aberrant 158P1H4 gene products in
XX biological sample.
XX
XX Claim 64: Page 149; 209pp; English.
XX
XX The present invention describes a method for monitoring 158P1H4 gene
XX products in a biological sample from a patient who has or is suspected
XX of having cancer. The method comprises determining the status of 158P1H4
XX gene products in a tissue sample from an individual, comparing the
XX status to the status of 158P1H4 gene products in a normal sample, and
XX identifying the presence of aberrant 158P1H4 gene products in the sample.
XX 158P1H4 sequences have cytostatic activity and can be used in vaccine
XX production. 158P1H4 polynucleotides may be used in monitoring genetic
XX abnormalities. The 158P1H4 proteins may be used in assessing the status
XX of 158P1H4 gene products in normal versus cancerous tissues and so
XX elucidating the malignant phenotype, in generating and characterizing
XX domain specific antibodies, for identifying agents or cellular factors
XX that bind to 158P1H4 or its particular domain, and for generating
XX cancer vaccines. Antibodies against 158P1H4 are useful in diagnostic
XX and prognostic assays. Antibodies against 158P1H4 are useful in diagnostic
XX and prognostic assays, in treating patients with cancer, in generating
XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,
XX and as immunological reagents for detecting 158P1H4 expressing cells.
XX The antibodies are particularly useful in bladder cancer diagnosis and
XX prognostic assays, and imaging methodologies. The 158P1H4 gene has been
XX located to chromosome 8q22-q23, and the 158P1H4 gene also described in
XX the present invention has been located to chromosome 8q23. ABL50400 to
XX ABL50429 and ABB94468 to ABB94468 represent sequences used in the
XX exemplification of the present invention.
XX
XX Sequence: 9 AA:
XX
XX Query Match: 36.4%, Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%, Pref. No. 9, 3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 RKSK 10
XX (11)
XX 4 RKSK 7
XX
XX RESULTS: 43
XX ABB94793
XX
XX ABB94793: standard; Peptide: 9 AA.
XX
XX ABB94793:
XX
XX 17-JUN-2002 (first entry)
XX
XX CTL epitope HLA peptide SEQ ID NO:122.
XX
XX Human, 158P1H4: chromosome 8q22-q23, 158P1H4, chromosome 8q23; cancer;
XX

```

KW bladder cancer; immune response; cytotoxic T lymphocyte; CIL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL;  
 US B-cell suppress.  
 US Synchetic.  
 PN W020216596 A2.  
 XX 48 FEB 2002.  
 XX 22 AUG 2001; 2001WO-US26411.  
 XX 22 AUG 2001; 2001US-2270981.  
 XX 10 APR 2001; 2001US-2627496.  
 XX (AGEN-) AGENSYS INC.  
 XX Chaitin Ed DM, Hubert RS, Kallans AB, Atar DEH, Levin E;  
 XX Faris M, Se W, Jakubovits A;  
 XX WPI: 2002-269357/31.  
 XX Monitoring 158PIH4 gene products in biological sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer,  
 XX comprises identifying presence of aberrant 158PIH4 gene products in  
 XX biological sample.  
 XX Claim 14; Page 153; 269pp; English.  
 XX The present invention describes a method for monitoring 158PIH4 gene  
 XX products in a biological sample from a patient who has or is suspected  
 XX of having cancer. The method comprises determining the status of 158PIH4  
 XX gene products in a tissue sample from an individual, comparing the  
 XX status to the status of 158PIH4 gene products in a normal sample, and  
 XX identifying the presence of aberrant 158PIH4 gene products in the sample.  
 XX 158PIH4 sequences have cytostatic activity and can be used in vaccine  
 XX production. 158PIH4 polynucleotides may be used in monitoring genetic  
 XX abnormalities. The 158PIH4 proteins may be used in assessing the status  
 XX of 158PIH4 gene products in normal versus cancerous tissues and so  
 XX elucidating the malignant phenotype, in generating and characterizing  
 XX diagnostic antibodies, for identifying agents or cellular factors  
 XX that bind to 158PIH4 or its particular domain, and for generating  
 XX cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 XX and prognostic assays. In treating patients with cancer, in generating  
 XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 XX and as immunization reagents for detecting 158PIH4-expressing cells.  
 XX The antibodies are particularly useful in bladder cancer diagnostic and  
 XX prognostic assays, and immunization reagents. The 158PIH4 gene has been  
 XX located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
 XX the present invention has been located to chromosome 8q23. AB050400 to  
 XX AB050429 and AB094468 to AB094498 represent sequences used in the  
 XX exemplification of the present invention.  
 XX Sequence 9 AA;  
 Query Match 36.4%, Score 4; DP 23; Length 9;  
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KSKK 16  
 LQ 4 KSKK 7  
 RESULT 44  
 ABB94797  
 XX ABB94797 Standard; Peptide: 9 AA.  
 AC ABB94797;  
 XX 17 JUN 2002 (first entry)  
 XX CIL epitope HLA peptide SEQ ID NO. 27.

XX Human: 158PIH4; chromosome 8q22-q23, 158PIH4; chromosome 8q23; cancer;  
 KW bladder cancer; immune response; cytotoxic T lymphocyte; CIL; HLA;  
 KW human leukocyte antigen; helper T lymphocyte; HTL;  
 US B-cell suppress.  
 US Synchetic.  
 PN W020216596 A2.  
 XX 48 FEB 2002.  
 XX 22 AUG 2001; 2001WO-US26411.  
 XX 22 AUG 2001; 2001US-2270981.  
 XX 10 APR 2001; 2001US-2627496.  
 XX (AGEN-) AGENSYS INC.  
 XX Chaitin Ed DM, Hubert RS, Kallans AB, Atar DEH, Levin E;  
 XX Faris M, Se W, Jakubovits A;  
 XX WPI: 2002-269357/31.  
 XX Monitoring 158PIH4 gene products in biological sample from patient who  
 XX has or is suspected of having cancer, useful for treating cancer, in  
 XX comprises identifying presence of aberrant 158PIH4 gene products in  
 XX biological sample.  
 XX Claim 14; Page 153; 209pp; English.  
 XX The present invention describes a method for monitoring 158PIH4 gene  
 XX products in a biological sample from a patient who has or is suspected  
 XX of having cancer. The method comprises determining the status of 158PIH4  
 XX gene products in a tissue sample from an individual, comparing the  
 XX status to the status of 158PIH4 gene products in a normal sample, and  
 XX identifying the presence of aberrant 158PIH4 gene products in the sample.  
 XX 158PIH4 sequences have cytostatic activity and can be used in vaccine  
 XX production. 158PIH4 polynucleotides may be used in monitoring genetic  
 XX abnormalities. The 158PIH4 proteins may be used in assessing the status  
 XX of 158PIH4 gene products in normal versus cancerous tissues and so  
 XX elucidating the malignant phenotype, in generating and characterizing  
 XX diagnostic antibodies, for identifying agents or cellular factors  
 XX that bind to 158PIH4 or its particular domain, and for generating  
 XX cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic  
 XX and prognostic assays. In treating patients with cancer, in generating  
 XX cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,  
 XX and as immunization reagents for detecting 158PIH4-expressing cells.  
 XX The antibodies are particularly useful in bladder cancer diagnostic and  
 XX prognostic assays, and immunization reagents. The 158PIH4 gene has been  
 XX located to chromosome 8q22-q23, and the 158PIH4 gene also described in  
 XX the present invention has been located to chromosome 8q23. AB050400 to  
 XX AB050429 and AB094468 to AB094498 represent sequences used in the  
 XX exemplification of the present invention.  
 XX Sequence 9 AA;  
 Query Match 36.4%, Score 4; DP 23; Length 9;  
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KSKK 16  
 LQ 4 KSKK 4  
 RESULT 45  
 ABB94867  
 XX ABB94867 Standard; Peptide: 9 AA.  
 AC ABB94867;  
 XX 17 JUN 2002 (first entry)



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XX  CTL epitope HLA peptide SEQ ID NO:416
XX
XX  BLADDER 158PIH4: chromosome 8q22-q24, 158PIH4: chromosome 8q23, cancer;
KW  bladder cancer, immune response: cytotoxic T lymphocyte, CTL, HLA;
KW  human leukocyte antigen: helper T lymphocyte, HTL;
XX
XX  Homo sapiens,
XX  Synthetic,
XX
XX  W420021598 A2,
XX
XX  28 FEB-2002,
XX
XX  22 AUG-2001: 2001WG-US2411,
XX
XX  22 AUG-2001: 2000US-227099P,
XX  10 APR-2001: 2001US-282719P,
XX
XX  (AGEN-) AGENSYS INC,
XX
XX  Charlotte Ed PM, Robert KS, Raitano AB, Afar DEH, Levin E;
XX  Paris M, Ge W, Jakobovits A,
XX
XX  WPI: 2002-264357/31,
XX
XX  Monitoring 158PIH4 gene products in biological sample from patient who
XX  has or is suspected of having cancer, useful for treating cancer,
XX  comprises identifying presence of aberrant 158PIH4 gene products in
XX  biological sample,
XX
XX  Claim 64: Page 156: 239pp: English,
XX
XX  The present invention describes a method for monitoring 158PIH4 gene
XX  products in a biological sample from a patient who has or is suspected
XX  of having cancer. The method comprises determining the status of 158PIH4
XX  gene products in a tissue sample from an individual, comparing the
XX  status to the status of 158PIH4 gene products in a normal sample, and
XX  identifying the presence of aberrant 158PIH4 gene products in the sample.
XX  158PIH4 sequences have cytostatic activity and can be used in vaccine
XX  products. 158PIH4 polynucleotides may be used in monitoring genetic
XX  abnormalities. The 158PIH4 proteins may be used in assessing the status
XX  of 158PIH4 gene products in normal versus cancerous tissues and so
XX  characterizing the malignant phenotype, in generating and characterizing
XX  domain specific antibodies, for identifying agents or cellular factors
XX  that bind to 158PIH4 or its particular domain, and for generating
XX  cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic
XX  and prognostic assays. In treating patients with cancer, in generating
XX  cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,
XX  and as immunomodulatory reagents for detecting 158PIH4-expressing cells,
XX  the antibodies are particularly useful in bladder cancer diagnostic and
XX  prognostic assays, and imaging methodologies. The 158PIH4 gene has been
XX  located to chromosome 8q22-q24, and the 158PIH4 gene also described in
XX  AB540429 and AB694468 to ABB95188 represent sequences used in the
XX  exemplification of the present invention.
XX
XX  Sequence 9 AA:
XX
XX  Query Match 36.4%; Score 4; DB 23; Length 9;
XX  Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX  Matches 4; Conservative 0; Mismatches 0; Gaps 0;
XX
XX  7 RRSK 10
XX  IIII
XX  3 RRSK 6
XX
XX  RESULT 47
XX  ABB9459P
XX  ID ABB9459P standard: Peptide: 9 AA.

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XX  17 JUN-2002 (first entry)
XX
XX  CTL epitope HLA peptide SEQ ID NO:527,
XX
XX  BLADDER 158PIH4: chromosome 8q22-q24, 158PIH4: chromosome 8q23, cancer;
KW  bladder cancer, immune response: cytotoxic T lymphocyte, CTL, HLA;
KW  human leukocyte antigen: helper T lymphocyte, HTL;
XX
XX  Homo sapiens,
XX  Synthetic,
XX
XX  W420021598 A2,
XX
XX  24 FEB-2002,
XX
XX  22 AUG-2001: 2001WG-US2411,
XX
XX  22 AUG-2001: 2000US-227099P,
XX  10 APR-2001: 2001US-282719P,
XX
XX  (AGEN-) AGENSYS INC,
XX
XX  Charlotte Ed PM, Robert KS, Raitano AB, Afar DEH, Levin E;
XX  Paris M, Ge W, Jakobovits A,
XX
XX  WPI: 2002-264357/31,
XX
XX  Monitoring 158PIH4 gene products in biological sample from patient who
XX  has or is suspected of having cancer, useful for treating cancer,
XX  comprises identifying presence of aberrant 158PIH4 gene products in
XX  biological sample,
XX
XX  Claim 64: Page 159: 239pp: English,
XX
XX  The present invention describes a method for monitoring 158PIH4 gene
XX  products in a biological sample from a patient who has or is suspected
XX  of having cancer. The method comprises determining the status of 158PIH4
XX  gene products in a tissue sample from an individual, comparing the
XX  status to the status of 158PIH4 gene products in a normal sample, and
XX  identifying the presence of aberrant 158PIH4 gene products in the sample.
XX  158PIH4 sequences have cytostatic activity and can be used in vaccine
XX  products. 158PIH4 polynucleotides may be used in monitoring genetic
XX  abnormalities. The 158PIH4 proteins may be used in assessing the status
XX  of 158PIH4 gene products in normal versus cancerous tissues and so
XX  characterizing the malignant phenotype, in generating and characterizing
XX  domain specific antibodies, for identifying agents or cellular factors
XX  that bind to 158PIH4 or its particular domain, and for generating
XX  cancer vaccines. Antibodies against 158PIH4 are useful in diagnostic
XX  and prognostic assays. In treating patients with cancer, in generating
XX  cytotoxic T lymphocyte (CTL) or helper T lymphocyte (HTL) responses,
XX  and as immunomodulatory reagents for detecting 158PIH4-expressing cells,
XX  the antibodies are particularly useful in bladder cancer diagnostic and
XX  prognostic assays, and imaging methodologies. The 158PIH4 gene has been
XX  located to chromosome 8q22-q24, and the 158PIH4 gene also described in
XX  AB540429 and AB694468 to ABB95188 represent sequences used in the
XX  exemplification of the present invention.
XX
XX  Sequence 9 AA:
XX
XX  Query Match 36.4%; Score 4; DB 23; Length 9;
XX  Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX  Matches 4; Conservative 0; Mismatches 0; Gaps 0;
XX
XX  7 RRSK 10
XX  IIII
XX  3 RRSK 6
XX
XX  RESULT 47
XX  ABB9459P
XX  ID ABB9459P standard: Peptide: 9 AA.

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```

KW human leukocyte antigen.
XX
GS Homo sapiens.
XX
PN W020028921-A2.
XX
EC 24-007-2002.
XX
PF 10-APR-2001: 2002WO-US11654.
XX
PF 10-APR-2001: 2001US-282739P.
XX
PF 10-APR-2001: 2001US-283112P.
XX
PF 25-APR-2001: 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakubovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
WP1: 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients.
XX
PS Claim 13; Page 272; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and AB278169-AB278186). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX the genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
SQ Sequence 9 AA;
XX
XX Query Match: 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. NO. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 IRR 7
XX 1-11
XX 2 IRR 5
XX
XX Search completed: September 30, 2003, 10:25:13
XX Job time : 48.1667 secs

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```

KW human leukocyte antigen.
XX
GS Homo sapiens.
XX
PN W020028921-A2.
XX
EC 24-007-2002.
XX
PF 10-APR-2002: 2002WO-US11654.
XX
PF 10-APR-2001: 2001US-282739P.
XX
PF 10-APR-2001: 2001US-283112P.
XX
PF 25-APR-2001: 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakubovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
WP1: 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response
XX in cancer patients.
XX
PS Claim 13; Page 272; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
XX proteins (AB278120-AB278168 and AB278169-AB278186). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX the genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention.
XX
SQ Sequence 9 AA;
XX
XX Query Match: 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 IRR 7
XX 1-11
XX 6 IRR 7
XX
XX ABR15209
XX ABR15209 standard; Peptide: 9 AA
XX
XX ABR15209.
XX
XX 19-FEB-2003 (first entry)
XX
XX Human cancer related protein 179907 HLA peptide #249.
XX
XX Human cytotoxic; vaccino; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX W020028921-A2.
XX
XX 24 OCT-2002.
XX
XX 10-APR-2002: 2002WO-US11654.
XX

```



103	18.2	10	2	855087	cytochrome c oxidase	176	2	18.2	12	2	SI5815	translation elonga
104	18.2	10	2	8X0050	lysosomal aspartate	177	2	18.2	12	2	S97206	kassinin - Senegal
105	18.2	10	2	A55095	proteoglycan core	178	2	18.2	12	2	A61359	vespakinin X - hor
106	18.2	10	2	835372	protein receptor fo	179	2	18.2	12	2	A55501	24K kidney and bla
107	18.2	10	2	880894	protein receptor fo	180	2	18.2	12	2	S34447	pink protein - Sta
108	18.2	10	2	830495	cytochrome c oxidase	181	2	18.2	12	2	A60757	enterotoxin C-1 -
109	18.2	10	2	814856	cytochrome c oxidase	182	2	18.2	12	2	PA3098	ribosomal protein
110	18.2	10	2	814976	cytochrome c oxidase	183	2	18.2	12	2	865730	hemoglobin, extrac
111	18.2	10	2	814957	cytochrome c oxidase	184	2	18.2	12	2	A56878	light yellow cell
112	18.2	10	2	814957	cytochrome c oxidase	185	2	18.2	12	2	865028	hemocyanin chain 6
113	18.2	10	2	814957	cytochrome c oxidase	186	2	18.2	12	2	SI0125	lipovitellin - Afr
114	18.2	10	2	814957	cytochrome c oxidase	187	2	18.2	12	2	S47463	T-cell antigen rec
115	18.2	10	2	814957	cytochrome c oxidase	188	2	18.2	12	2	8H174	T-cell receptor al
116	18.2	10	2	814957	cytochrome c oxidase	189	2	18.2	12	2	S74196	3-hydroxy-3-methyl
117	18.2	10	2	814957	cytochrome c oxidase	190	2	18.2	12	2	S68402	NAO(+)-glycolol
118	18.2	10	2	814957	cytochrome c oxidase	191	2	18.2	12	2	A37934	lq lambda chain J
119	18.2	10	2	854226	lipoic acid oxidase	192	2	18.2	12	2	PH4605	lq H chain V-D-J r
120	18.2	10	2	854226	lipoic acid oxidase	193	2	18.2	12	2	PH4606	lq H chain V-D-J r
121	18.2	10	2	854226	lipoic acid oxidase	194	2	18.2	12	2	PH4611	lq H chain V-D-J r
122	18.2	10	2	854226	lipoic acid oxidase	195	2	18.2	12	2	PH4611	lq H chain V-D-J r
123	18.2	10	2	A44871	monodehydroascorbate	196	2	18.2	12	2	S25039	lq heavy chain V r
124	18.2	10	2	840794	NAO(+)-glycolol	197	2	18.2	12	2	S68271	major urinary prot
125	18.2	11	2	S42073	ribosomal protein	198	2	18.2	12	2	R39690	neural cell adhesi
126	18.2	11	2	A40743	transferrin - Sheep	199	2	18.2	12	2	860931	T-cell receptor be
127	18.2	11	2	A26740	oral loader - polyar	200	2	18.2	12	2	864577	telomeric and tet
128	18.2	11	2	Y881	monophenolase neur	201	2	18.2	12	2	856049	urinary tract ston
129	18.2	11	2	Y881	monophenolase neur	202	2	18.2	12	2	S21163	NAO Ape-ribosyltra
130	18.2	11	2	Y881	monophenolase neur	203	2	18.2	12	2	PH0776	NAO(+)-glycolol
131	18.2	11	2	Y881	monophenolase neur	204	2	18.2	12	2	8X0315	AMN2 dehydrogenas
132	18.2	11	2	826744	modulator of cytokin	205	2	18.2	12	2	S49073	transferrin - bovin
133	18.2	11	2	826744	modulator of cytokin	206	2	18.2	12	2	8X0315	transferrin - bovin
134	18.2	11	2	826744	modulator of cytokin	207	2	18.2	12	2	8X0315	transferrin - bovin
135	18.2	11	2	826744	modulator of cytokin	208	2	18.2	12	2	8X0315	transferrin - bovin
136	18.2	11	2	826744	modulator of cytokin	209	2	18.2	12	2	8X0315	transferrin - bovin
137	18.2	11	2	826744	modulator of cytokin	210	2	18.2	12	2	8X0315	transferrin - bovin
138	18.2	11	2	826744	modulator of cytokin	211	2	18.2	12	2	8X0315	transferrin - bovin
139	18.2	11	2	826744	modulator of cytokin	212	2	18.2	12	2	8X0315	transferrin - bovin
140	18.2	11	2	826744	modulator of cytokin	213	2	18.2	12	2	8X0315	transferrin - bovin
141	18.2	11	2	826744	modulator of cytokin	214	2	18.2	12	2	8X0315	transferrin - bovin
142	18.2	11	2	826744	modulator of cytokin	215	2	18.2	12	2	8X0315	transferrin - bovin
143	18.2	11	2	826744	modulator of cytokin	216	2	18.2	12	2	8X0315	transferrin - bovin
144	18.2	11	2	826744	modulator of cytokin	217	2	18.2	12	2	8X0315	transferrin - bovin
145	18.2	11	2	826744	modulator of cytokin	218	2	18.2	12	2	8X0315	transferrin - bovin
146	18.2	11	2	826744	modulator of cytokin	219	2	18.2	12	2	8X0315	transferrin - bovin
147	18.2	11	2	826744	modulator of cytokin	220	2	18.2	12	2	8X0315	transferrin - bovin
148	18.2	11	2	826744	modulator of cytokin	221	2	18.2	12	2	8X0315	transferrin - bovin
149	18.2	11	2	826744	modulator of cytokin	222	2	18.2	12	2	8X0315	transferrin - bovin
150	18.2	11	2	826744	modulator of cytokin	223	2	18.2	12	2	8X0315	transferrin - bovin
151	18.2	11	2	826744	modulator of cytokin	224	2	18.2	12	2	8X0315	transferrin - bovin
152	18.2	11	2	826744	modulator of cytokin	225	2	18.2	12	2	8X0315	transferrin - bovin
153	18.2	11	2	826744	modulator of cytokin	226	2	18.2	12	2	8X0315	transferrin - bovin
154	18.2	11	2	826744	modulator of cytokin	227	2	18.2	12	2	8X0315	transferrin - bovin
155	18.2	11	2	826744	modulator of cytokin	228	2	18.2	12	2	8X0315	transferrin - bovin
156	18.2	11	2	826744	modulator of cytokin	229	2	18.2	12	2	8X0315	transferrin - bovin
157	18.2	11	2	826744	modulator of cytokin	230	2	18.2	12	2	8X0315	transferrin - bovin
158	18.2	11	2	826744	modulator of cytokin	231	2	18.2	12	2	8X0315	transferrin - bovin
159	18.2	11	2	826744	modulator of cytokin	232	2	18.2	12	2	8X0315	transferrin - bovin
160	18.2	11	2	826744	modulator of cytokin	233	2	18.2	12	2	8X0315	transferrin - bovin
161	18.2	11	2	826744	modulator of cytokin	234	2	18.2	12	2	8X0315	transferrin - bovin
162	18.2	11	2	826744	modulator of cytokin	235	2	18.2	12	2	8X0315	transferrin - bovin
163	18.2	11	2	826744	modulator of cytokin	236	2	18.2	12	2	8X0315	transferrin - bovin
164	18.2	11	2	826744	modulator of cytokin	237	2	18.2	12	2	8X0315	transferrin - bovin
165	18.2	11	2	826744	modulator of cytokin	238	2	18.2	12	2	8X0315	transferrin - bovin
166	18.2	11	2	826744	modulator of cytokin	239	2	18.2	12	2	8X0315	transferrin - bovin
167	18.2	11	2	826744	modulator of cytokin	240	2	18.2	12	2	8X0315	transferrin - bovin
168	18.2	11	2	826744	modulator of cytokin	241	2	18.2	12	2	8X0315	transferrin - bovin
169	18.2	11	2	826744	modulator of cytokin	242	2	18.2	12	2	8X0315	transferrin - bovin
170	18.2	11	2	826744	modulator of cytokin	243	2	18.2	12	2	8X0315	transferrin - bovin
171	18.2	11	2	826744	modulator of cytokin	244	2	18.2	12	2	8X0315	transferrin - bovin
172	18.2	11	2	826744	modulator of cytokin	245	2	18.2	12	2	8X0315	transferrin - bovin
173	18.2	11	2	826744	modulator of cytokin	246	2	18.2	12	2	8X0315	transferrin - bovin
174	18.2	11	2	826744	modulator of cytokin	247	2	18.2	12	2	8X0315	transferrin - bovin
175	18.2	11	2	826744	modulator of cytokin	248	2	18.2	12	2	8X0315	transferrin - bovin
176	18.2	11	2	826744	modulator of cytokin	249	2	18.2	12	2	8X0315	transferrin - bovin
177	18.2	11	2	826744	modulator of cytokin	250	2	18.2	12	2	8X0315	transferrin - bovin
178	18.2	11	2	826744	modulator of cytokin	251	2	18.2	12	2	8X0315	transferrin - bovin
179	18.2	11	2	826744	modulator of cytokin	252	2	18.2	12	2	8X0315	transferrin - bovin
180	18.2	11	2	826744	modulator of cytokin	253	2	18.2	12	2	8X0315	transferrin - bovin
181	18.2	11	2	826744	modulator of cytokin	254	2	18.2	12	2	8X0315	transferrin - bovin
182	18.2	11	2	826744	modulator of cytokin	255	2	18.2	12	2	8X0315	transferrin - bovin
183	18.2	11	2	826744	modulator of cytokin	256	2	18.2	12	2	8X0315	transferrin - bovin
184	18.2	11	2	826744	modulator of cytokin	257	2	18.2	12	2	8X0315	transferrin - bovin
185	18.2	11	2	826744	modulator of cytokin	258	2	18.2	12	2	8X0315	transferrin - bovin
186	18.2	11	2	826744	modulator of cytokin	259	2	18.2	12	2	8X0315	transferrin - bovin
187	18.2	11	2	826744	modulator of cytokin	260	2	18.2	12	2	8X0315	transferrin - bovin
188	18.2	11	2	826744	modulator of cytokin	261	2	18.2	12	2	8X0315	transferrin - bovin
189	18.2	11	2	826744	modulator of cytokin	262	2	18.2	12	2	8X0315	transferrin - bovin
190	18.2	11	2	826744	modulator of cytokin	263	2	18.2	12	2	8X0315	transferrin - bovin
191	18.2	11	2	826744	modulator of cytokin	264	2	18.2	12	2	8X0315	transferrin - bovin
192	18.2	11	2	826744	modulator of cytokin	265	2	18.2	12	2	8X0315	transferrin - bovin
193	18.2	11	2	826744	modulator of cytokin	266	2	18.2	12	2	8X0315	transferrin - bovin
194	18.2	11	2	826744	modulator of cytokin	267	2	18.2	12	2	8X0315	transferrin - bovin
195	18.2	11	2	826744	modulator of cytokin	268	2	18.2	12	2	8X0315	transferrin - bovin
196	18.2	11	2	826744	modulator of cytokin	269	2	18.2	12	2	8X0315	transferrin - bovin
197	18.2	11	2	826744	modulator of cytokin	270	2	18.2	12	2	8X0315	transferrin - bovin
198	18.2	11	2	826744	modulator of cytokin	271	2	18.2	12	2	8X0315	transferrin - bovin
199	18.2	11	2	826744	modulator of cytokin	272	2	18.2	12	2	8X0315	transferrin - bovin
200	18.2	11	2	826744	modulator of cytokin	273	2	18.2	12	2	8X0315	transferrin - bovin
201	18.2	11	2	826744	modulator of cytokin	274	2	18.2	12	2	8X0315	transferrin - bovin
202	18.2	11	2	826744	modulator of cytokin	275	2	18.2	12	2	8X0315	transferrin - bovin
203	18.2	11	2	826744	modulator of cytokin	276	2	18.2	12	2	8X0315	transferrin - bovin
204	18.2	11	2	826744	modulator of cytokin	277	2	18.2	12	2	8X0315	transferrin - bovin
205	18.2	11	2	826744	modulator of cytokin	278	2	18.2	12	2	8X0315	transferrin - bovin
206	18.2	11	2	826744	modulator of cytokin	279	2	18.2	12	2	8X0315	transferrin - bovin
207	18.2	11	2	826744	modulator of cytokin	280	2	18.2	12	2	8X0315	transferrin - bovin
208	18.2	11	2	826744	modulator of cytokin	281	2	18.2	12	2	8X0315	transferrin - bovin
209	18.2	11	2	826744	modulator of cytokin	282	2	18.2	12	2	8X	





A:Reference number: PQ0775; M010:94151437; PMID:8126709

A:Accession: PQ0785

A:Molecule type: protein

A:Residues: 1-13 <DET>

C:Comment: Complex 1, mitochondrial NADH-ubiquinone reductase, is the first of the three

translating from 5K to 7SK.

C:Comment: This enzyme catalyzes electron transfer from ubiquinol to ubiquinone by

conjugated.

A:Comment: Mitochondrial

C:Keywords: electron transfer; mitochondrial; oxidoreductase

Query Match 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SKD 8

DB 8 SKD 10

#### RESULT 3

QY 6

A:Reference number: PQ0775; M010:94151437; PMID:8126709

A:Accession: PQ0785

A:Molecule type: protein

A:Residues: 1-13 <DET>

C:Comment: Complex 1, mitochondrial NADH-ubiquinone reductase, is the first of the three

translating from 5K to 7SK.

C:Comment: This enzyme catalyzes electron transfer from ubiquinol to ubiquinone by

conjugated.

A:Comment: Mitochondrial

C:Keywords: electron transfer; mitochondrial; oxidoreductase

Query Match 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SKD 8

DB 8 SKD 10

#### RESULT 4

QY 9

DB 9

SKD 11

SKD 5

SKD 5

SKD 5

SKD 5

SKD 5

SKD 5

SKD 5

SKD 5

SKD 5

SKD 5

SKD 5

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SKD 5

SKD 5

SKD 5

A:Reference number: PQ0775; M010:94151437; PMID:8126709

A:Accession: PQ0785

A:Molecule type: protein

A:Residues: 1-13 <DET>

C:Comment: Complex 1, mitochondrial NADH-ubiquinone reductase, is the first of the three

translating from 5K to 7SK.

C:Comment: This enzyme catalyzes electron transfer from ubiquinol to ubiquinone by

conjugated.

A:Comment: Mitochondrial

C:Keywords: electron transfer; mitochondrial; oxidoreductase

Query Match 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SKD 8

DB 8 SKD 10

#### RESULT 5

QY 4

DB 4

SKD 5

SKD 7

SKD 7

SKD 7

SKD 7

SKD 7

SKD 7

SKD 7

SKD 7

SKD 7

SKD 7

SKD 7

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A: Molecule type: DNA  
 A: Accession: U01452  
 A: Reference: EMBL:248957; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1995  
 A: Species: Homo sapiens  
 A: Gene: tpep

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SK 1c  
 ID 1 SK 2

RESULT 41  
 11052  
 Hypothetical protein, t - spring water  
 C: Species: Vitula saligna (Spring water, Euro)  
 C: Date: 14-Jul-1999 #sequence\_revision 31-Jul-1999 #text\_change 16-Jul-1999  
 C: Accession: F10952  
 C: Reference: EMBL:248957; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1995  
 A: Species: Homo sapiens  
 A: Gene: tpep

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SK 1c  
 ID 1 SK 2

RESULT 42  
 871979  
 Alcohol dehydrogenase (EC 1.1.1.1) - mouse (fragment)  
 C: Species: Mus musculus (mouse, mouse)  
 C: Date: 14-Apr-1994 #sequence\_revision 24-Apr-1994 #text\_change 07-May-1994  
 C: Accession: S71979  
 C: Reference: EMBL:248957; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Note: The source is designated as a mouse (fragment)  
 A: Species: Mus musculus (mouse, mouse)  
 A: Gene: tpep

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SK 1c  
 ID 1 SK 2

RESULT 43  
 11052  
 Hypothetical protein, t - spring water  
 C: Species: Vitula saligna (Spring water, Euro)  
 C: Date: 14-Jul-1999 #sequence\_revision 31-Jul-1999 #text\_change 16-Jul-1999  
 C: Accession: F10952  
 C: Reference: EMBL:248957; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1995  
 A: Species: Homo sapiens  
 A: Gene: tpep

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SK 1c  
 ID 1 SK 2

R: Yamada, M.; Wasserman, R.; Reichardt, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 495-507, 1991  
 A: Title: Preferential utilization of specific immunoglobulin heavy chain diversity  
 A: Reference number: P10222; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Accession: P10222  
 A: Molecule type: DNA  
 A: Residues: 1-8 <YAM>  
 A: Experimental source: B lymphocyte  
 C: Keywords: heterotetramer; immunoglobulin

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RE 6  
 ID 7 RE 8

RESULT 34  
 845800  
 Serum albumin - dog (fragment)  
 C: Species: Canis lupus familiaris (dog)  
 C: Date: 01-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 31-Dec-1993  
 C: Accession: B45800  
 C: Reference: EMBL:248957; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Note: The source is designated as a dog (fragment)  
 A: Species: Canis lupus familiaris (dog)  
 A: Gene: tpep

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AR 2  
 ID 2 AR 3

RESULT 35  
 845800  
 Serum albumin - dog (fragment)  
 C: Species: Canis lupus familiaris (dog)  
 C: Date: 01-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 31-Dec-1993  
 C: Accession: B45800  
 C: Reference: EMBL:248957; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Note: The source is designated as a dog (fragment)  
 A: Species: Canis lupus familiaris (dog)  
 A: Gene: tpep

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AR 2  
 ID 2 AR 3

RESULT 36  
 845800  
 Serum albumin - dog (fragment)  
 C: Species: Canis lupus familiaris (dog)  
 C: Date: 01-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 31-Dec-1993  
 C: Accession: B45800  
 C: Reference: EMBL:248957; M10-39295880; P18-00000021.1; P18-00000021.2  
 A: Note: The source is designated as a dog (fragment)  
 A: Species: Canis lupus familiaris (dog)  
 A: Gene: tpep

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AR 2  
 ID 2 AR 3









GenCore version 5.1.6  
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OM protein protein search, using sw model

Run on: September 30, 2003, 16:07:14, Search time 4.25 Seconds

(with 1000 alignments)

82 717 alignments with updates/score

Title: US-09-787-443-14

Perfect score: 11

Sequence: 1 ARKIRKRSKG 11

Scoring table: G1G2

Gapop 60.0, Gapext 60.0

Searches: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 737

Minimum hit seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

Database: SwissProt\_41.0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	length	DB ID	Description
1	3	27.3	9	1	DEAK_MOUSE
2	4	27.3	11	1	TKN_ELM
3	4	27.3	11	1	UXB2_YEAST
4	4	27.3	14	1	RYCA_MELAR
5	4	18.2	8	1	ACT1_CARMA
6	4	18.2	8	1	ACT1_CYTO
7	2	18.2	8	1	ALB5_CYTO
8	2	18.2	8	1	NS3_MYD1
9	2	18.2	8	1	SL1_FHWT
10	2	18.2	8	1	RS7_MYD1
11	2	18.2	8	1	PRG9_FAT
12	2	18.2	9	1	HTUL_KIDNEY
13	2	18.2	9	1	DETA_SILVER
14	2	18.2	9	1	NEF_HV128
15	2	18.2	9	1	NEUF_HUMAN
16	2	18.2	9	1	SAMP_MOUSE
17	2	18.2	9	1	THYF_PIG
18	2	18.2	10	1	CATB_SHEEP
19	2	18.2	10	1	COXM_RAT
20	2	18.2	10	1	COXQ_RAT
21	2	18.2	10	1	COXQ_SHEEP
22	2	18.2	10	1	PRB_PERSI
23	2	18.2	10	1	MALE_KOFEIN
24	2	18.2	10	1	SLAP_BAT10
25	2	18.2	10	1	SP34_DROME
26	2	18.2	10	1	SP1_HAIRB
27	2	18.2	10	1	SPK_CAMP
28	2	18.2	10	1	TEMK_RANIE
29	2	18.2	10	1	TKNB_CHICK
30	2	18.2	10	1	TKNB_CARMA
31	2	18.2	10	1	TKN2_DROME
32	2	18.2	10	1	JPAN_HUMAN
33	2	18.2	10	1	UXA6_CHLTP

34	2	18.2	10	1	XYNB_DICB4
35	2	18.2	11	1	BRK_MEGFL
36	2	18.2	11	1	F51_RAI
37	2	18.2	11	1	MORN_HUMAN
38	2	18.2	11	1	O20A_COMTE
39	2	18.2	11	1	RR2_CONAM
40	2	18.2	11	1	RS30_ONCMY
41	2	18.2	11	1	TKN2_GPERO
42	2	18.2	11	1	TKNA_RANR1
43	2	18.2	11	1	TKND_RANCA
44	2	18.2	12	1	PAR2_PENMG
45	2	18.2	12	1	H2AX_ONCMY
46	2	18.2	12	1	HCTB_MESCR
47	2	18.2	12	1	NO40_LOTJA
48	2	18.2	12	1	NO40_SESRO
49	2	18.2	12	1	RR16_GINBI
50	2	18.2	12	1	RS19_GLYEP
51	2	18.2	12	1	RS19_ELYEP
52	2	18.2	12	1	RS19_TORBP
53	2	18.2	12	1	TKN_KASSE
54	2	18.2	12	1	V14K_WSSV
55	2	18.2	12	1	VZPV_ECOLI
56	2	18.2	13	1	BRK_PAPID
57	2	18.2	13	1	CH60_CANFA
58	2	18.2	13	1	CRB1_VESCR
59	2	18.2	13	1	EP65_HUMAN
60	2	18.2	13	1	FIBB_HYLLA
61	2	18.2	13	1	FIBB_RAB11
62	2	18.2	13	1	LMAL1_LOCI
63	2	18.2	13	1	LPAA_PORGI
64	2	18.2	13	1	NEUT_BUFMA
65	2	18.2	13	1	NEUT_GAVPO
66	2	18.2	13	1	NEUT_CHICK
67	2	18.2	13	1	NEUT_RANTE
68	2	18.2	13	1	NEUT_TRIVU
69	2	18.2	13	1	NG40_PEA
70	2	18.2	13	1	NO40_VICSA
71	2	18.2	13	1	PSA3_PEA
72	2	18.2	13	1	SA2A_ONCMY
73	2	18.2	13	1	SA2B_ONCMY
74	2	18.2	13	1	TEML_RANTE
75	2	18.2	13	1	UN02_PINPS
76	2	18.2	13	1	CALL_CALGT
77	2	18.2	14	1	CAT2_FASHE
78	2	18.2	14	1	EF10_CANFA
79	2	18.2	14	1	HY14_PIG
80	2	18.2	14	1	IF26_RAT
81	2	18.2	14	1	JAP1_RANJA
82	2	18.2	14	1	LPW_RHINE
83	2	18.2	14	1	MAST_VESBA
84	2	18.2	14	1	MY14_EISFO
85	2	18.2	14	1	RS19_PWBPP
86	2	18.2	14	1	RS19_PRUAP
87	2	18.2	14	1	SMS1_MYOSC
88	2	18.2	14	1	SMS1_LIMI
89	2	18.2	14	1	TKN1_SCHCK
90	2	18.2	15	1	ACEA_ALICA
91	2	18.2	15	1	AF11_MALPA
92	2	18.2	15	1	AFP3_MALPA
93	2	18.2	15	1	AH2_PRUSE
94	2	18.2	15	1	C10A_RAT
95	2	18.2	15	1	CKX_WHEAT
96	2	18.2	15	1	DCMM_PSECH
97	2	18.2	15	1	FIBA_ANAPL
98	2	18.2	15	1	ITRB_ALBJU
99	2	18.2	15	1	MCRA_METTE
100	2	18.2	15	1	MM01_RAT
101	2	18.2	15	1	ND03_SOLTU
102	2	18.2	15	1	ND08_SOLTU
103	2	18.2	15	1	ONC1_ONCMY
104	2	18.2	15	1	PGKH_PHYPA
105	2	18.2	15	1	RL11_STRAC
106	2	18.2	15	1	RS20_BACST

P80717	dictyolomu
P12797	megascolia
P56571	rattus norv
P01163	homo sapien
P80464	comamonas t
P42341	conopholis
P83328	oncorhynch
P08616	uperoleia r
P29207	rana ridibu
P22691	rana catesb
P83322	percaeus mon
P83327	oncorhynch
Q10584	megathura c
O22426	lotus japon
Q24369	sesbania ro
Q46207	ginkgo bilb
Q46490	clover yell
Q47881	elm yellow
Q56251	tomato big
P08611	kassina sen
P82006	white spot
P17776	escherichia
P42717	parapolybia
P49818	canis famli
P01518	vespa crabr
P54963	homo sapien
P14472	hylobates l
P14478	oryctolagus
P38496	locusta mig
P81411	porphyromon
P81796	bufo marinu
P32560	cavia porce
P13724	gallus gall
P41536	rana tempor
P31745	trichosurus
P55959	pisum sativ
P55961	vicia sativ
U17229	pisum sativ
P82238	oncorhynch
P82239	oncorhynch
P57104	rana tempor
P61667	pinus pinas
P20768	calotropis
P80342	fasciola he
P54835	canis famli
P01155	sus scrofa
P81795	rattus norv
P83305	rana japoni
P18854	rhizobium m
P21654	vespa basai
P46979	eisenia foe
U52053	pigeon pea
Q4160	prunus arme
P20750	myoxocephal
P31895	alligator m
P82470	schistocerc
P28467	acinetobact
P83141	malva parvi
P83137	malva parvi
P29260	prunus sero
P31720	rattus norv
P58763	trilicium ae
P19917	pseudomonas
P12801	anas platyr
P24927	albizzia ju
P22948	methanosarc
P81563	rattus norv
P80263	solanum tub
P80731	solanum tub
P83287	oncorhynch
P80659	physcomitre
Q95520	streptomyce
P59661	bacillus st

107	2	18.2	15	1	RS6_BOVIN	P5942	baet. taur. st	180	1	9.1	9	1	BUK_CLOPA	P81337	clostridium
108	2	18.2	15	1	R032_BOVIN	P8297	bos. taurus	181	1	9.1	9	1	CCAP_CARMA	P38556	carcinus ma
109	2	18.2	13	1	SR01_RAT	P0158	rattus. torv	182	1	9.1	9	1	CONO_CONGE	P05486	conus geogr
110	2	18.2	15	1	TERO_HPM2	P29837	baet. trophi	183	1	9.1	9	1	CONO_CONST	P05487	conus strit
111	2	18.2	15	1	UC16_MALZE	P80522	zea. mays (m	184	1	9.1	9	1	COM_CONVE	P83047	conus ventr
112	2	18.2	15	1	UC27_MALZE	P80644	zea. mays (m	185	1	9.1	9	1	COXE_THUOB	P80975	thunius obe
113	2	18.2	15	1	WAKA_METEM	P80937	act. hant. bact	186	1	9.1	9	1	DL_NEPNO	P24816	neptiops no
114	2	18.2	15	1	YAA3_BOPPA	P82036	theog. sesto	187	1	9.1	9	1	DNF1_LOCM1	P16339	locusta mig
115	1	9.1	8	1	AK11_HIBAL	P18691	theonius. alb	188	1	9.1	9	1	DSIP_RAHIT	P01158	oryz. tollagus
116	1	9.1	8	1	AKB2_ORPAT	P14065	gryllus. tim	189	1	9.1	9	1	PAR1_CALVO	P41856	calliphora
117	1	9.1	8	1	AKB3_HIBAL	P25425	lebelli. a. a	190	1	9.1	9	1	PAR2_CALVO	P41857	calliphora
118	1	9.1	8	1	AKB4_METEM	P25425	lebelli. a. a	191	1	9.1	9	1	PAR2_PANRE	P41873	panagrellus
119	1	9.1	8	1	AKB5_HIBAL	P14596	fabar. st. at	192	1	9.1	9	1	PAR3_CALVO	P41858	calliphora
120	1	9.1	8	1	ALL2_CARMA	P21815	car. taurus ma	193	1	9.1	9	1	PAR3_MACRS	P83276	macrobrachi
121	1	9.1	8	1	ALL3_CARMA	P21816	car. taurus ma	194	1	9.1	9	1	PAR4_PENMO	P83318	penaeus mon
122	1	9.1	8	1	ALL4_CARMA	P21816	car. taurus ma	195	1	9.1	9	1	PAR4_CALVO	P41859	calliphora
123	1	9.1	8	1	ALL5_CARMA	P21816	car. taurus ma	196	1	9.1	9	1	PAR4_PENMO	P83319	penaeus mon
124	1	9.1	8	1	ALL6_CARMA	P21816	car. taurus ma	197	1	9.1	9	1	PAR5_ASCSU	P43170	ascaris suu
125	1	9.1	8	1	ALL7_CARMA	P21816	car. taurus ma	198	1	9.1	9	1	PAR5_CALVO	P41860	calliphora
126	1	9.1	8	1	ALL8_CYDIP	P21816	cyd. a. pomor	199	1	9.1	9	1	PAR5_PANRE	P82661	panagrellus
127	1	9.1	8	1	ALL9_CALVO	P21816	cyd. a. pomor	200	1	9.1	9	1	PAR5_PENMO	P83320	penaeus mon
128	1	9.1	8	1	ALL10_CALVO	P21816	cyd. a. pomor	201	1	9.1	9	1	PAR6_CALVO	P41861	calliphora
129	1	9.1	8	1	ALL11_CALVO	P21816	cyd. a. pomor	202	1	9.1	9	1	PAR6_MACRS	P83279	macrobrachi
130	1	9.1	8	1	ALL12_CARMA	P21816	car. taurus ma	203	1	9.1	9	1	PAR7_CALVO	P41862	calliphora
131	1	9.1	8	1	ALL13_CARMA	P21816	car. taurus ma	204	1	9.1	9	1	PAR9_MACRS	P83281	macrobrachi
132	1	9.1	8	1	ALL14_CARMA	P21816	car. taurus ma	205	1	9.1	9	1	PAR9_ASCSU	P43172	ascaris suu
133	1	9.1	8	1	ALL15_CARMA	P21816	car. taurus ma	206	1	9.1	9	1	PARA_CALVO	P41865	calliphora
134	1	9.1	8	1	ALL16_CARMA	P21816	car. taurus ma	207	1	9.1	9	1	PARA_CALVO	P41868	calliphora
135	1	9.1	8	1	ALL17_CARMA	P21816	car. taurus ma	208	1	9.1	9	1	PARA_CALVO	P41868	calliphora
136	1	9.1	8	1	ALL18_CARMA	P21816	car. taurus ma	209	1	9.1	9	1	PARA_CALVO	P41868	calliphora
137	1	9.1	8	1	ALL19_CARMA	P21816	car. taurus ma	210	1	9.1	9	1	PARA_CALVO	P41868	calliphora
138	1	9.1	8	1	ALL20_CARMA	P21816	car. taurus ma	211	1	9.1	9	1	PARA_CALVO	P41868	calliphora
139	1	9.1	8	1	ALL21_CARMA	P21816	car. taurus ma	212	1	9.1	9	1	PARA_CALVO	P41868	calliphora
140	1	9.1	8	1	ALL22_CARMA	P21816	car. taurus ma	213	1	9.1	9	1	PARA_CALVO	P41868	calliphora
141	1	9.1	8	1	ALL23_CARMA	P21816	car. taurus ma	214	1	9.1	9	1	PARA_CALVO	P41868	calliphora
142	1	9.1	8	1	ALL24_CARMA	P21816	car. taurus ma	215	1	9.1	9	1	PARA_CALVO	P41868	calliphora
143	1	9.1	8	1	ALL25_CARMA	P21816	car. taurus ma	216	1	9.1	9	1	PARA_CALVO	P41868	calliphora
144	1	9.1	8	1	ALL26_CARMA	P21816	car. taurus ma	217	1	9.1	9	1	PARA_CALVO	P41868	calliphora
145	1	9.1	8	1	ALL27_CARMA	P21816	car. taurus ma	218	1	9.1	9	1	PARA_CALVO	P41868	calliphora
146	1	9.1	8	1	ALL28_CARMA	P21816	car. taurus ma	219	1	9.1	9	1	PARA_CALVO	P41868	calliphora
147	1	9.1	8	1	ALL29_CARMA	P21816	car. taurus ma	220	1	9.1	9	1	PARA_CALVO	P41868	calliphora
148	1	9.1	8	1	ALL30_CARMA	P21816	car. taurus ma	221	1	9.1	9	1	PARA_CALVO	P41868	calliphora
149	1	9.1	8	1	ALL31_CARMA	P21816	car. taurus ma	222	1	9.1	9	1	PARA_CALVO	P41868	calliphora
150	1	9.1	8	1	ALL32_CARMA	P21816	car. taurus ma	223	1	9.1	9	1	PARA_CALVO	P41868	calliphora
151	1	9.1	8	1	ALL33_CARMA	P21816	car. taurus ma	224	1	9.1	9	1	PARA_CALVO	P41868	calliphora
152	1	9.1	8	1	ALL34_CARMA	P21816	car. taurus ma	225	1	9.1	9	1	PARA_CALVO	P41868	calliphora
153	1	9.1	8	1	ALL35_CARMA	P21816	car. taurus ma	226	1	9.1	9	1	PARA_CALVO	P41868	calliphora
154	1	9.1	8	1	ALL36_CARMA	P21816	car. taurus ma	227	1	9.1	9	1	PARA_CALVO	P41868	calliphora
155	1	9.1	8	1	ALL37_CARMA	P21816	car. taurus ma	228	1	9.1	9	1	PARA_CALVO	P41868	calliphora
156	1	9.1	8	1	ALL38_CARMA	P21816	car. taurus ma	229	1	9.1	9	1	PARA_CALVO	P41868	calliphora
157	1	9.1	8	1	ALL39_CARMA	P21816	car. taurus ma	230	1	9.1	9	1	PARA_CALVO	P41868	calliphora
158	1	9.1	8	1	ALL40_CARMA	P21816	car. taurus ma	231	1	9.1	9	1	PARA_CALVO	P41868	calliphora
159	1	9.1	8	1	ALL41_CARMA	P21816	car. taurus ma	232	1	9.1	9	1	PARA_CALVO	P41868	calliphora
160	1	9.1	8	1	ALL42_CARMA	P21816	car. taurus ma	233	1	9.1	9	1	PARA_CALVO	P41868	calliphora
161	1	9.1	8	1	ALL43_CARMA	P21816	car. taurus ma	234	1	9.1	9	1	PARA_CALVO	P41868	calliphora
162	1	9.1	8	1	ALL44_CARMA	P21816	car. taurus ma	235	1	9.1	9	1	PARA_CALVO	P41868	calliphora
163	1	9.1	8	1	ALL45_CARMA	P21816	car. taurus ma	236	1	9.1	9	1	PARA_CALVO	P41868	calliphora
164	1	9.1	8	1	ALL46_CARMA	P21816	car. taurus ma	237	1	9.1	9	1	PARA_CALVO	P41868	calliphora
165	1	9.1	8	1	ALL47_CARMA	P21816	car. taurus ma	238	1	9.1	9	1	PARA_CALVO	P41868	calliphora
166	1	9.1	8	1	ALL48_CARMA	P21816	car. taurus ma	239	1	9.1	9	1	PARA_CALVO	P41868	calliphora
167	1	9.1	8	1	ALL49_CARMA	P21816	car. taurus ma	240	1	9.1	9	1	PARA_CALVO	P41868	calliphora
168	1	9.1	8	1	ALL50_CARMA	P21816	car. taurus ma	241	1	9.1	9	1	PARA_CALVO	P41868	calliphora
169	1	9.1	8	1	ALL51_CARMA	P21816	car. taurus ma	242	1	9.1	9	1	PARA_CALVO	P41868	calliphora
170	1	9.1	8	1	ALL52_CARMA	P21816	car. taurus ma	243	1	9.1	9	1	PARA_CALVO	P41868	calliphora
171	1	9.1	8	1	ALL53_CARMA	P21816	car. taurus ma	244	1	9.1	9	1	PARA_CALVO	P41868	calliphora
172	1	9.1	8	1	ALL54_CARMA	P21816	car. taurus ma	245	1	9.1	9	1	PARA_CALVO	P41868	calliphora
173	1	9.1	8	1	ALL55_CARMA	P21816	car. taurus ma	246	1	9.1	9	1	PARA_CALVO	P41868	calliphora
174	1	9.1	8	1	ALL56_CARMA	P21816	car. taurus ma	247	1	9.1	9	1	PARA_CALVO	P41868	calliphora
175	1	9.1	8	1	ALL57_CARMA	P21816	car. taurus ma	248	1	9.1	9	1	PARA_CALVO	P41868	calliphora
176	1	9.1	8	1	ALL58_CARMA	P21816	car. taurus ma	249	1	9.1	9	1	PARA_CALVO	P41868	calliphora
177	1	9.1	8	1	ALL59_CARMA	P21816	car. taurus ma	250	1	9.1	9	1	PARA_CALVO	P41868	calliphora
178	1	9.1	8	1	ALL60_CARMA	P21816	car. taurus ma	251	1	9.1	9	1	PARA_CALVO	P41868	calliphora
179	1	9.1	8	1	ALL61_CARMA	P21816	car. taurus ma	252	1	9.1	9	1	PARA_CALVO	P41868	calliphora

254	1	9	1	UPA5_HUMAN	P15992	homo sapien	326	1	9	1	TKL2_L10CM1	P16224	locusta miq
255	1	9	1	UPA7_HUMAN	P16093	homo sapien	327	1	9	1	TKL3_L10CM1	P30249	locusta miq
256	1	9	1	XELA_STRSQ	P19149	streptomyce	328	1	9	1	TKL4_L10CM1	P30250	locusta miq
257	1	9	1	YHER_AZAV	P23425	azotobacter	329	1	9	1	TKN1_SYCA	P08608	steyliorhino
258	1	10	1	AEGL_AGRAE	P61495	eurocybe ae	330	1	9	1	TKN2_ONCMY	P28500	oncorhynchu
259	1	9	1	ABX_PUGSH	P39261	pinus sero	331	1	9	1	TKNB_RANR1	P29135	rana ridiibu
260	1	9	1	AKHX_L10CM	P61426	locusta miq	332	1	9	1	TKN2_RANR1	P22690	rana ratiab
261	1	9	1	AL39_CANNA	P36422	narctonius ma	333	1	9	1	TKN2_PUG	P12492	sus scrofa
262	1	9	1	AMEN_BELAN	P81731	belontrichu	334	1	9	1	TKN_PRYBI	P08610	phyllomedus
263	1	9	1	AN31_BOTLA	P20541	batulops ja	335	1	9	1	TKS1_AEDAE	P42634	aedes aegyp
264	1	9	1	AN21_BOVIN	P01019	bos taur us	336	1	9	1	TKS2_AEDAE	P42635	aedes aegyp
265	1	9	1	AN21_CHICK	P01019	galus gall	337	1	9	1	TKU1_UREUN	P40751	urechis uni
266	1	9	1	AP22_CADPH	P00471	caprae capra	338	1	9	1	TKM0_AEDAE	P19425	aedes aegyp
267	1	9	1	B022_BOLIA	P11022	batulops ja	339	1	9	1	TKPIS_NICPG	P19118	nicotiana gl
268	1	9	1	BPP_VIPAS	P10351	vipera aspi	340	1	9	1	TRP5_LEUMA	P81738	leucophaea
269	1	9	1	BRK_ONCMY	P01077	oncorhynch	341	1	9	1	TRP6_LEUMA	P81738	leucophaea
270	1	9	1	CA12_LITCI	P02086	litoria cit	342	1	9	1	TRP7_LEUMA	P81740	leucophaea
271	1	9	1	CAER_LITXA	P06264	litoria xan	343	1	9	1	TRP8_LEUMA	P81741	leucophaea
272	1	9	1	COXA_ONCMY	P00348	oncorhynch	344	1	9	1	TRP9_LEUMA	P56573	rattus norv
273	1	9	1	COXR_ONCMY	P00331	oncorhynch	345	1	9	1	UB05_RAT	P40910	homo sapien
274	1	9	1	COXR_KAT	P00332	oncorhynch	346	1	9	1	UBA3_HUMAN	P30088	homo sapien
275	1	9	1	COXO_THICK	P00332	rattus norv	347	1	9	1	UBA4_HUMAN	P30090	homo sapien
276	1	9	1	ESL_LACZA	P05982	thomomys obe	348	1	9	1	UBA5_HUMAN	P30091	homo sapien
277	1	9	1	ESTA_SCHCA	P01072	schizopelis	349	1	9	1	UBA5_HUMAN	P30095	homo sapien
278	1	9	1	FAR4_PENNA	P03333	penaeus aen	350	1	9	1	UBA5_HUMAN	P32080	homo sapien
279	1	9	1	FAR4_MAKES	P04278	macrotetrach	351	1	9	1	UBA5_HUMAN	P32080	homo sapien
280	1	9	1	FAR4_PANRE	P02560	panastrellus	352	1	9	1	UBA5_HUMAN	P34590	homo sapien
281	1	9	1	FAR7_MAKES	P04280	macrotetrach	353	1	9	1	UBA5_HUMAN	P17339	mordanella
282	1	9	1	FAR8_CAVUS	P14967	calliphora	354	1	9	1	UBA5_HUMAN	P38003	chlamydia t
283	1	9	1	FAR9_L10CM	P14967	calliphora	355	1	9	1	UBA5_HUMAN	P38003	chlamydia t
284	1	9	1	FARP_MANSE	P14967	calliphora	356	1	9	1	UBA5_HUMAN	P38003	chlamydia t
285	1	9	1	FARP_MYF13	P14967	calliphora	357	1	9	1	UBA5_HUMAN	P38003	chlamydia t
286	1	9	1	GADU_HUMAN	P01458	homo sapien	358	1	9	1	UBA5_HUMAN	P38003	chlamydia t
287	1	9	1	GEM_HUMAN	P02728	homo sapien	359	1	9	1	UBA5_HUMAN	P38003	chlamydia t
288	1	9	1	GEM2_ALANI	P02728	homo sapien	360	1	9	1	UBA5_HUMAN	P38003	chlamydia t
289	1	9	1	GEM2_CHICK	P02728	homo sapien	361	1	9	1	UBA5_HUMAN	P38003	chlamydia t
290	1	9	1	GEM2_CHICK	P02728	homo sapien	362	1	9	1	UBA5_HUMAN	P38003	chlamydia t
291	1	9	1	GEM2_CHICK	P02728	homo sapien	363	1	9	1	UBA5_HUMAN	P38003	chlamydia t
292	1	9	1	GEM2_CHICK	P02728	homo sapien	364	1	9	1	UBA5_HUMAN	P38003	chlamydia t
293	1	9	1	GEM2_CHICK	P02728	homo sapien	365	1	9	1	UBA5_HUMAN	P38003	chlamydia t
294	1	9	1	GEM2_CHICK	P02728	homo sapien	366	1	9	1	UBA5_HUMAN	P38003	chlamydia t
295	1	9	1	GEM2_CHICK	P02728	homo sapien	367	1	9	1	UBA5_HUMAN	P38003	chlamydia t
296	1	9	1	GEM2_CHICK	P02728	homo sapien	368	1	9	1	UBA5_HUMAN	P38003	chlamydia t
297	1	9	1	GEM2_CHICK	P02728	homo sapien	369	1	9	1	UBA5_HUMAN	P38003	chlamydia t
298	1	9	1	GEM2_CHICK	P02728	homo sapien	370	1	9	1	UBA5_HUMAN	P38003	chlamydia t
299	1	9	1	GEM2_CHICK	P02728	homo sapien	371	1	9	1	UBA5_HUMAN	P38003	chlamydia t
300	1	9	1	GEM2_CHICK	P02728	homo sapien	372	1	9	1	UBA5_HUMAN	P38003	chlamydia t
301	1	9	1	GEM2_CHICK	P02728	homo sapien	373	1	9	1	UBA5_HUMAN	P38003	chlamydia t
302	1	9	1	GEM2_CHICK	P02728	homo sapien	374	1	9	1	UBA5_HUMAN	P38003	chlamydia t
303	1	9	1	GEM2_CHICK	P02728	homo sapien	375	1	9	1	UBA5_HUMAN	P38003	chlamydia t
304	1	9	1	GEM2_CHICK	P02728	homo sapien	376	1	9	1	UBA5_HUMAN	P38003	chlamydia t
305	1	9	1	GEM2_CHICK	P02728	homo sapien	377	1	9	1	UBA5_HUMAN	P38003	chlamydia t
306	1	9	1	GEM2_CHICK	P02728	homo sapien	378	1	9	1	UBA5_HUMAN	P38003	chlamydia t
307	1	9	1	GEM2_CHICK	P02728	homo sapien	379	1	9	1	UBA5_HUMAN	P38003	chlamydia t
308	1	9	1	GEM2_CHICK	P02728	homo sapien	380	1	9	1	UBA5_HUMAN	P38003	chlamydia t
309	1	9	1	GEM2_CHICK	P02728	homo sapien	381	1	9	1	UBA5_HUMAN	P38003	chlamydia t
310	1	9	1	GEM2_CHICK	P02728	homo sapien	382	1	9	1	UBA5_HUMAN	P38003	chlamydia t
311	1	9	1	GEM2_CHICK	P02728	homo sapien	383	1	9	1	UBA5_HUMAN	P38003	chlamydia t
312	1	9	1	GEM2_CHICK	P02728	homo sapien	384	1	9	1	UBA5_HUMAN	P38003	chlamydia t
313	1	9	1	GEM2_CHICK	P02728	homo sapien	385	1	9	1	UBA5_HUMAN	P38003	chlamydia t
314	1	9	1	GEM2_CHICK	P02728	homo sapien	386	1	9	1	UBA5_HUMAN	P38003	chlamydia t
315	1	9	1	GEM2_CHICK	P02728	homo sapien	387	1	9	1	UBA5_HUMAN	P38003	chlamydia t
316	1	9	1	GEM2_CHICK	P02728	homo sapien	388	1	9	1	UBA5_HUMAN	P38003	chlamydia t
317	1	9	1	GEM2_CHICK	P02728	homo sapien	389	1	9	1	UBA5_HUMAN	P38003	chlamydia t
318	1	9	1	GEM2_CHICK	P02728	homo sapien	390	1	9	1	UBA5_HUMAN	P38003	chlamydia t
319	1	9	1	GEM2_CHICK	P02728	homo sapien	391	1	9	1	UBA5_HUMAN	P38003	chlamydia t
320	1	9	1	GEM2_CHICK	P02728	homo sapien	392	1	9	1	UBA5_HUMAN	P38003	chlamydia t
321	1	9	1	GEM2_CHICK	P02728	homo sapien	393	1	9	1	UBA5_HUMAN	P38003	chlamydia t
322	1	9	1	GEM2_CHICK	P02728	homo sapien	394	1	9	1	UBA5_HUMAN	P38003	chlamydia t
323	1	9	1	GEM2_CHICK	P02728	homo sapien	395	1	9	1	UBA5_HUMAN	P38003	chlamydia t
324	1	9	1	GEM2_CHICK	P02728	homo sapien	396	1	9	1	UBA5_HUMAN	P38003	chlamydia t
325	1	9	1	GEM2_CHICK	P02728	homo sapien	397	1	9	1	UBA5_HUMAN	P38003	chlamydia t





```

C1 6 AA, 155 MW, 15: 45 kDa.
C2 1 SIMILARITY: BELONGS TO THE ACTIN FAMILY.
C3 InterPro: IPR004091; Actin-like.
C4 PROSITE: PS00406; ACTINS_17 PARTIAL.
C5 PROSITE: PS00432; ACTINS_2 PARTIAL.
C6 PROSITE: PS01142; ACTINS_ACTIN_LIKE PARTIAL.
C7 Structural protein.
C8 Non-ter 1
C9 Non-ter 1
C10 SEQUENCE 8 AA: 976 MW: 142400 DALTONS (99%)

Query Match: 18.2% Score 2; DB 1; Length 8;
Best Local Similarity: 100.0%; Pred. No. 1; 4e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 2 PK 4
Q2 7 PK 8

RESULT 7
ALIA_CYB01 STANDARD; FR: 8 AA.
AC PR156;
C1 60-MAY-2000 (Rel. 39, Created)
C2 30 MAY 2000 (Rel. 39, Last sequence update)
C3 30 MAY 2000 (Rel. 39, Last annotation update)
C4 Cydia pomonella.
C5 Cydia pomonella (Coding motif).
C6 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Pitystia; Tortricidae; Tortricidae; Olethreutinae; Cydia.
C7 NCBI_TaxID: 22600;
C8 1;
C9 SEQUENCE.
C10 TISSUE: Fat.
C11 MECHANISM: 9925299; PubMed:9925299.

RA Dave H., Johnson A.B., Maestre J., Scott A.G., Winstanley D., Gavey M., East P.B., Thorpe A.J. "Lepidopteran peptides of the allatostatin superfamily." Peptides 18:141-159(1997).
C1 SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
C2 Non-ter 1
C3 Non-ter 1
C4 SEQUENCE 8 AA: 976 MW: 142400 DALTONS (99%)

Query Match: 18.2% Score 2; DB 1; Length 8;
Best Local Similarity: 100.0%; Pred. No. 1; 4e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 2 PK 4
Q2 7 PK 8

RESULT 8
NSA_MY011 STANDARD; FR: 8 AA.
AC PR152;
C1 15-JUL-1999 (Rel. 38, Created)
C2 15-JUL-1999 (Rel. 38, Last sequence update)
C3 15-JUL-2001 (Rel. 40, Last annotation update)
C4 43 kDa non-secretory protein 3 (Fragment).
C5 Mycobacterium tuberculosis.
C6 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
C7 NCBI_TaxID: 1774;
C8 1;
C9 SEQUENCE.
C10 STRAIN H-789;
C11 Submitted (DEC 1997) to the SWISS-PROT data bank.
C12 CAUTION: We are unable to find this protein in the translation of the genome of strain H789.
C13 Non-ter 1
C14 Non-ter 1
C15 SEQUENCE 8 AA: 919 MW: 80960 DALTONS (99%)

Query Match: 18.2% Score 2; DB 1; Length 8;
Best Local Similarity: 100.0%; Pred. No. 1; 4e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q1 2 PK 4
Q2 7 PK 8

RESULT 9
RSL_ERW01 STANDARD; FR: 8 AA.
AC PR156;
C1 01-NOV-1994 (Rel. 38, Created)
C2 01-NOV-1994 (Rel. 40, Last sequence update)
C3 01-NOV-1995 (Rel. 42, Last annotation update)
C4 30S ribosomal protein S1 (Fragment).
C5 ERW01 chrysalis host.
C6 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
C7 NCBI_TaxID: 556;
C8 1;
C9 SEQUENCE FROM N.A.
C10 STRAIN 3987;
C11 Submitted (AUG 1994) to the EMBL/GenBank/DBJ databases.
C12 FUNCTION: BINDS MRNA, THUS FACILITATING RECOGNITION OF THE SHINE DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
C13 SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.

```

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X44750; CAA52769.1;  
 DR DDB: S47141; S47141;  
 KW Ribosomal protein; Repeat: KNAAT000001;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 517 MW: 91887.866 Da; 100% (100%)

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KS 9  
 DB 3 KS 4  
 AC P35661  
 ID R52\_MYC1 STANDARD: PRT; 8 AA  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DI 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN RPS1  
 OS Mycobacterium intracellulare  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium  
 CC NCBI\_TaxID: 1767;  
 RN 1;  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 9197130; PubMed: 8451173;  
 RA Nair J., House D.A., Morris S.G.  
 RE "Nucleotide sequence analysis of the ribosomal S12 gene of  
 RE Mycobacterium intracellulare."  
 RA Nucleic Acids Res. 21:1039-1049(1993)  
 CC 1- FUNCTION: one of the primary rRNA binding proteins; it binds  
 CC directly to 16S rRNA where it is located at the head  
 CC domain of the 30S subunit; is located at the subunit interface  
 CC close to the decoding center, probably blocks exit of the E-site  
 CC tRNA (by similarity).  
 CC 1- SUBUNIT: part of the 30S ribosomal subunit; contacts proteins S2  
 CC and S1 (by similarity).  
 CC 1- SIMILARITY: BELONGS TO THE 27S LAM: Y1 - 5S-RAL PROTEINS.

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DR EMBL: F0871; AAA25376.1;  
 DR DDB: S05598; S05598;  
 DR HANAP: RF\_004801; 1;  
 DR InterPro: IPR000235; Ribosomal\_S7;  
 DR ProSITE: PS00052; RIBOSOMAL\_S7; PAR.1AL;  
 KW Ribosomal protein; RNA-binding; tRNA binding;  
 FT INIT\_MK1 0  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 850 MW: 63276.076 Da; 100% (100%)

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KS 9  
 DB 3 KS 4  
 AC P35661  
 ID R52\_MYC1 STANDARD: PRT; 8 AA  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DI 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN RPS1  
 OS Mycobacterium intracellulare  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium  
 CC NCBI\_TaxID: 1767;  
 RN 1;  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 9197130; PubMed: 8451173;  
 RA Nair J., House D.A., Morris S.G.  
 RE "Nucleotide sequence analysis of the ribosomal S12 gene of  
 RE Mycobacterium intracellulare."  
 RA Nucleic Acids Res. 21:1039-1049(1993)  
 CC 1- FUNCTION: one of the primary rRNA binding proteins; it binds  
 CC directly to 16S rRNA where it is located at the head  
 CC domain of the 30S subunit; is located at the subunit interface  
 CC close to the decoding center, probably blocks exit of the E-site  
 CC tRNA (by similarity).  
 CC 1- SUBUNIT: part of the 30S ribosomal subunit; contacts proteins S2  
 CC and S1 (by similarity).  
 CC 1- SIMILARITY: BELONGS TO THE 27S LAM: Y1 - 5S-RAL PROTEINS.

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DR EMBL: X44750; CAA52769.1;  
 DR DDB: S47141; S47141;  
 KW Ribosomal protein; Repeat: KNAAT000001;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 517 MW: 91887.866 Da; 100% (100%)

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KS 9  
 DB 3 KS 4  
 AC P35661  
 ID R52\_MYC1 STANDARD: PRT; 8 AA  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DI 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN RPS1  
 OS Mycobacterium intracellulare  
 CC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;  
 CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium  
 CC NCBI\_TaxID: 1767;  
 RN 1;  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 9197130; PubMed: 8451173;  
 RA Nair J., House D.A., Morris S.G.  
 RE "Nucleotide sequence analysis of the ribosomal S12 gene of  
 RE Mycobacterium intracellulare."  
 RA Nucleic Acids Res. 21:1039-1049(1993)  
 CC 1- FUNCTION: one of the primary rRNA binding proteins; it binds  
 CC directly to 16S rRNA where it is located at the head  
 CC domain of the 30S subunit; is located at the subunit interface  
 CC close to the decoding center, probably blocks exit of the E-site  
 CC tRNA (by similarity).  
 CC 1- SUBUNIT: part of the 30S ribosomal subunit; contacts proteins S2  
 CC and S1 (by similarity).  
 CC 1- SIMILARITY: BELONGS TO THE 27S LAM: Y1 - 5S-RAL PROTEINS.

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DR EMBL: X44750; CAA52769.1;  
 DR DDB: S47141; S47141;  
 KW Ribosomal protein; Repeat: KNAAT000001;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 517 MW: 91887.866 Da; 100% (100%)

QY 2 RK 3  
 DB 2 RK 3  
 AC P56575;  
 ID 15-DEC-1998 (Rel. 37, Created)  
 DI 15-DEC-1998 (Rel. 37, Last sequence update)  
 DE 15-DEC-1998 (Rel. 37, Last annotation update)  
 GN Unknown protein from 20 page of heart tissue (Spot P9) (Fragment).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus  
 CC NCBI\_TaxID 10116;  
 RN 1;  
 RE SEQUENCE;  
 RA STRAIN-Wistar; TISSUE-Heart;  
 RA CC X-P.P.; Pileissner K.-P.; Scheier C.; Regitz-Zagrosek V.; Salikov J.;  
 RA Jungblut P.R.;  
 RE Submitted (SEP 1998) to the SWISS-PROT data bank.  
 CC 1- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED P1 OF THIS UNKNOWN  
 CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 1029 MW: 960775.604 Da; 100% (100%)

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 AC P12381;  
 ID HUTU\_KDEAE STANDARD: PRT; 9 AA  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN Crocinate hydratase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 GN hydrolase) (Fragment).  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella;  
 CC NCBI\_TaxID: 2845;  
 RN 1;  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neuhaus A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;  
 RE "A bidirectional promoter in the hut(P) region of the histidine  
 RE utilization (hut) operons from Klebsiella aerogenes.";  
 RA J. Bacteriol. 170:2240-2246(1988).  
 RN 121  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 90368611; PubMed: 2263754;  
 RA Schwacha A., Bender R.A.;

CC "Nucleotide sequence of the gene encoding the repressor for the  
 CC histidine utilization genes of Klebsiella aerogenes.";  
 CC J. Bacteriol. 172:5477-5481(1990).  
 CC 1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-  
 CC yl)propanoate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

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DR EMBL: X44750; CAA52769.1;  
 DR DDB: S47141; S47141;  
 KW Ribosomal protein; Repeat: KNAAT000001;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 517 MW: 91887.866 Da; 100% (100%)

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 AC P12381;  
 ID HUTU\_KDEAE STANDARD: PRT; 9 AA  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN Crocinate hydratase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 GN hydrolase) (Fragment).  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella;  
 CC NCBI\_TaxID: 2845;  
 RN 1;  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neuhaus A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;

CC "Nucleotide sequence of the gene encoding the repressor for the  
 CC histidine utilization genes of Klebsiella aerogenes.";  
 CC J. Bacteriol. 172:5477-5481(1990).  
 CC 1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-  
 CC yl)propanoate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

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DR EMBL: X44750; CAA52769.1;  
 DR DDB: S47141; S47141;  
 KW Ribosomal protein; Repeat: KNAAT000001;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 517 MW: 91887.866 Da; 100% (100%)

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 AC P12381;  
 ID HUTU\_KDEAE STANDARD: PRT; 9 AA  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN Crocinate hydratase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 GN hydrolase) (Fragment).  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella;  
 CC NCBI\_TaxID: 2845;  
 RN 1;  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neuhaus A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;

CC "Nucleotide sequence of the gene encoding the repressor for the  
 CC histidine utilization genes of Klebsiella aerogenes.";  
 CC J. Bacteriol. 172:5477-5481(1990).  
 CC 1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-  
 CC yl)propanoate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

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DR EMBL: X44750; CAA52769.1;  
 DR DDB: S47141; S47141;  
 KW Ribosomal protein; Repeat: KNAAT000001;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 517 MW: 91887.866 Da; 100% (100%)

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1; 1e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7  
 DB 2 ER 5  
 AC P12381;  
 ID HUTU\_KDEAE STANDARD: PRT; 9 AA  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DI 01-OCT-1989 (Rel. 12, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 GN Crocinate hydratase (EC 4.2.1.49) (Urocanase) (imidazolonepropionate  
 GN hydrolase) (Fragment).  
 OS Klebsiella aerogenes;  
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 CC Enterobacteriaceae; Klebsiella;  
 CC NCBI\_TaxID: 2845;  
 RN 1;  
 RE SEQUENCE FROM N.A.  
 RA MEDLINE: 88198018; PubMed: 2834335;  
 RA Neuhaus A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;

CC "Nucleotide sequence of the gene encoding the repressor for the  
 CC histidine utilization genes of Klebsiella aerogenes.";  
 CC J. Bacteriol. 172:5477-5481(1990).  
 CC 1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-  
 CC yl)propanoate + urocanate + H(2O).  
 CC 1- COFACTOR: Binds 1 NAD per subunit (By similarity).  
 CC 1- PATHWAY: Histidine degradation; second step.  
 CC 1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC 1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.

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Query Match 18.2% Score 21 DB 11 Length 10;  
 Best Local Similarity 100.0% Prot No. 9, 6e-03;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 21  
 CXXC\_RAT 10 CXXC\_SHEEP STANDARD: PRT 10 AA  
 A\* PROCEE  
 D1 01-JUL-1994 (Rel. 32, created)  
 D2 01-JUL-1994 (Rel. 32, last sequence update)  
 D3 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII [liver/heart] (EC 1.9.3.1)  
 EE (Fragment)  
 EN P0XBB  
 ES Oryzotadas conchylus (Ratt.)  
 EC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 EC Mammalia; Eutheria; Lagomorpha; Caprimulgidae; Cryptolagus  
 EX NCPI\_TaxID=9986;  
 EN 11  
 SE SEQUENCE  
 RA Tissue heart, and liver  
 RA Freund R. Kadenbach, B.  
 RA Submitted (Mar-1994) to the Swiss Prot data bank  
 CC 1 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT  
 CC 1 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O  
 CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 FT NON\_TFR 10  
 SQ SEQUENCE 10 AA: 1177 MW: 87077614 AAIDBA 6664

Query Match 18.2% Score 21 DB 11 Length 10;  
 Best Local Similarity 100.0% Prot No. 9, 6e-03;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 21  
 CXXC\_RAT 10 CXXC\_SHEEP STANDARD: PRT 10 AA  
 A\* PROCEE  
 D1 01-JUL-1994 (Rel. 32, created)  
 D2 01-JUL-1994 (Rel. 32, last sequence update)  
 D3 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII [liver/heart] (EC 1.9.3.1)  
 EE (Fragment)  
 EN P0XBB  
 ES Oryzotadas conchylus (Ratt.)  
 EC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 EC Mammalia; Eutheria; Lagomorpha; Caprimulgidae; Cryptolagus  
 EX NCPI\_TaxID=9986;  
 EN 11  
 SE SEQUENCE  
 RA Tissue heart, and liver  
 RA Freund R. Kadenbach, B.  
 RA Submitted (Mar-1994) to the Swiss Prot data bank  
 CC 1 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT  
 CC 1 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O  
 CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 FT NON\_TFR 10  
 SQ SEQUENCE 10 AA: 1210 MW: 87077614 AAIDBA 6664

Query Match 18.2% Score 21 DB 11 Length 10;  
 Best Local Similarity 100.0% Prot No. 9, 6e-03;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 21  
 CXXC\_RAT 10 CXXC\_SHEEP STANDARD: PRT 10 AA  
 A\* PROCEE  
 D1 01-JUL-1994 (Rel. 32, created)  
 D2 01-JUL-1994 (Rel. 32, last sequence update)  
 D3 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII [liver/heart] (EC 1.9.3.1)  
 EE (Fragment)  
 EN P0XBB  
 ES Oryzotadas conchylus (Ratt.)  
 EC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 EC Mammalia; Eutheria; Lagomorpha; Caprimulgidae; Cryptolagus  
 EX NCPI\_TaxID=9986;  
 EN 11  
 SE SEQUENCE  
 RA Tissue heart, and liver  
 RA Freund R. Kadenbach, B.  
 RA Submitted (Mar-1994) to the Swiss Prot data bank  
 CC 1 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT  
 CC 1 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O  
 CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 FT NON\_TFR 10  
 SQ SEQUENCE 10 AA: 1027 MW: 2022507430076338 CRC64

Query Match 18.2% Score 21 DB 11 Length 10;  
 Best Local Similarity 100.0% Prot No. 9, 6e-03;  
 Matches 21 Conservative 0 Mismatches 0 Indels 0 Gaps 0

SV 1 AP 2  
 IL 7 AP 7

RESULT 21  
 CXXC\_RAT 10 CXXC\_SHEEP STANDARD: PRT 10 AA  
 A\* PROCEE  
 D1 01-JUL-1994 (Rel. 32, created)  
 D2 01-JUL-1994 (Rel. 32, last sequence update)  
 D3 28-FEB-2003 (Rel. 41, last annotation update)  
 DE Cytochrome c oxidase polypeptide VIII [liver/heart] (EC 1.9.3.1)  
 EE (Fragment)  
 EN P0XBB  
 ES Oryzotadas conchylus (Ratt.)  
 EC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;  
 EC Mammalia; Eutheria; Lagomorpha; Caprimulgidae; Cryptolagus  
 EX NCPI\_TaxID=9986;  
 EN 11  
 SE SEQUENCE  
 RA Tissue heart, and liver  
 RA Freund R. Kadenbach, B.  
 RA Submitted (Mar-1994) to the Swiss Prot data bank  
 CC 1 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT  
 CC 1 CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) -> 4 ferricytochrome  
 CC c + 2 H(2)O  
 CC 1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.  
 FT NON\_TFR 10  
 SQ SEQUENCE 10 AA: 1210 MW: 87077614 AAIDBA 6664

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FT MEN_HER 10 10
SQ SEQUENCE 10 AA: 1027 MW: C45956A40C76330-DR 664

Query Match:
Best Local Similarity 100.0%: Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0

CY 3 KT 4
DB 7 KT 8

RESULT 24
FIBR_CERSI STANDARD: PRT: 10 AA
AC F4547
DI 01 JAN 1990 (Rel. 13, Last sequence update)
DI 01 JAN 1990 (Rel. 13, Last sequence update)
DI 24 FEB 2003 (Rel. 41, Last annotation update)
DI Fibrinogen beta chain [Contains: Fibrinogen beta, (Fragment)]
GN FGB
OS Crustaceorum stum (White rhineros) (Square tipped rhineros)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostei;
OC Mammalia; Eutheria; Perissodactyla; Solimovetidae; Cervidae;
OX NCBI TaxID 9837
LN 111
SQ SEQUENCE 10 AA: 1097 MW: 949262020304000-DR 664

Query Match:
Best Local Similarity 100.0%: Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Gaps 0

CY 3 KT 2
DB 9 KT 10

RESULT 24
MALE_KLEIN STANDARD: PRT: 10 AA
AC Q05564
DI 01 OCT 1994 (Rel. 30, Created)
DI 01 OCT 1994 (Rel. 30, Last sequence update)
DI 01 MAY 2000 (Rel. 39, Last annotation update)
DI Maltose binding periplasmic Protein (80.1 kDa) (partial protein)
DI (MBP) (Fragment)
GN MBP
OS Klebsiella pneumoniae
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella
OX NCBI TaxID 573
LN 111
SQ SEQUENCE FROM N.A.
RP STRAIN-1033-5014 / KAY2026
RX MEDLINE 93211295; PubMed 8455773;

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KA Bachelier S., Perrin D., Hofnung M., Gilsos E.;
RC "Bacterial interspersed mosaic elements (BIMES) are present in the
RI genome of Klebsiella".
RG Mol. Microbiol. 7:537-544(1993).
CC -1- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CC CHEM. EXAS: TOWARD MALTOSE-LIGOSACCHARIDES.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE BINDING
CC PROTEIN FAMILY 1.
CC
CC THIS SWISS PROTEIN ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC ENTITIES REQUIRES A LICENSE AGREEMENT (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X68329; CAA48404.1;
CC InterPro: IPR006060; SBI_dsm1
CC PROSITE: PS01037; SHP_BACTERIAL_1; PARTIAL.
CC Transport: Sugar transport; Periplasmic.
CC NON_TER 1
CC FT 1
CC SQ SEQUENCE 10 AA: 1159 MW: 8F08DC4415A6DDDA CRC64:

Query Match:
Best Local Similarity 100.0%: Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 10 KT 11
DB 2 KT 4

RESULT 24
SLAP_RACTS STANDARD: PRT: 10 AA
AC P43325
DI 01-FEB-1996 (Rel. 34, Created)
DI 01-FEB-1996 (Rel. 34, Last sequence update)
DI 01-FEB-1996 (Rel. 34, Last annotation update)
DI S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae)
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI TaxID: 29330
LN 111
SQ SEQUENCE.
RP STRAIN-NKRL 4047;
RX MEDLINE 90078131; PubMed-2592449;
KA Luckovich M.D., Peterlin E.
RC "Characterization of a dynamic S-layer on Bacillus thuringiensis".
RG J. Bacteriol. 173:656-667(1999).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HELIQUOUS (P2) SYMMETRY.
CC PIR: A60476; A60476.
CC Cell wall: S-layer.
CC NON_TER 10
CC FT 10
CC SQ SEQUENCE 10 AA: 1080 MW: 57AB7ACAB769C1A3 CRC64:

Query Match:
Best Local Similarity 100.0%: Pred. No. 9.6e-03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KT 4
DB 3 KT 4

RESULT 25
SP34_DJCMO

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ID SP14_HALBO STANDARD; PRI: 10 AA.
AC P41545;
DI 15-JUL-1999 (Rel. 38, Created)
DI 15-DEC-1999 (Rel. 38, Last sequence update)
DI 15-JUL-1999 (Rel. 38, Last annotation update)
DE Surface protein P44 (Fragment)
GN P44
OS Dictyostelium discoideum (Slime mold)
OC Eukaryota; Metazoa; Dictyosteliales; Dictyostelaceae
GX NCBI_FaxID: 41287;
LN 1;
RP SEQUENCE
RC STRAIN: DM-2;
RA Schreiner, S.J.;
RT Characterization of a surface protein in macrophages of early stadium
RT macrophages.
RL Submitted (NCBI-1498) to the SWISS PROT data bank
CC -! FUNCTION: THIS PROTEIN IS PRESENT IN THE MATURE CYST PRIMARY WALL
CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
CC REPRODUCTION.
CC -! SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
KW Cell wall.
FT Non_Ter
SC SEQUENCE 10 AA: 10 MW: 1184767AA1444852 (Rel. 34)
Query Match 18.2% Score 2; D8 I; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 KD 11
LA 1
RESULT 26
ID SP1_HALBO STANDARD; PRI: 10 AA.
AC Q13997;
DI 01-JUL-1996 (Rel. 34, Created)
DI 01-DEC-1996 (Rel. 34, Last sequence update)
DI 15-DEC-1996 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment)
OS Haliocynthia roretzi (Sea squirt)
OC Eukaryota; Metazoa; Chordata; Haliocinetidae; Ascidiacea;
OC Stolidobranchia; Pyrosidae; Haliocinetidae
GX NCBI_FaxID: 7729;
LN 1;
RP SEQUENCE
RC TISSUE: Hemolymph;
RA Shishikura, E.; Abe, F.; Otake, S.;
RT "Purification and characterization of a serine proteinase
RT inhibitor from the hemolymph of a solitary ascidian, Haliocynthia
RT roretzi."
RC Catechism, Physiol., 114B:1-9(1996)
CC -! FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA KINASE(S) ACTIVITY
CC -! SUBUNIT: Monomer.
CC -! SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DI InterPro: IPR002157; Serpin.
DI PROSITE: PS00284; SERPIN: PARTIAL.
DE Serpin: Serine protease inhibitor; Glycylproline plasma.
FT Non_Ter
SC SEQUENCE 10 AA: 1104 MW: 422567A018107AA (Rel. 10)
Query Match 18.2% Score 2; D8 I; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 KD 11
LA 3 KD 4

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RESULT 27
ID SYK_CAMUP STANDARD; PRI: 10 AA.
AC Q46454;
DI 15-DEC-1996 (Rel. 37, Created)
DI 15-DEC-1996 (Rel. 37, Last sequence update)
DI 24-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
DE (Fragment)
GX NCBI_FaxID: 26360;
LN 1;
RP SEQUENCE FROM N.A.
RC STRAIN: ATCC 43954;
RA MEHLINE-97149102; PubMed: 8996110;
RA Bourke, B.; Rashid, S.T.; Hindham H.L.; Chan V.L.;
RT Characterization of Campylobacter upsaliensis fur and its
RT localization in a highly conserved region of the Campylobacter
RT genome.
RL Gene 183:219-224(1996)
CC -! CATALYTIC ACTIVITY: ATP + L-lysine -> tRNA(Lys) - AMP + diphosphate
CC + L-lysyl-tRNA(Lys).
CC -! COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC -! SUBUNIT: Homodimer (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! SIMILARITY: Belongs to class-I aminocacyl-tRNA synthetase family.
CC
CC This SWISS PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: L77076; AAA41342.1;
CC HAMAP: MF_00252; 1;
DI InterPro: IPR006195; tRNA_Ligase_11;
DI PROSITE: PS00862; AA_TRNA_LIGASE_11; PARTIAL.
KW Aminocacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Metal-binding; Magnesium.
FT Non_Ter
SC SEQUENCE 10 AA: 1218 MW: 90EA46A813372B05 CRC64;
Query Match 18.2% Score 2; D8 I; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 KS 9
LA 2 KS 3
RESULT 28
ID TEMK_PANTE STANDARD; PRI: 10 AA.
AC P6923;
DI 30-MAY-2000 (Rel. 39, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Terporin K.
OS Rana temporaria (European common frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
GX NCBI_FaxID: 8407;
LN 1;
RP SEQUENCE
RC TISSUE: Skin secretion;
RA MEHLINE-9715050; PubMed: 9022713;
RA Simmare, M.; Mianzeta, S.; Canofari, S.; Miele, R.; Mangoni, M.L.;

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RA Rana catesbeiana (Bull frog).
RT *Temporary, antimicrobial peptides from the European tree frog Rana
RT temporaria.
RL Eur. J. Biochem. 242:788-792(1996).
SC -1- FUNCTION: Has antibacterial activity against Gram-positive
SC bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the protease family.
KW Amphibian defense peptide; Antimicrobial; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1123 MW: 3995496.47272577 (RefSeq).

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KS 9
EB 7 KS 8

RESULT 29
TKNB_CHICK
ID TKNB_CHICK STANDARD; PPT: 10 AA.
AC P22687.
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuropeptide A (Substance K) (Neurokinin B).
GS Gallus gallus (Chicken).
CC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Artosauria; Aves; Neognathae; Galliformes; Phasianidae; Thaumelidae;
CC Gallus.
CC NCBI_TaxID 9081;
FN 111
RP SEQUENCE.
TX MEDLINE:68204263; PubMed:24244611.
RA Gannon J.M., Katsoulis S., Schmitt W.R., Chim J.
RT *Amino acid substance P and neurokinin A from chicken small intestine.
RL Regul. Pept. 20:171-180(1988).
SC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
SC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
SC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: B61034; R61033.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1134 MW: 8668452.970664 (RefSeq).

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KS 4
EB 2 KS 3

RESULT 30
TKNB_RAN_A
ID TKNB_RAN_A STANDARD; PPT: 10 AA.
AC P22687.
DT 01-APR-1991 (Rel. 19, Created)
DT 01-APR-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Kanatachykinin B (R1K B).

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OS Rana catesbeiana (Bull frog).
CC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
CC NCBI_TaxID 8450;
FN 111
RP SEQUENCE, AND SYNTHESIS.
TX MEDLINE:91254437; PubMed:25445443.
RA Kozawa H., Hino J., Minamino N., Kanyawa K., Matsuo H.
RT *Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN 121
RP SEQUENCE.
TX MEDLINE:94024716; PubMed:840506;
RA Kanyawa K., Kozawa H., Hino J., Minamino N., Matsuo H.
RT *Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.
RL Regul. Pept. 46:81-88(1993).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: B61034; R61033.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1210 MW: 9175564.5905845 CRC64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KS 9
EB 2 KS 3

RESULT 31
TKU2_URECH
ID TKU2_URECH STANDARD; PPT: 10 AA.
AC P40752.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
LE Urechis tachykinin 11.
OS Urechis unicinctus.
CC Eukaryote; Metazoa; Echinoda; Xenophenista; Urechidae; Urechis.
CC NCBI_TaxID 6432;
FN 111
RP SEQUENCE, AND SYNTHESIS.
TX MEDLINE:93236558; PubMed:8476410;
RA Ikeda T., Minakata H., Numoto K., Kubota I., Muneoka Y.
RT *Two novel tachykinin related neuropeptides in the echinoid worm,
RT Urechis unicinctus.
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
CC MUSCLE OF THE ANIMAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 984 MW: 3F58D079C87698 CRC64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KW Headache, Migraine, Vasodilation.
PI PEPIDE 1 11 MEGASTROPHILIN.
PI PEPIDE 1 9 BRADYKININ-LIKE PEPTIDE.
SQ SEQUENCE 11 AA: 1274 MW: 3486749.07716978 CR662.

Query Match 18.2% Score 27 DB 1 Length 11
Best Local Similarity 100.0% Pred No. 1e+04
Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 2 SK 1
LD 3 SK 10

RESULT 38
EST_LSI
LC EST LSI STANDARD: PEP 11 AA
AC 194521.
DE 15 DEC 1998 (Ref. 47, Created)
DE 15 DEC 1998 (Ref. 47, Last sequence added)
DE 16 OCT 2001 (Ref. 40, Last annotation update)
DE EST protein: Mitochondrial (Fragment)
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae;
OC Mus musculus (Mus)
PI NCBI TaxID 10116;
RN 11
RP SEQUENCE.
RC STRAIN:Wistar; Tissue:Heart;
KA Li X, P, Weissner K, P, Schaller H, C, Reilly J, Zdzienicka V, Salnikow K,
KA Gurevich P, K,
KL Submitted (SHR-1998) TO THE SWISS PROTEIN BANK.
CC 1: SUBCELLULAR LOCATION: Mitochondrion (predicted)
CC 1: MUSCULAR LOCATION: ON THE Z-DISK THE DEFERRED FORM OF THIS PROTEIN
CC (SLOC 12) IS: 8.9, ITS MW IS: 25 KDa
CC 1: SIMILARITY: BELONGS TO THE EST FAMILY.
KW Mitochondrion.
RN 11
RP SEQUENCE.
FT 1142 MW: 3486749.07716978 CR662.

Query Match 18.2% Score 27 DB 1 Length 11
Best Local Similarity 100.0% Pred No. 1e+04
Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 1 AR 2
LD 2 AR 4

RESULT 47
RN HUMAN
LC EST LSI STANDARD: PEP 11 AA
AC 194521.
DE 21 JUL 1998 (Ref. 41, Created)
DE 21 JUL 1998 (Ref. 41, Last sequence added)
DE 28 FEB 2004 (Ref. 41, Last annotation update)
DE Morphogenetic neuroepitope (head activator) (HNC)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
OC Homo sapiens (Human)
PI NCBI TaxID 9606; 10116; 9913; 6112; 6062;
RN 11
RP SEQUENCE.
RC SPECIES Human, Rat, and Bovine;
KA MEDLINE:82035850; PubMed-7293191;
KA Bodenmuller H, C, Schaller H, C;
KA "Conserved amino acid sequence of a morphogenetic peptide from
KA term co-ordinates to humans".
KL NATURE 293:579-580(1981);

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RN 121
RP SEQUENCE.
RC SPECIES: Aequiactissima, and H. attenuata;
KA Schaller H, C, Bodenmuller H, C;
KA "Isolation and amino acid sequence of a morphogenetic peptide from
KA Hydra".
KL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN 31
RP SEQUENCE.
RC MEDLINE:82035850; PubMed-7293191;
KA Bodenmuller H, C, Schaller H, C;
KA "Synthesis of a new morphogenetic peptide, the head activator from Hydra".
KA FEBS Lett. 133:317-322(1982).
RN 41
RP SEQUENCE.
RC MEDLINE:90056924; PubMed-2581311;
KA Schaller H, C, Bodenmuller H, C, Reilly J, Zdzienicka V, Salnikow K,
KA "Head activator acts as an autocrine growth factor for NIH3T3 cells
KA in the G2/mitosis transition".
KA EMBO J. 8:311-318(1989).
CC 1: FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
CC IN THE G2/MITOSIS TRANSITION.
CC 1: CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
CC
CC PIR: A01427; YUKI
CC PIR: A91906; YHXA.
CC PIR: R01427; YAMC.
CC PIR: B91906; YEDPHY.
CC PIR: G01427; YHKG.
CC GK: P01263;
KW Growth factor; cell cycle; mitosis; pyrrolidone carboxylic acid.
FT M22_ERS 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA: 1142 MW: 379274173255878 CR664.

Query Match 18.2% Score 27 DB 1 Length 11
Best Local Similarity 100.0% Pred No. 1e+04
Matches 2: Conservative 0; Mismatches 0; Gaps 0

QY 9 SK 10
LD 6 SK 7

RESULT 38
Q20A_COMIF
LC Q20A_COMIF STANDARD: PEP 11 AA.
AC 194564.
DE 01-NV-1995 (Ref. 42, Created)
DE 01-NV-1995 (Ref. 42, Last sequence update)
DE 16 OCT 2001 (Ref. 40, Last annotation update)
DE Quinolone 2-oxo-reductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Camponotus testaceus (Pseudomyrmex testaceus)
OC Arthropoda; Insecta; Hymenoptera; Belontiidae; Burkholderiales;
OC Camponotidae; Camponotus.
CC NCBI TaxID: 285;
RN 11
RP SEQUENCE.
RC STRAIN:64;
KA MEDLINE:96045589; PubMed-756264;
KA Sebach S, Tetsuoka H, Fetzner S, Lingens F, J
KA "Quinolone 2-oxo-reductase and 2-oxo-1,2-dihydroquinoline 5,6-
KA dioxygenase from Camponotus testaceus, 63. The first two enzymes in
KA quinolone and 3-methyl-quinoline degradation.".
KL Eur. J. Biochem. 232:536-544(1995).
CC 1: FUNCTION: CONVERTS (3-METHYL)-QUINOLINE TO (3-METHYL)-2-OXO-
CC 3,2-DIHYDROQUINOLINE.
CC 1: CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-
CC 3(2H)-one + reduced acceptor.
CC 1: COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC 1: PATHWAY: Degradation of quinoline and (3-methyl)-quinoline; first
CC step.

```





```

QY 3 KT 4
   II
DB 5 KT 6

RESULT 44
TKNA_RANR1
ID TKNA_RANR1 STANDARD: PRT: 11 AA.
AC P24207
BI 01-DEC-1992 (rel. 24, Created)
BI 01-DEC-1992 (rel. 24, Last sequence update)
BI 15-SEP-2003 (rel. 42, Last annotation update)
DB Rankinidin (Substance-p-related peptide)
CS Rankinidin (Caqching frog) (Marsie frog)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bute (testes)
CC Amphibia; Batrachia; Anura; Neobatrachia; Rana; Rana
CX NCBI_TaxID: 8406;
RN 11
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE: 9204454; PubMed: 1656243;
RA O'Harte P., Barcher E., Iovas S., Smith L.B., Vaudry H., Carlson J.M.;
RI "Rankinidin: a novel NK1 tachykinin receptor agonist isolated with
RI rankinidin B from the brain of the frog Rana sibilandii."
RI J. Neurochem. 57:2086-2091(1991);
RC 1.
BI FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WITH EXCIT. NEURONS.
BI EVOKE BEHAVIORAL RESPONSES. ARE POTENT VASODILATORS AND
BI SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
BI MUSCLES.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DE InterPro: IP000580; Protachykinin.
DE InterPro: IP002040; Tachykinin.
DB SMART: SM00253; TK: 1.
DB PROSITE: PS0267; TACHYKININ_1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA: 1352 MW: 3A2456N5940400? CRC64:

Query Match: 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7
   II
DB 5 ER 6

RESULT 43
TKNA_RANR1
ID TKNA_RANR1 STANDARD: PRT: 11 AA.
AC P22693
BI 01-AUG-1993 (rel. 19, Created)
BI 01-AUG-1993 (rel. 19, Last sequence update)
BI 15-SEP-2003 (rel. 42, Last annotation update)
DB Rankinidin 2 (RTK D).
CS Rana catesbeiana (Bull. frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Batrachia; Stomyl.
CC Amphibia; Batrachia; Anura; Neobatrachia; Rana; Rana
CX NCBI_TaxID: 8406;
RN 11
RP SEQUENCE.
RC TISSUE: Intestine;
RX MEDLINE: 91254337; PubMed: 2043143;
RA Kozawa H., Hino J., Minamino N., Katsawa K., Matsuo H.;
RI "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RI brain and intestine."
RI Brain and Biophys. Res. Commun. 177:586-595(1991)
RN 121
RP SEQUENCE.
RC TISSUE: Intestine;

```

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RX MEDLINE: 94023216; PubMed: 8210506;
RA Katsawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RI "Four novel tachykinins in frog (Rana catesbeiana) brain and
RI intestine."
RI Regul. Pept. 46:181-188(1993).
BI FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS.
BI EVOKE BEHAVIORAL RESPONSES. ARE POTENT VASODILATORS AND
BI SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
BI MUSCLES.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DE InterPro: IP002040; Tachykinin.
DB PROSITE: PS00267; TACHYKININ; FALSE_NEG.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA: 1356 MW: 3A34256C59D43B07 CRC64:

Query Match: 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ER 7
   II
DB 5 ER 6

RESULT 44
FAR7_PENMO
ID FAR7_PENMO STANDARD: PRT: 12 AA.
AC P83322
BI 28-FEB-2003 (rel. 41, Created)
BI 28-FEB-2003 (rel. 41, Last sequence update)
BI 28-FEB-2003 (rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP7 (GYRKPPFNGSIF-amide).
CS Penaeus monodon (Penaeid shrimp).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
CC Penaeidae; Penaeus.
CX NCBI_TaxID: 6687;
RN 11
RP SEQUENCE. AND MASS SPECTROMETRY.
RC TISSUE: Eye stalk;
RX MEDLINE: 21956277; PubMed: 11959515;
RA Sathigornquai P., Pupum J., Krungkarn C., Longyant S.,
RA Chaisivuthakul P., Sithigornquai W., Petsom A.;
RI "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RI of the giant tiger prawn Penaeus monodon."
RI Comp. Biochem. Physiol. 131B:325-337(2002).
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- MASS SPECTROMETRY: MW: 1381.4; RET: 900=MALDI.
CC 1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA: 1483 MW: 31209192EF49D777 CRC64:

Query Match: 18.2%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RK 3
   II
DB 3 RK 4

RESULT 45
HZAX_ONCMY
ID HZAX_ONCMY STANDARD: PRT: 12 AA.
AC P83327
BI 28-FEB-2003 (rel. 41, Created)
BI 28-FEB-2003 (rel. 41, Last sequence update)
BI 15-SEP-2003 (rel. 42, Last annotation update)

```



**CX** conserved in Fibrales; Fabaceae; Papilionoidae; Retinidae; Saxifraga  
**RN** NERI\_LuxID=3895;  
**II** |||  
**RN** SEQUENCE FROM N.A.  
**KP** TISSUE: Stem nodules;  
**RC** MEDLINE: 96291575; PubMed: 9629265;  
**RX** Carlsen V., Gockmachling S., Lievens S., Van Marck M., Holsters M.,  
**RT** Patterns of ENOD40 gene expression in stem nodule locules of Sesbania  
**KT** rostrata.\*  
**KZ** Plant Mol Biol. 37:67-75(1998).  
**CC** 1 FUNCTION: MODULATES THE ACTION OF AUXIN AND KAY SERGIN AS PLANT  
**CC** GROWTH REGULATOR THAT ALTERS PHYTOCHROME RESPONSES (BY  
**CC** SEMIARITY)  
**CC** 1 DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE  
**CC** DEVELOPMENT.  
**CC** |||  
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**EMBL:** Y12734; CAA73252.1;  
**CC** |||  
**KW** Regulation.  
**SQ** SEQUENCE 12 AA: 1418 MW: 305951876 Da; 30% ID:  
Query Match 18.2%; Score 21; DB: UniProtKB; 125  
Best local Similarity 100.0%; Prod No: 1; Id: 41  
Matches 27 Conservative 0; Mismatches 12 Gaps 0; Daps 0;  
**QY** 8 KS 9  
**IL** 7 KS 8  
**RESULT 49**  
**R3D\_GINKR**  
**ID** R616.GINKR STANDARD; PDB: 1Z AA:  
**AC** 136,267;  
**DT** 01 JUN 1994 (Rev. 29, Created)  
**DI** 01 JUN 1994 (Rev. 25, Last sequence update)  
**DE** 24 FEB 2003 (Rev. 41, Last annotation of date)  
**GN** chloroplast 30S ribosomal protein S16 (fragment).  
**GE** 68516  
**OS** Ginkgo biloba (Ginkgo).  
**OC** Chlorophyta.  
**OC** Eukaryota; Viridiplantae; Streptophyta; Charophyta; Embryophyta.  
**OX** Sporophyta; Ginkgophyta; Ginkgoales; Taxaceae; Ginkgo  
**CX** NERI\_LuxID=3895;  
**RN** |||  
**RP** SEQUENCE FROM N.A.  
**EX** MEDLINE: 95094313; PubMed: 9501171;  
**KC** Richard M., Tremblay C., Bellemare A.  
**KA** "Chloroplast genomes of Ginkgo biloba and Pinus strobus contain  
**KI** a chla gene encoding the subunit of a self-independent  
**GI** protochlorophyllide reductase." \*  
**HL** Curr. Genet. 23:159-165(1994).  
**CC** 1 SIMILARITY: BELONGS TO THE S16 FAMILY OF RIBOSOMAL PROTEINS.  
**CC** |||  
**CC** THIS SWISS-PROT entry is copyright © 1997 provided by a collaboration  
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**CC** or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
**EMBL:** U0531; AAA66977.1;  
**DR** 6AARP; MF\_00385; -;  
**DR** IncePhos; PF080307; Ribosomal S16  
**DR** ProSDH; PS0732; RIBOSOMAL S16

```

KW Ribosomal proteins: Chloroplast.
FT NON_TER 12 12
SQ SEQUENCE 12 AA: 1488 MW: 6700EDAF9D033734 CRC64:

Query Match 12.2% Score 2: DB 1: Length 12:
Best local Similarity 100.0% Prod. No. 1.1e+04:
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 2 RK 3
   11
   11 RK 12

En

RESULT 1:
RS19_CLEP
ID RS19_CLEP STANDARD: 141: 12 AA.
AC Q464450:
ET 30-MAY-2000 (Ref. 19, created)
ET 30-MAY-2000 (Ref. 19, last sequence update)
ET 28-FEB-2003 (Ref. 41, last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPSS OR RPS19.
OS clover yellow-edge phytoplasm.
OC Bacteria: Firmicutes: Mollicutes: Acholeplasmales:
OC Acholeplasmales: Acholeplasma.
OC NCBI Taxid 35775:
RN [1]
RX MEDLINE:94350832: PMID:971195:
KA Gundersen D.E., Lee I.M., Reiner S.A., Davis K.E., Kingsbury D.T.:
ET "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
ET their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC 1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.
CC
CC This SWISS Prot entry is copyright. It is produced through a collaboration
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CC
CC EM62: 12319: AAA89431:
CC HAMAN: ME_00541: 1:
CC ESTPRO: DPK02222: Ribosomal S19.
CC PROSITE: PS00433: Ribosomal S19: PARTIAL.
CC Ribosomal protein S19A-binding.
FT NON_TER 1
SQ SEQUENCE 12 AA: 1479 MW: 40478EFC833AA3 CRC64:

Query Match 18.2% Score 2: DB 1: Length 12:
Best local Similarity 100.0% Prod. No. 1.1e+04:
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 10 KD 1:
   11
   5 KD 6

En

Search completed: September 08, 2003, 10:26:05
Job time: 7.25 secs

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Search completed: September 10, 2005, 13:26:05  
 Job time: 7.25 secs

Genre version 5.1.6  
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2. protein-protein search, using sw method.

Rev. on: September 30, 2003, 10:17:04 (Section: the 31st and Section 15  
(with a 1,000,000)  
89, 89 million dollars/31st

File: US-99-787-443-14

... AKKIREKSKU...

[illegible]

**Figure 1** | **(A)** Schematic representation of the experimental setup. The subject was seated at a distance of 60 cm from the screen. The screen displayed a target area (red circle) and a starting point (black dot). The subject was asked to move the hand from the starting point to the target area. The movement was recorded by a video camera. **(B)** Example of a movement trajectory. The red line indicates the path of the hand. The black dots indicate the starting and ending points. The green arrow indicates the direction of movement.

See: *Chad*; 830.25 says, 258052234 (p. 1, 10)

[illegible]

Total number of hits satisfying chosen parameters, of

# MUMUKSHU BHASINI

Model	Min. length	Max. length
Model 1	1.5	1.5
Model 2	1.5	1.5
Model 3	1.5	1.5
Model 4	1.5	1.5
Model 5	1.5	1.5
Model 6	1.5	1.5
Model 7	1.5	1.5
Model 8	1.5	1.5
Model 9	1.5	1.5
Model 10	1.5	1.5
Model 11	1.5	1.5
Model 12	1.5	1.5
Model 13	1.5	1.5
Model 14	1.5	1.5
Model 15	1.5	1.5
Model 16	1.5	1.5
Model 17	1.5	1.5
Model 18	1.5	1.5
Model 19	1.5	1.5
Model 20	1.5	1.5
Model 21	1.5	1.5
Model 22	1.5	1.5
Model 23	1.5	1.5
Model 24	1.5	1.5
Model 25	1.5	1.5
Model 26	1.5	1.5
Model 27	1.5	1.5
Model 28	1.5	1.5
Model 29	1.5	1.5
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Model 31	1.5	1.5
Model 32	1.5	1.5
Model 33	1.5	1.5
Model 34	1.5	1.5
Model 35	1.5	1.5
Model 36	1.5	1.5
Model 37	1.5	1.5
Model 38	1.5	1.5
Model 39	1.5	1.5
Model 40	1.5	1.5
Model 41	1.5	1.5
Model 42	1.5	1.5
Model 43	1.5	1.5
Model 44	1.5	1.5
Model 45	1.5	1.5
Model 46	1.5	1.5
Model 47	1.5	1.5
Model 48	1.5	1.5
Model 49	1.5	1.5
Model 50	1.5	1.5
Model 51	1.5	1.5
Model 52	1.5	1.5
Model 53	1.5	1.5
Model 54	1.5	1.5
Model 55	1.5	1.5
Model 56	1.5	1.5
Model 57	1.5	1.5
Model 58	1.5	1.5
Model 59	1.5	1.5
Model 60	1.5	1.5
Model 61	1.5	1.5
Model 62	1.5	1.5
Model 63	1.5	1.5
Model 64	1.5	1.5
Model 65	1.5	1.5
Model 66	1.5	1.5
Model 67	1.5	1.5
Model 68	1.5	1.5
Model 69	1.5	1.5
Model 70	1.5	1.5
Model 71	1.5	1.5
Model 72	1.5	1.5
Model 73	1.5	1.5
Model 74	1.5	1.5
Model 75	1.5	1.5
Model 76	1.5	1.5
Model 77	1.5	1.5
Model 78	1.5	1.5
Model 79	1.5	1.5
Model 80	1.5	1.5
Model 81	1.5	1.5
Model 82	1.5	1.5
Model 83	1.5	1.5
Model 84	1.5	1.5
Model 85	1.5	1.5
Model 86	1.5	1.5
Model 87	1.5	1.5
Model 88	1.5	1.5
Model 89	1.5	1.5
Model 90	1.5	1.5
Model 91	1.5	1.5
Model 92	1.5	1.5
Model 93	1.5	1.5
Model 94	1.5	1.5
Model 95	1.5	1.5
Model 96	1.5	1.5
Model 97	1.5	1.5
Model 98	1.5	1.5
Model 99	1.5	1.5
Model 100	1.5	1.5

THE UNIVERSITY OF CHICAGO

id: abase : SPIRITMBL 23 : \*

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;; sp arched:
;; sp arched:

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[illegible]

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sp_func1;
sp_func2;
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1 : sp_human : *
2 : human : *

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sp\_lover:ale:

6. *Sp. nana*! : \*

sp\_mhc: \*

α: sp. of value 1

9. Sp. page: \*

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.:): sp_plant:

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1.: sp_rotent:
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12: sp. virus:

Isabel

4: 22. 10. 1941

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:star_05
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sp\_bacteri

./: src\_archive

Prod 80 is the number of residents of the 100 countries having a score greater than or equal to the score for the country to be compared and subtracted by the number of the countries having a score less than or equal to the score for the country to be compared.

Result	No.	Score	Entry	Match	Length	DB	ID	Location
1	1	4	35.4	18	4	Q90285	270.85	Home Station
2	2	3	27.3	3	4	Q44763	247.7	China Station
3	3	4	27.3	9	4	Q93684	29.804	Home Station
4	4	4	27.3	9	4	Q91211	29.211	Spain Station
5	5	4	27.3	9	8	Q91211	29.211	Spain Station
6	6	3	27.3	5	10	Q61493	261.05	Sea Mays (0)
7	7	3	27.3	9	13	Q51A33	Q9145	Sea Mays (0)
8	8	3	27.3	10	2	Q50839	Q9145	Sea Mays (0)
9	9	4	27.3	10	5	Q82221	Q9145	Sea Mays (0)
10	10	3	27.3	10	8	P82136	182.1	Spain Station
11	11	4	27.3	10	10	Q41333	Q9145	Sea Mays (0)
12	12	4	27.3	10	10	Q82134	182.1	Spain Station
13	13	4	27.3	10	12	Q84266	Q9145	Sea Mays (0)
14	14	4	27.3	10	13	Q71831	Q9145	Sea Mays (0)
15	15	4	27.3	11	4	Q34785	Q9145	Sea Mays (0)
16	16	3	27.3	11	4	Q34785	Q9145	Sea Mays (0)

90	2	18.2	8	2	Q95453	Q95453	psodactonus	153	2	18.2	8	8	Q94VF9	Q94VF9	varanus ind
91	2	18.2	8	4	Q15889	Q15889	homo sapien	154	2	18.2	8	8	Q8MC16	Q8MC16	indwigia hy
92	2	18.2	8	4	Q15895	Q15895	homo sapien	155	2	18.2	8	8	Q8MC34	Q8MC34	heimia myrt
93	2	18.2	8	4	Q16428	Q16428	homo sapien	156	2	18.2	8	8	P93992	P93992	australopyr
94	2	18.2	8	4	Q94PK3	Q94PK3	homo sapien	157	2	18.2	8	8	Q8MC32	Q8MC32	rotala indi
95	2	18.2	8	5	Q15899	Q15899	tabesia avi	158	2	18.2	8	8	Q8MC42	Q8MC42	sonneratia
96	2	18.2	8	5	Q94624	Q94624	manduca sox	159	2	18.2	8	8	Q15959	Q15959	quossypium t
97	2	18.2	8	5	Q8MUNE	Q8MUNE	hericium	160	2	18.2	8	8	Q8MC40	Q8MC40	hesana lued
98	2	18.2	8	5	Q15896	Q15896	tabesia hox	161	2	18.2	8	8	P92426	P92426	pseudoroegn
99	2	18.2	8	6	Q18854	Q18854	tabesia fami	162	2	18.2	8	8	Q15956	Q15956	gossypium a
100	2	18.2	8	6	Q95593	Q95593	meplatiza b	163	2	18.2	8	8	P92431	P92431	aegilops ta
101	2	18.2	8	6	Q95597	Q95597	coris fami	164	2	18.2	8	8	Q94VF3	Q94VF3	varanus kei
102	2	18.2	8	6	Q95597	Q95597	coris fami	165	2	18.2	8	8	Q94VA7	Q94VA7	varanus sal
103	2	18.2	8	6	Q95597	Q95597	coris fami	166	2	18.2	8	8	Q94VA5	Q94VA5	varanus sal
104	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	167	2	18.2	8	8	P92422	P92422	psathyrosta
105	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	168	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
106	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	169	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
107	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	170	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
108	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	171	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
109	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	172	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
110	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	173	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
111	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	174	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
112	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	175	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
113	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	176	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
114	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	177	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
115	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	178	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
116	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	179	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
117	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	180	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
118	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	181	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
119	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	182	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
120	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	183	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
121	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	184	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
122	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	185	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
123	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	186	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
124	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	187	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
125	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	188	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
126	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	189	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
127	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	190	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
128	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	191	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
129	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	192	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
130	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	193	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
131	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	194	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
132	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	195	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
133	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	196	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
134	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	197	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
135	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	198	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
136	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	199	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
137	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	200	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
138	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	201	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
139	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	202	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
140	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	203	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
141	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	204	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
142	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	205	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
143	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	206	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
144	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	207	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
145	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	208	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
146	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	209	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
147	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	210	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
148	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	211	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
149	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	212	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
150	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	213	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
151	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	214	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
152	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	215	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
153	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	216	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
154	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	217	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
155	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	218	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
156	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	219	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
157	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	220	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
158	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	221	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
159	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	222	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
160	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	223	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
161	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	224	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph
162	2	18.2	8	8	Q8MUN4	Q8MUN4	sonneratia	225	2	18.2	8	8	Q8MUN4	Q8MUN4	bacterioph

245	2	18.2	9	8	Q952N1	Q9501 pericardium	309	2	18.2	10	5	P82217	P82217 bombyx mori
247	2	18.2	9	8	Q91NE4	Q9404 magnolia sa	310	2	18.2	10	5	P82224	P82224 bombyx mori
248	2	18.2	9	8	Q95DS6	Q95DS6 magnolia w2	311	2	18.2	10	5	P82224	P82224 bombyx mori
249	2	18.2	9	8	Q91NE6	Q91NE6 magnolia q7	312	2	18.2	10	6	Q9TRC1	Q9TRC1 bos taurus
249	2	18.2	9	8	Q91NE6	Q91NE6 magnolia q7	313	2	18.2	10	6	Q9XSR4	Q9XSR4 equus caball
241	2	18.2	9	8	Q91NE1	Q91NE1 magnolia be	314	2	18.2	10	6	Q9M178	Q9M178 bos mutus g
242	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	315	2	18.2	10	6	Q9M270	Q9M270 trichosurus
243	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	316	2	18.2	10	6	P82205	P82205 ovis aries
244	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	317	2	18.2	10	7	Q95HE8	Q95HE8 papio anubi
245	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	318	2	18.2	10	7	Q95HE9	Q95HE9 papio anubi
246	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	319	2	18.2	10	6	Q9H4W1	Q9H4W1 triturus vu
247	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	320	2	18.2	10	6	Q9SHC6	Q9SHC6 furcifer be
248	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	321	2	18.2	10	8	Q99224	Q99224 elgaria pan
249	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	322	2	18.2	10	8	Q94616	Q94616 aspidosceli
250	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	323	2	18.2	10	8	Q95HE9	Q95HE9 rana boylii
251	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	324	2	18.2	10	8	Q9H4W1	Q9H4W1 pachytriton
252	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	325	2	18.2	10	8	Q95HE12	Q95HE12 rana tempor
253	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	326	2	18.2	10	8	Q91NE4	Q91NE4 diplolossu
254	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	327	2	18.2	10	8	Q9XMR4	Q9XMR4 aegilops ta
255	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	328	2	18.2	10	8	Q95HE14	Q95HE14 xantusia he
256	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	329	2	18.2	10	8	Q91NE6	Q91NE6 diplolossu
257	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	330	2	18.2	10	8	Q94VGS	Q94VGS varanus gri
258	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	331	2	18.2	10	8	Q94VH1	Q94VH1 varanus gle
259	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	332	2	18.2	10	8	Q91NE6	Q91NE6 abronia oax
260	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	333	2	18.2	10	8	Q94V97	Q94V97 varanus spe
261	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	334	2	18.2	10	8	Q91NE5	Q91NE5 elgaria mul
262	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	335	2	18.2	10	8	Q94VGS	Q94VGS mertensiell
263	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	336	2	18.2	10	8	Q91NE8	Q91NE8 shinisaurus
264	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	337	2	18.2	10	8	P92766	P92766 varanus gri
265	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	338	2	18.2	10	8	Q95HE18	Q95HE18 rana catesb
266	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	339	2	18.2	10	8	Q91NE9	Q91NE9 mertensiell
267	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	340	2	18.2	10	8	Q94VGS	Q94VGS varanus oli
268	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	341	2	18.2	10	8	Q91NE8	Q91NE8 ophiodes st
269	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	342	2	18.2	10	8	Q94VGS	Q94VGS mertensiell
270	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	343	2	18.2	10	8	Q91NE6	Q91NE6 e-daria kin
271	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	344	2	18.2	10	8	Q94VGS	Q94VGS varanus pan
272	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	345	2	18.2	10	8	Q94VGS	Q94VGS mertensiell
273	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	346	2	18.2	10	8	Q95HE10	Q95HE10 magnolia po
274	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	347	2	18.2	10	8	Q91NE1	Q91NE1 barisia imb
275	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	348	2	18.2	10	8	Q91NE8	Q91NE8 sauromalus
276	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	349	2	18.2	10	8	Q95HE8	Q95HE8 magnolia de
277	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	350	2	18.2	10	8	Q91NE6	Q91NE6 acanthusar
278	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	351	2	18.2	10	8	Q94VGS	Q94VGS varanus kin
279	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	352	2	18.2	10	8	Q95HE9	Q95HE9 magnolia sp
280	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	353	2	18.2	10	8	Q91NE2	Q91NE2 teratoscinc
281	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	354	2	18.2	10	8	Q94VGS	Q94VGS tylotriton
282	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	355	2	18.2	10	8	Q95HE6	Q95HE6 rana pretio
283	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	356	2	18.2	10	8	Q91NE1	Q91NE1 heloderma s
284	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	357	2	18.2	10	8	Q95HE8	Q95HE8 rana cascad
285	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	358	2	18.2	10	8	Q95HE15	Q95HE15 rana sylvat
286	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	359	2	18.2	10	8	Q94VGS	Q94VGS mertensiell
287	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	360	2	18.2	10	8	Q91NE4	Q91NE4 ophiisaurus
288	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	361	2	18.2	10	8	P92771	P92771 xenosaurus
289	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	362	2	18.2	10	8	Q94VGS	Q94VGS varanus var
290	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	363	2	18.2	10	8	Q91NE8	Q91NE8 elgaria coe
291	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	364	2	18.2	10	8	Q94VGS	Q94VGS mertensiell
292	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	365	2	18.2	10	8	Q95HE8	Q95HE8 rana aurora
293	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	366	2	18.2	10	8	Q95HE8	Q95HE8 xantusia ar
294	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	367	2	18.2	10	8	Q91NE2	Q91NE2 ophiisaurus
295	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	368	2	18.2	10	8	Q94VGS	Q94VGS salamandra
296	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	369	2	18.2	10	8	Q95HE8	Q95HE8 magnolia me
297	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	370	2	18.2	10	8	Q94VGS	Q94VGS magnolia me
298	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	371	2	18.2	10	8	Q91NE4	Q91NE4 gambelia w
299	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	372	2	18.2	10	8	Q91NE1	Q91NE1 crotophytus
300	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	373	2	18.2	10	8	Q91NE8	Q91NE8 gerrophotus
301	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	374	2	18.2	10	8	Q91NE4	Q91NE4 anguis frag
302	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	375	2	18.2	10	8	Q94VGS	Q94VGS varanus sca
303	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	376	2	18.2	10	8	Q91NE1	Q91NE1 mertensiell
304	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	377	2	18.2	10	8	Q91NE8	Q91NE8 ophiisaurus
305	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	378	2	18.2	10	8	Q91NE2	Q91NE2 annieia pu
306	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	379	2	18.2	10	8	Q91NE4	Q91NE4 bipes bipor
307	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	380	2	18.2	10	8	Q91NE4	Q91NE4 ophiisaurus
308	2	18.2	9	8	Q91NE4	Q91NE4 rotulus gla	381	2	18.2	10	8	Q91NE4	Q91NE4 mertensiell

452	2	18.2	10	9	Q92Y12	Q92Y12	ectomorphala
453	2	18.2	10	8	Q95D12	Q95D12	maritima pa
454	2	18.2	10	8	Q97G25	Q97G25	cartaria pa
455	2	18.2	10	8	Q94NH4	Q94NH4	tata muscus
456	2	18.2	10	8	Q94VD2	Q94VD2	varanus pa
457	2	18.2	10	8	Q91374	Q91374	weimoria h
458	2	18.2	10	8	Q94A55	Q94A55	westerncell
459	2	18.2	10	8	Q94G26	Q94G26	salamandra
460	2	18.2	10	8	Q91377	Q91377	sauresta ad
461	2	18.2	10	8	Q91B65	Q91B65	calatus o
462	2	18.2	10	8	Q91362	Q91362	hesapus mo
463	2	18.2	10	8	Q94D11	Q94D11	maritima yu
464	2	18.2	10	8	Q91359	Q91359	annulata de
465	2	18.2	10	8	Q91389	Q91389	celestus co
466	2	18.2	10	8	Q92YV4	Q92YV4	discomus
467	2	18.2	10	8	Q92374	Q92374	xanthostyl
468	2	18.2	10	8	Q95J07	Q95J07	xanthostyl
469	2	18.2	10	8	Q95J01	Q95J01	xanthostyl
470	2	18.2	10	8	Q95J04	Q95J04	atomotum
471	2	18.2	10	8	Q95J06	Q95J06	atomotum
472	2	18.2	10	8	Q95J08	Q95J08	atomotum
473	2	18.2	10	8	Q95J10	Q95J10	atomotum
474	2	18.2	10	8	Q95J12	Q95J12	atomotum
475	2	18.2	10	8	Q95J14	Q95J14	atomotum
476	2	18.2	10	8	Q95J16	Q95J16	atomotum
477	2	18.2	10	8	Q95J18	Q95J18	atomotum
478	2	18.2	10	8	Q95J20	Q95J20	atomotum
479	2	18.2	10	8	Q95J22	Q95J22	atomotum
480	2	18.2	10	8	Q95J24	Q95J24	atomotum
481	2	18.2	10	8	Q95J26	Q95J26	atomotum
482	2	18.2	10	8	Q95J28	Q95J28	atomotum
483	2	18.2	10	8	Q95J30	Q95J30	atomotum
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485	2	18.2	10	8	Q95J34	Q95J34	atomotum
486	2	18.2	10	8	Q95J36	Q95J36	atomotum
487	2	18.2	10	8	Q95J38	Q95J38	atomotum
488	2	18.2	10	8	Q95J40	Q95J40	atomotum
489	2	18.2	10	8	Q95J42	Q95J42	atomotum
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492	2	18.2	10	8	Q95J48	Q95J48	atomotum
493	2	18.2	10	8	Q95J50	Q95J50	atomotum
494	2	18.2	10	8	Q95J52	Q95J52	atomotum
495	2	18.2	10	8	Q95J54	Q95J54	atomotum
496	2	18.2	10	8	Q95J56	Q95J56	atomotum
497	2	18.2	10	8	Q95J58	Q95J58	atomotum
498	2	18.2	10	8	Q95J60	Q95J60	atomotum
499	2	18.2	10	8	Q95J62	Q95J62	atomotum
500	2	18.2	10	8	Q95J64	Q95J64	atomotum
501	2	18.2	10	8	Q95J66	Q95J66	atomotum
502	2	18.2	10	8	Q95J68	Q95J68	atomotum
503	2	18.2	10	8	Q95J70	Q95J70	atomotum
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505	2	18.2	10	8	Q95J74	Q95J74	atomotum
506	2	18.2	10	8	Q95J76	Q95J76	atomotum
507	2	18.2	10	8	Q95J78	Q95J78	atomotum
508	2	18.2	10	8	Q95J80	Q95J80	atomotum
509	2	18.2	10	8	Q95J82	Q95J82	atomotum
510	2	18.2	10	8	Q95J84	Q95J84	atomotum
511	2	18.2	10	8	Q95J86	Q95J86	atomotum
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513	2	18.2	10	8	Q95J90	Q95J90	atomotum
514	2	18.2	10	8	Q95J92	Q95J92	atomotum
515	2	18.2	10	8	Q95J94	Q95J94	atomotum
516	2	18.2	10	8	Q95J96	Q95J96	atomotum
517	2	18.2	10	8	Q95J98	Q95J98	atomotum
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519	2	18.2	10	8	Q95J02	Q95J02	atomotum
520	2	18.2	10	8	Q95J04	Q95J04	atomotum
521	2	18.2	10	8	Q95J06	Q95J06	atomotum
522	2	18.2	10	8	Q95J08	Q95J08	atomotum
523	2	18.2	10	8	Q95J10	Q95J10	atomotum
524	2	18.2	10	8	Q95J12	Q95J12	atomotum
525	2	18.2	10	8	Q95J14	Q95J14	atomotum
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527	2	18.2	10	8	Q95J18	Q95J18	atomotum
528	2	18.2	10	8	Q95J20	Q95J20	atomotum
529	2	18.2	10	8	Q95J22	Q95J22	atomotum
530	2	18.2	10	8	Q95J24	Q95J24	atomotum
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532	2	18.2	10	8	Q95J28	Q95J28	atomotum
533	2	18.2	10	8	Q95J30	Q95J30	atomotum
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535	2	18.2	10	8	Q95J34	Q95J34	atomotum
536	2	18.2	10	8	Q95J36	Q95J36	atomotum
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547	2	18.2	10	8	Q95J58	Q95J58	atomotum
548	2	18.2	10	8	Q95J60	Q95J60	atomotum
549	2	18.2	10	8	Q95J62	Q95J62	atomotum
550	2	18.2	10	8	Q95J64	Q95J64	atomotum
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554	2	18.2	10	8	Q95J72	Q95J72	atomotum
555	2	18.2	10	8	Q95J74	Q95J74	atomotum
556	2	18.2	10	8	Q95J76	Q95J76	atomotum
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560	2	18.2	10	8	Q95J84	Q95J84	atomotum
561	2	18.2	10	8	Q95J86	Q95J86	atomotum
562	2	18.2	10	8	Q95J88	Q95J88	atomotum
563	2	18.2	10	8	Q95J90	Q95J90	atomotum
564	2	18.2	10	8	Q95J92	Q95J92	atomotum
565	2	18.2	10	8	Q95J94	Q95J94	atomotum
566	2	18.2	10	8	Q95J96	Q95J96	atomotum
567	2	18.2	10	8	Q95J98	Q95J98	atomotum
568	2	18.2	10	8	Q95J00	Q95J00	atomotum
569	2	18.2	10	8	Q95J02	Q95J02	atomotum
570	2	18.2	10	8	Q95J04	Q95J04	atomotum
571	2	18.2	10	8	Q95J06	Q95J06	atomotum
572	2	18.2	10	8	Q95J08	Q95J08	atomotum
573	2	18.2	10	8	Q95J10	Q95J10	atomotum
574	2	18.2	10	8	Q95J12	Q95J12	atomotum
575	2	18.2	10	8	Q95J14	Q95J14	atomotum
576	2	18.2	10	8	Q95J16	Q95J16	atomotum
577	2	18.2	10	8	Q95J18	Q95J18	atomotum
578	2	18.2	10	8	Q95J20	Q95J20	atomotum
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586	2	18.2	10	8	Q95J36	Q95J36	atomotum
587	2	18.2	10	8	Q95J38	Q95J38	atomotum
588	2	18.2	10	8	Q95J40	Q95J40	atomotum
589	2	18.2	10	8	Q95J42	Q95J42	atomotum
590	2	18.2	10	8	Q95J44	Q95J44	atomotum
591	2	18.2	10	8	Q95J46	Q95J46	atomotum
592	2	18.2	10	8	Q95J48	Q95J48	atomotum
593	2	18.2	10	8	Q95J50	Q95J50	atomotum
594	2	18.2	10	8	Q95J52	Q95J52	atomotum
595	2	18.2	10	8	Q95J54	Q95J54	atomotum
596	2	18.2	10	8	Q95J56	Q95J56	atomotum
597	2	18.2	10	8	Q95J58	Q95J58	atomotum
598	2	18.2	10	8	Q95J60	Q95J60	atomotum
599	2	18.2	10	8	Q95J62	Q95J62	atomotum
600	2	18.2	10	8	Q95J64	Q95J64	atomotum
601	2	18.2	10	8	Q95J66	Q95J66	atomotum
602	2	18.2	10	8	Q95J68	Q95J68	atomotum
603	2	18.2	10	8	Q95J70	Q95J70	atomotum
604	2	18.2	10	8	Q95J72	Q95J72	atomotum
605	2	18.2	10	8	Q95J74	Q95J74	atomotum
606	2	18.2	10	8	Q95J76	Q95J76	atomotum
607	2	18.2	10	8	Q95J78	Q95J78	atomotum
608	2	18.2	10	8	Q95J80	Q95J80	atomotum
609	2	18.2	10	8	Q95J82	Q95J82	atomotum
610	2	18.2	10	8	Q95J84	Q95J84	atomotum
611	2	18.2	10	8	Q95J86	Q95J86	atomotum
612	2	18.2	10	8	Q95J88	Q95J88	atomotum
613	2	18.2	10	8	Q95J90	Q95J90	atomotum
614	2	18.2	10	8	Q95J92	Q95J92	atomotum
615	2	18.2	10	8	Q95J94	Q95J94	atomotum
616	2	18.2	10	8	Q95J96	Q95J96	atomotum
617	2	18.2	10	8	Q95J98	Q95J98	atomotum
618	2	18.2	10	8	Q95J00	Q95J00	atomotum
619	2	18.2	10	8	Q95J02	Q95J02	atomotum
620	2	18.2	10	8	Q95J04	Q95J04	atomotum
621	2	18.2	10	8	Q95J06	Q95	

SQ SEQUENCE 14 AA: 1609 MW: 4E29F5352729A3 (6074)  
 Query Match: 36.4% Score 3: 10 11: 1000000 13:  
 Best Local Similarity: 100.0% Pred. No. 9 3e+05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 3 KIR 5  
 10 11  
 10 7 KIR 10  
 RESULT 4  
 Q91210 PRELIMINARY: PRT: 9 AA:  
 AC Q91210  
 DT 01-MAY-2000 (EMBLrel. 13: Created)  
 DT 01-MAY-2000 (EMBLrel. 13: Last sequence update)  
 DT 01-JUN-2002 (EMBLrel. 21: Last annotation update)  
 DE LHC II LIGHT-HARVESTING CHLOROPHYLL PROTEIN II (Fragment).  
 OS Spinacia oleracea (Spinach).  
 GN Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.  
 CX NCBI TaxID 3562;  
 RN 11  
 RP SEQUENCE  
 RX MEDLINE:9137386; PubMed:1894541;  
 RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.L.  
 RT "Tandem mass spectrometry identifies sites of three post-translational  
 RT modifications of spinach light-harvesting chlorophyll protein II.  
 RT Proteolytic cleavage, acetylation, and phosphorylation.";  
 RL J. Biol. Chem. 266:17584-17591(1991).  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 799 MW: 54D9276387D51A3 (38064)  
 Query Match: 27.3% Score 3: 08 8: Length 9:  
 Best Local Similarity: 100.0% Pred. No. 8 3e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 2 RKT 4  
 10 11  
 10 1 RKT 3

Query Match: 27.3% Score 3: 08 8: Length 9:  
 Best Local Similarity: 100.0% Pred. No. 8 3e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 8 KSK 10  
 10 11  
 10 4 KSK 5  
 RESULT 5  
 Q91211 PRELIMINARY: PRT: 9 AA:  
 AC Q91211  
 DT 01-MAY-2000 (EMBLrel. 13: Created)  
 DT 01-MAY-2000 (EMBLrel. 13: Last sequence update)  
 DT 01-JUN-2002 (EMBLrel. 21: Last annotation update)  
 DE LHC II LIGHT-HARVESTING CHLOROPHYLL PROTEIN II (Fragment).  
 OS Spinacia oleracea (Spinach).  
 GN Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.  
 CX NCBI TaxID 3562;  
 RN 11  
 RP SEQUENCE  
 RX MEDLINE:9137386; PubMed:1894541;  
 RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.L.  
 RT "Tandem mass spectrometry identifies sites of three post-translational  
 RT modifications of spinach light-harvesting chlorophyll protein II.  
 RT Proteolytic cleavage, acetylation, and phosphorylation.";  
 RL J. Biol. Chem. 266:17584-17591(1991).  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 985 MW: 54D9276387D51A3 (38064)  
 Query Match: 27.3% Score 3: 08 8: Length 9:  
 Best Local Similarity: 100.0% Pred. No. 8 3e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 7 PKS 9  
 10 11  
 10 1 KKS 3

Query Match: 27.3% Score 3: 08 8: Length 9:  
 Best Local Similarity: 100.0% Pred. No. 8 3e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 4 KSK 1  
 10 11  
 10 2 KSK 3  
 RESULT 6  
 Q91214 PRELIMINARY: PRT: 9 AA:  
 AC Q91214  
 DT 01-MAY-2000 (EMBLrel. 13: Created)  
 DT 01-MAY-2000 (EMBLrel. 13: Last sequence update)  
 DT 01-MAY-2000 (EMBLrel. 13: Last annotation update)  
 DE LHC II LIGHT-HARVESTING CHLOROPHYLL PROTEIN II (Fragment).  
 OS Spinacia oleracea (Spinach).  
 GN Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;  
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.  
 CX NCBI TaxID 3562;  
 RN 11  
 RP SEQUENCE  
 RX MEDLINE:9137386; PubMed:1894541;  
 RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.L.  
 RT "Tandem mass spectrometry identifies sites of three post-translational  
 RT modifications of spinach light-harvesting chlorophyll protein II.  
 RT Proteolytic cleavage, acetylation, and phosphorylation.";  
 RL J. Biol. Chem. 266:17584-17591(1991).  
 FT NON\_TER 1 9  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA: 1125 MW: 614A253630P411 (38064)  
 Query Match: 27.3% Score 3: 08 8: Length 9:  
 Best Local Similarity: 100.0% Pred. No. 8 3e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 4 KSK 1  
 10 11  
 10 2 KSK 3

RESULT 7





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DB: 5 KSK 5

RESULT 11
C8LPT7 PRELIMINARY: PRT: 10 AA.
ID C8LPT7
AC C8LPT7
DT 01-JUN-2002 (ITEMHIST: 22, Created)
DT 01-JUN-2002 (ITEMHIST: 22, Last sequence update)
DT 01-JUN-2002 (ITEMHIST: 22, Last annotation update)
DE beta expansin-like protein (fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Monocotyledons; Poales; Poaceae;
OC PACAD clade; Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID:4577;
EN 11;
RP SEQUENCE FROM N.A.
RC STRAIN CV: H96;
RA China A.S., Caldwell K.S., Long M., Dolan M., Smith O.S., Magee S.,
RA Morante M., Ralski J.A.;
RT *SNP frequency, haplotype structure and linkage disequilibrium in
RT elite maize inbred lines.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
ER EMBL: AY594306; AAM21834.1;
FI NCN_TIER 1
FI NCN_TIER 1
SQ SEQUENCE 10 AA: 1348 MW: 50556702cblaaa3 CRC64;

Query Match 27.4% Score 3; DB 10; Length 10;
Best local similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKD 11
DB 2 SKD 4

RESULT 12
P82434 PRELIMINARY: PRT: 10 AA.
ID P82434
AC P82434
DT 01-JUN-2000 (ITEMHIST: 14, Created)
DT 01-JUN-2000 (ITEMHIST: 14, Last sequence update)
DT 01-JUN-2000 (ITEMHIST: 14, Last annotation update)
DE 28 kDa cell wall protein (fragment).
OS Nicotiana tabacum (common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID:4597;
EN 11;
RP SEQUENCE.
RC STRAIN CV: PETH: HAVANA;
RA Bleg K.A., Bohner V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolewell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco cultures";
RL Planta 216-0(2000).
OC 1- SUBCELLULAR LOCATION: CELL WALL.
CC 1- TISSUE SPECIFICITY: XYLEM.
FI NCN_TIER 10
FI NCN_TIER 10
SQ SEQUENCE 10 AA: 1054 MW: 1A4K96DDAH2C444 CRC64;

Query Match 27.4% Score 3; DB 10; Length 10;
Best local similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARK 3
DB 8 ARK 10

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RS0911: 13
845256
ID 084526 PRELIMINARY: PRT: 10 AA
AC 084526
DT 01-NOV-1999 (TrEMBLrel. 01, Created)
DI 01-NOV-1999 (TrEMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 08, Last annotation update)
DE (HIV-1) gNA (Fragment)
DN E6
OS Human papillomavirus type 11
OC Viruses: dsDNA viruses, no RNA stage; Papillomaviridae
OC Papillomavirus
CX NCBI_TaxID:13590
RN 11
RP SEQUENCE FROM N.A.
RC STEADIN Boushey
RA MEDLINE 4929475; PubMed:4545074
RA Collado S.C., Chow L.T., Kreider J.W., Probst L.S., Li L., N.L.,
RA Bowers M.K.
RT "Characterization of an HIV type 1 isolate propagated in human
RT foreskin explants in nude mice."
RC Virus 17:294-297(1999)
DR EMBL:354511; AAA66865.1
FT NON_TER 10
SV SEQUENCE 10 AA: 1026 MW: 97895SRHAA125 CR664
Query Match 27.8% Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKD 11
ID 6 SKD 5

RESULT 14
Q98J01
ID Q98J01 PRELIMINARY: PRT: 10 AA
AC Q98J01
DT 01-MAY-2000 (TrEMBLrel. 14, Created)
DI 01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
DE "SODIUM FEMALE attractant pheromone"
OS Cynops pyrrhogaster (Japanese common toad)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Anura; Caudata; Salamandridae; Gyraps
CX NCBI_TaxID:8159
RP SEQUENCE
RC MEDLINE 7890452
RA Kikuchi S., Toyoda F., Shimizu Y.
RA "Sodium female attractant pheromone in toad"
RC "Quodas"
DR EMBL:354511; AAA66865.1
FT NON_TER 10
SV SEQUENCE 10 AA: 1071 MW: 995782LAA52047 CR664
Query Match 27.3% Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKD 11
ID 4 SKD 6

RESULT 15
Q94785
ID Q94785 PRELIMINARY: PRT: 11 AA
AC Q94785
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DI 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE Thrombospondin (Fragment)
OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta eudicotyledons; core eudicots; Rosidae;
OC Eurosidia 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
CX NCBI_TaxID: 6847;

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OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 11
RP SEQUENCE FROM N.A.
RC Sasaki Y., Takahashi T., Nakagawa K., Okuno Y., Nakao K.,
RT "Production of Thrombospondin by Human Carcinomas and Its Novel mRNA
RT Isoforms."
RI Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL:AB014683; BAA34312.1
FT NON_TER 1
SV SEQUENCE 11 AA: 1233 MW: 5FE19F44B6C1A877 CR664
Query Match 27.8% Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TRE 6
ID 8 TRE 10

RESULT 16
Q98J07
ID Q98J07 PRELIMINARY: PRT: 11 AA
AC Q98J07
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Aquaporin-4 (Fragment)
DE Aquaporin-4 (Fragment)
DN AQP4
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE 97008105; PubMed 8855281;
RA Li M., Lee M.B., Smith B.L., Susq J.S., Agre P., Verdijk M.A.J.,
RA Borck G., Rjess J.P.L., Beem P.M.T.
RT "The human AQP4 gene: definition of the locus encoding two water
RT channel polypeptides in brain."
RL Proc. Natl. Acad. Sci. U.S.A. 93:10908-10912(1996).
DR EMBL: U63613; AAG37964.1
FT NON_TER 1
FT NON_TER 11
SV SEQUENCE 11 AA: 1233 MW: 47956A331AEH737 CR664
Query Match 27.8% Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TRE 4
ID 7 TRE 9

RESULT 17
Q98X84
ID Q98X84 PRELIMINARY: PRT: 11 AA
AC Q98X84
DT 01-MAY-2001 (TrEMBLrel. 15, Created)
DI 01-MAY-2001 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vegetative storage protein 54 peptide 3, VSP94-LIPOXYGENASE
DE (Fragment)
DN Glycine max (Soybean)
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta eudicotyledons; core eudicots; Rosidae;
OC Eurosidia 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine
CX NCBI_TaxID: 6847;

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FN SEQUENCE.
RX MEDLINE 92361246; PubMed 1822994;
RA Truberg T.J., Franceschi V.K., Alderman D.F., Graves B.D.
KI "The soybean 94-kilodalton vegetative storage protein is a
RL lipoxxygenase that is localized to paracuticular mesophyll cell
RL Plant Cell 3:973-987(1991).
FL NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1366 MW; 90412618E35A5B3 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RKS 7
LB 4 RKS 4

RESULT 19
Q26404
ID Q26404 PRELIMINARY; PKI; 12 AA.
AC Q26404;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-2000 (TrEMBLrel. 01, Last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PROPOSCIPEDIA protein (Fragment).
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7242;
XX 11
RP SEQUENCE FROM N.A.
KA MEDLINE 92111489; PubMed-1684942;
KA Randazzo F.M., Citrus D.L., Kaufman T.C.
KI "Rescue and regulation of proboscipedia: a homeotic gene of the
RL Antennapedia Complex."
RL Development 113:257-271(1991).
DR EMBL: S77929; AAB20845.1; -.
DR FlyBase: FBgn012734; DpseXpb.
FL NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1377 MW; 4608D18E355A5B3 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKS 9
LB 4 RKS 4

RESULT 21
P82364
ID P82364 PRELIMINARY; PKI; 12 AA.
AC P82364;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 35S ribosomal protein S14 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID:3562;
XX 11
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RA STRAIN-GV, ALVARO; TISSUE-Leaf;
RX MEDLINE 20435797; PubMed-10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
KI "The plastid ribosomal proteins: Identification of all the proteins in
RL the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN PL. S14 ALPHA

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CC 1- FROM IS THE LEAST BASIC FORM.
CC 1- MASS SPECTROMETRY: MW 11745.9; PHEMO4 ELECTRO SPRAY.
CC 1- MASS SPECTROMETRY: MW 11747; MEMED-MA201.
CC 1- MISCELLANEOUS: ON THE 2D GEL ITS MW IS 14 KDA.
CC 1- SIMILARITY: BELONGS TO THE S14E FAMILY OF RIBOSOMAL PROTEINS
DE INTERPRO: IPRO01209; Ribosomal_S14
DE PLANT: PR01249; Ribosomal_S14; PARTIAL
DE PROSITE: PS01144; RIBOSOMAL_S14; PARTIAL
DE RIBOSOMAL PROTEIN: Chloroplast: tRNA-binding.
DE NON_TER 12 12
SQ SEQUENCE 12 AA: 1513 MW: 54240.1; 1513 MW: 54240.1
Query Match 27.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RKS 9
DB 1 RKS 4
RESULT 22
P82247
AC P82247 PRELIMINARY; PRI: 12 AA.
DE GENE: 2002 (EMBL:rel. 22; Last sequence update)
DE GENE: 2002 (EMBL:rel. 22; Last sequence update)
DE beta expansion like protein (Fragment)
DE Zea mays (Maize)
DE Eukaryota; Viridiplantae; Streptophyta; Charophyta;
DE Spermatophyta; Magnoliophyta; Liliopsida; Liliaceae;
DE PAVAR clade; Parnicoideae; Andropogoneae; Zea
DE NCBI_TaxID: 4577;
DE SEQUENCE FROM K.A.
DE STRAIN: cv. TX503;
DE Zaidi A.S.; Caldwell K.S.; Jang M.; Jordan M.; Shetty S.S.; Hickey S.;
DE Meradze M.; Katsaki J.A.;
DE SNF frequency, haplotype structure and linkage disequilibrium in
DE rice and rice inbred lines.
DE Published (APR 2002) to the EMBL/Genbank/Tran databases
DE DMC: AY094609; AAM21845.1;
DE NON_TER 12 12
SQ SEQUENCE 12 AA: 1260 MW: 54240.1; 1260 MW: 54240.1
Query Match 27.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 RKS 11
DB 4 RKS 6
RESULT 23
P82248
AC P82248 PRELIMINARY; PRI: 12 AA.
DE GENE: 2002 (EMBL:rel. 14; Created)
DE GENE: 2001 (EMBL:rel. 14; Last sequence update)
DE GENE: 2001 (EMBL:rel. 17; Last annotation update)
DE chloroplast 5S ribosomal protein L31 (Fragment)
DE Spinacia oleracea (Spinach)
DE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
DE Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
DE NCBI_TaxID: 3562;
DE SEQUENCE FROM K.A.
DE STRAIN: cv. ALVARO; TISSUE: leaf;
DE MEDLINE: 2445799; PubMed: 10474046;
DE Yamauchi K.; Subramanian A.K.;
DE The 50 S subunit of an organelle ribosome (chloroplast).
DE 2D Gel Electrometry: 275, 28466, 28482(2.9e3)
DE FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
DE SUBCELLULAR LOCATION: CHLOROPLAST.
DE TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES
DE MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
DE DIFFER IN CHARGE.
DE SIMILARITY: BELONGS TO THE L31E FAMILY OF RIBOSOMAL PROTEINS.
DE INTERPRO: IPRO02150; Ribosomal_L31
DE PLANT: PR01197; Ribosomal_L31; PARTIAL
DE PROSITE: PS01144; RIBOSOMAL_L31; PARTIAL
DE PRINTS: PR01249; RIBOSOMAL_L31; PARTIAL
DE PROSITE: PS01144; RIBOSOMAL_L31; PARTIAL
DE RIBOSOMAL PROTEIN: chloroplast: tRNA-binding.
DE NON_TER 12 12
SQ SEQUENCE 12 AA: 1529 MW: 14898.95; 1529 MW: 14898.95
Query Match 27.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RKS 9
DB 1 RKS 4
RESULT 24
P82249
AC P82249 PRELIMINARY; PRI: 12 AA.
DE GENE: 2000 (EMBL:rel. 14; Created)
DE GENE: 2000 (EMBL:rel. 14; Last sequence update)
DE GENE: 2000 (EMBL:rel. 17; Last annotation update)
DE chloroplast 50S ribosomal protein L31 gamma (Fragment)
DE Spinacia oleracea (Spinach)
DE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
DE Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
DE NCBI_TaxID: 3562;
DE SEQUENCE FROM K.A.
DE STRAIN: cv. ALVARO; TISSUE: leaf;
DE MEDLINE: 2445799; PubMed: 10474046;
DE Yamauchi K.; Subramanian A.K.;
DE The 50 S subunit of an organelle ribosome (chloroplast).
DE 2D Gel Electrometry: 275, 28466, 28482(2.9e3)
DE FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
DE SUBCELLULAR LOCATION: CHLOROPLAST.
DE TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES
DE MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
DE DIFFER IN CHARGE.
DE SIMILARITY: BELONGS TO THE L31E FAMILY OF RIBOSOMAL PROTEINS.
DE INTERPRO: IPRO02150; Ribosomal_L31
DE PLANT: PR01197; Ribosomal_L31; PARTIAL
DE PRINTS: PR01249; RIBOSOMAL_L31; PARTIAL
DE PROSITE: PS01144; RIBOSOMAL_L31; PARTIAL
DE RIBOSOMAL PROTEIN: chloroplast: tRNA-binding.
DE NON_TER 12 12
SQ SEQUENCE 12 AA: 1529 MW: 14898.95; 1529 MW: 14898.95
Query Match 27.0%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RKS 9
DB 1 RKS 4
RESULT 25
P82250
AC P82250 PRELIMINARY; PRI: 12 AA.
DE GENE: 2000 (EMBL:rel. 14; Created)
DE GENE: 2000 (EMBL:rel. 14; Last sequence update)
DE GENE: 2000 (EMBL:rel. 17; Last annotation update)
DE chloroplast 50S ribosomal protein L31 gamma (Fragment)
DE Spinacia oleracea (Spinach)
DE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
DE Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
DE NCBI_TaxID: 3562;
DE SEQUENCE FROM K.A.
DE STRAIN: cv. ALVARO; TISSUE: leaf;
DE MEDLINE: 2445799; PubMed: 10474046;
DE Yamauchi K.; Subramanian A.K.;
DE The 50 S subunit of an organelle ribosome (chloroplast).
DE 2D Gel Electrometry: 275, 28466, 28482(2.9e3)
DE FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
DE SUBCELLULAR LOCATION: CHLOROPLAST.
DE TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES
DE MISCELLANEOUS: THERE ARE THREE FORMS, ALPHA, BETA AND GAMMA WHICH
DE DIFFER IN CHARGE.
DE SIMILARITY: BELONGS TO THE L31E FAMILY OF RIBOSOMAL PROTEINS.
DE INTERPRO: IPRO02150; Ribosomal_L31
DE PLANT: PR01197; Ribosomal_L31; PARTIAL
DE PRINTS: PR01249; RIBOSOMAL_L31; PARTIAL
DE PROSITE: PS01144; RIBOSOMAL_L31; PARTIAL
DE RIBOSOMAL PROTEIN: chloroplast: tRNA-binding.
DE NON_TER 12 12
SQ SEQUENCE 12 AA: 1529 MW: 14898.95; 1529 MW: 14898.95

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CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45685.1;
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid. 1.
KW Polypeptide. 14 13
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 34
Q81774 ID Q81774 PRELIMINARY; PRT; 13 AA.
AC Q81774;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genomic polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus
OX NCBI_TaxID:11103;
KN 11
RP SEQUENCE FROM N.A.
RC STRAIN-SA1;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45715.1;
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid. 1.
KW Polypeptide. 14 14
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 35
Q81766 ID Q81766 PRELIMINARY; PRT; 13 AA.
AC Q81766;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genomic polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus
OX NCBI_TaxID:11103;
KN 11
RP SEQUENCE FROM N.A.
RC STRAIN-HK2;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45684.1;
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid. 1.
KW Polypeptide. 14 13
FT NON_TER
SQ SEQUENCE 13 AA: 1571 MW: 46410E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 36
Q81793 ID Q81793 PRELIMINARY; PRT; 13 AA.
AC Q81793;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

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CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45685.1;
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid. 1.
KW Polypeptide. 14 13
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464197E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 35
Q81766 ID Q81766 PRELIMINARY; PRT; 13 AA.
AC Q81766;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Genomic polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus
OX NCBI_TaxID:11103;
KN 11
RP SEQUENCE FROM N.A.
RC STRAIN-HK2;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84863; AAA45684.1;
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid. 1.
KW Polypeptide. 14 13
FT NON_TER
SQ SEQUENCE 13 AA: 1571 MW: 46410E1A42FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 36
Q81793 ID Q81793 PRELIMINARY; PRT; 13 AA.
AC Q81793;
DI 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

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DE Genome polyprotein (Fragment).
GN POLYPROTEIN
GS Hepatitis C virus.
CA* Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepacivirus.
EX NCBI_LaXID:11103;
EN 1;
SC SEQUENCE FROM N.A.
RX MEDLINE-92279243; PubMed 1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
CR EMBL: M84865; AAA45717.1;
IR InterPro: IPR002522; HCV_capsid
IK Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 4549761A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 47
Q81768
ID Q81768 PRELIMINARY: PRT: 13 AA.
AC Q81768;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN
GS Hepatitis C virus.
CA* Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepacivirus.
EX NCBI_LaXID:11103;
EN 1;
SC SEQUENCE FROM N.A.
RX MEDLINE-92279243; PubMed 1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
CR EMBL: M84865; AAA45686.1;
IR InterPro: IPR002522; HCV_capsid; 1;
IK Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 4549761A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

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RESULT 38
Q81785
ID Q81785 PRELIMINARY: PRT: 13 AA.
AC Q81785;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN
GS Hepatitis C virus.
CA* Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepacivirus.
EX NCBI_LaXID:11103;
EN 1;
SC SEQUENCE FROM N.A.
RX MEDLINE-92279243; PubMed 1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
CR EMBL: M84865; AAA45702.1;
IR InterPro: IPR002522; HCV_capsid
IK Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 4549761A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RKT 4
DB 9 RKT 11

RESULT 39
Q81800
ID Q81800 PRELIMINARY: PRT: 13 AA.
AC Q81800;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN
GS Hepatitis C virus.
CA* Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Hepacivirus.
EX NCBI_LaXID:11103;
EN 1;
SC SEQUENCE FROM N.A.
RX MEDLINE-92279243; PubMed 1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
  Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC 1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
  LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
  PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
  PROTEIN C AND MRNA (BY SIMILARITY).
CR EMBL: M84865; AAA45717.1;
IR InterPro: IPR002522; HCV_capsid
IK Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 4549761A42FC763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;

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DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1557 MW: 464656FA42PC763 CRC64:
      Query Match: 27.9%, Score 3; DR 12; Length 13;
      Best Local Similarity 100.0%; Prod. No. 1004;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PKT 4
DB 111
DB 9 RKT 11
      PRELIMINARY; PRI: 13 AA.
RESULT 4:
Q81759 Q81759 PRELIMINARY; PRI: 13 AA.
AC Q81759
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID:11103;
CX NCBI_TaxID:11103;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-P8;
RC MEDLINE:92279243; PubMed:1417578;
RA Bukh J., Purcell R.H., Miller R.H.;
RI Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992);
RL 01- SURFING THE VISION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND RNA (BY SIMILARITY).
CC EMBL: M84856; AAA45687 1;
DR InterPro: IPR002522; RV Capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1557 MW: 465465FA42PC763 CRC64:
      Query Match: 27.9%, Score 3; DR 12; Length 13;
      Best Local Similarity 100.0%; Prod. No. 1004;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PKT 4
DB 111
DB 9 RKT 11
      PRELIMINARY; PRI: 13 AA.
RESULT 4:
Q81759 Q81759 PRELIMINARY; PRI: 13 AA.
AC Q81759
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID:11103;
CX NCBI_TaxID:11103;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-S9;
RC MEDLINE:92279243; PubMed:1417578;
RA Bukh J., Purcell R.H., Miller R.H.;
RI "Sequence analysis of the 5' noncoding region of hepatitis C virus."

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99 01 NOV 2002, Acad. Sci., U.S.A. 8914942 4946(1992).
100 1. SUBUNIT, THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
101 LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
102 PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
103 PROTEIN E AND MRNA (BY SIMILARITY).
104 EMBL: M64944, AAA45691.1.
105 DR 01 NOV 1996 (199602522) HCV_capsid.1
106 1. SUBUNIT, THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
107 LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
108 PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
109 PROTEIN E AND MRNA (BY SIMILARITY).
110 NC_017687 13 AA: 1572 MW: 4049761A42FC763 CRC64:
111 SEQUENCE 13 AA: 1572 MW: 4049761A42FC763 CRC64:
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113 Quality Match: 27.9% Score 4; DB 12; Length 13;
114 Best Local Similarity: 100.0%; Pred. No. 1004;
115 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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117 2 RRT 4
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119 4 RRT 11
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DI 01-NOV-1996 (TEMBLETON, 01, Last sequence update)
DE 01-NOV-2002 (TEMBLETON, 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae
OX NCBI_TaxID:11163
XN 11
KP SEQUENCE FROM N.A.
RC STRAIN:HK1
KA Bokh J., Perceval R.H., Miller R.H.
KI "Sequence analysis of the 5' noncoding region of hepatitis C virus."
KL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC 1-1 SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84809; AAA45681.1;
DR InterPro: IP8092522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON-TER 14 14
SQ SEQUENCE 14 AA: 1572 MW: 46419216421076; 25.94;
Query Match 27.4%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1004;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RKT 4
QZ 9 RKT 11
RESULT 4b
Q81794 PRELIMINARY, PRI: 14 AA.
AC Q81794;
DI 01-NOV-1996 (TEMBLETON, 01, Created)
DE 01-NOV-1996 (TEMBLETON, 01, Last sequence update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae
OX NCBI_TaxID:11163
XN 11
KP SEQUENCE FROM N.A.
RC STRAIN:HK1
KA Bokh J., Perceval R.H., Miller R.H.
KI "Sequence analysis of the 5' noncoding region of hepatitis C virus."
KL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC 1-1 SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84809; AAA45681.1;
DR InterPro: IP8092522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON-TER 14 14
SQ SEQUENCE 14 AA: 1572 MW: 46419216421076; 25.94;
Query Match 27.4%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1004;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RKT 4
QZ 9 RKT 11

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RESULT 4c
Q81796 PRELIMINARY, PRI: 14 AA.
AC Q81796;
DI 01-NOV-1996 (TEMBLETON, 01, Created)
DE 01-NOV-1996 (TEMBLETON, 01, Last sequence update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae
OX NCBI_TaxID:11163
XN 11
KP SEQUENCE FROM N.A.
RC STRAIN:SS2;
KA Bokh J., Perceval R.H., Miller R.H.
KI "Sequence analysis of the 5' noncoding region of hepatitis C virus."
KL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC 1-1 SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84847; AAA5713.1;
DR InterPro: IP8092522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON-TER 14 14
SQ SEQUENCE 14 AA: 1571 MW: 464016164210763; 25.93;
Query Match 27.4%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1004;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RKT 4
QZ 9 RKT 11
RESULT 5c
Q8179c PRELIMINARY, PRI: 14 AA.
AC Q8179c;
DI 01-NOV-1996 (TEMBLETON, 01, Created)
DE 01-NOV-1996 (TEMBLETON, 01, Last sequence update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae
OX NCBI_TaxID:11163
XN 11
KP SEQUENCE FROM N.A.
RC STRAIN:HK1;
KA Bokh J., Perceval R.H., Miller R.H.
KI "Sequence analysis of the 5' noncoding region of hepatitis C virus."
KL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC 1-1 SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84832; AAA45706.1;
DR InterPro: IP8092522; HCV_capsid; 1;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON-TER 14 14
SQ SEQUENCE 14 AA: 1572 MW: 464192164210763; 25.93;

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Query Match: 27.9%; Score: 93.00; Len: 100; Length: 200  
Best Local Similarity: 100.0%; Pred. No.: 34;  
Matches: 31; Conservative: 0; Mismatches: 0; Labels: 0; Gaps: 0;

QY 2 RRI 4  
IU 111  
DL 9 RRI 2

Search Completed: September 30, 2003, 11:06:54  
Lab Time: 0.36 6667 Secs

GenEdit version 5.1.6  
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CM protein: protein search, using sw model

Run on: September 30, 2003, 11:06:52, 5.1.6 Search engine: BLAST Sequences  
(without all duplicates)  
97,011,111,606,063 updates/sec

Title: US-09-787-443-14  
Perfect score: 11  
Sequence: 1 ARMTREKSKD 11

Scoring table: GIGU  
Gapop 66.6, Gapext 60.9

Searched: 128717 seqs, 4231058 residues

Word size: 3

Total number of hits satisfying chosen parameters: 7809

Minimum hit seq length: 8  
Maximum hit seq length: 15

Post-processing: listing first 500 summaries

Database: Issued\_Patents\_AA\*  
1: /cqn2\_6/ptodata/1/aa/SA/08b.fdb\*  
2: /cqn2\_6/ptodata/1/aa/SA/08b.fdb\*  
3: /cqn2\_6/ptodata/1/aa/SA/08b.fdb\*  
4: /cqn2\_6/ptodata/1/aa/SA/08b.fdb\*  
5: /cqn2\_6/ptodata/1/aa/SA/08b.fdb\*  
6: /cqn2\_6/ptodata/1/aa/backfiles.fdb\*

Prod. No. is the number of results predicted by engine to have a  
Score greater than or equal to the Score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Prod. No.	Description
1	46.4	8	1	US-09-444-040-36	Sequence 7, Appl	
2	46.4	8	2	US-09-444-040-36	Sequence 57, Appl	
3	46.4	8	2	US-09-444-040-36	Sequence 4, Appl	
4	46.4	8	4	US-09-444-040-36	Sequence 23, Appl	
5	46.4	8	3	US-09-444-040-36	Sequence 40, Appl	
6	46.4	8	3	US-09-444-040-36	Sequence 57, Appl	
7	46.4	8	3	US-09-444-040-36	Sequence 57, Appl	
8	46.4	8	4	US-09-444-040-36	Sequence 18, Appl	
9	46.4	8	4	US-09-444-040-36	Sequence 39, Appl	
10	46.4	8	4	US-09-444-040-36	Sequence 64, Appl	
11	46.4	8	4	US-09-444-040-36	Sequence 91, Appl	
12	46.4	8	4	US-09-444-040-36	Sequence 111, Appl	
13	46.4	8	4	US-09-444-040-36	Sequence 18, Appl	
14	46.4	8	6	US-09-444-040-36	Patent No. 547984	
15	46.4	9	2	US-09-444-040-36	Sequence 10, Appl	
16	46.4	9	2	US-09-444-040-36	Sequence 10, Appl	
17	46.4	9	3	US-09-444-040-36	Sequence 9, Appl	
18	46.4	9	3	US-09-444-040-36	Sequence 27, Appl	
19	46.4	9	3	US-09-444-040-36	Sequence 44, Appl	
20	46.4	9	3	US-09-444-040-36	Sequence 51, Appl	
21	46.4	9	3	US-09-444-040-36	Sequence 60, Appl	
22	46.4	9	3	US-09-444-040-36	Sequence 70, Appl	
23	46.4	9	4	US-09-444-040-36	Sequence 41, Appl	
24	46.4	9	4	US-09-444-040-36	Sequence 58, Appl	
25	46.4	9	4	US-09-444-040-36	Sequence 74, Appl	
26	46.4	9	4	US-09-444-040-36	Sequence 95, Appl	
27	46.4	9	4	US-09-444-040-36	Sequence 112, Appl	

28	4	35.4	10	2	US-08-808-277A-43	Sequence 43, Appl
29	4	35.4	10	4	US-08-265-222-1	Sequence 1, Appl
30	4	35.4	11	3	US-08-746-160-51	Sequence 51, Appl
31	4	36.4	11	3	US-08-810-324-46	Sequence 46, Appl
32	4	36.4	11	3	US-08-679-006-16	Sequence 16, Appl
33	4	36.4	11	3	US-08-147-592A-41	Sequence 41, Appl
34	4	36.4	11	4	US-08-292-694A-41	Sequence 41, Appl
35	4	36.4	11	4	US-08-292-694A-46	Sequence 46, Appl
36	4	36.4	11	4	US-08-292-694A-46	Sequence 46, Appl
37	4	36.4	11	4	US-08-495-308-2	Sequence 2, Appl
38	4	36.4	11	4	US-07-652-648-1	Sequence 1, Appl
39	4	36.4	11	4	US-08-249-387-5	Sequence 5, Appl
40	4	36.4	11	4	US-08-483-415-17	Sequence 17, Appl
41	4	36.4	11	4	US-08-616-855-3	Sequence 3, Appl
42	4	36.4	11	4	US-08-259-550A-35	Sequence 35, Appl
43	4	36.4	11	4	US-08-452-724A-38	Sequence 38, Appl
44	4	36.4	11	4	US-08-373-190-48	Sequence 48, Appl
45	4	36.4	11	4	US-08-481-337A-17	Sequence 17, Appl
46	4	36.4	11	4	US-08-147-777-4	Sequence 4, Appl
47	4	36.4	11	4	US-08-461-216-7	Sequence 7, Appl
48	4	36.4	11	4	US-08-350-260A-467	Sequence 467, App
49	4	36.4	11	4	US-08-438-190A-48	Sequence 48, Appl
50	4	36.4	11	4	US-08-232-539D-21	Sequence 21, Appl
51	4	36.4	11	4	US-08-696-268B-7	Sequence 7, Appl
52	4	36.4	11	4	US-08-464-025A-2	Sequence 2, Appl
53	4	36.4	11	4	US-08-350-215-48	Sequence 48, Appl
54	4	36.4	11	4	US-08-616-854-3	Sequence 3, Appl
55	4	36.4	11	4	US-08-466-151-10	Sequence 10, Appl
56	4	36.4	11	4	US-08-466-151-27	Sequence 27, Appl
57	4	36.4	11	4	US-08-925-002-21	Sequence 21, Appl
58	4	36.4	11	4	US-08-452-872-4	Sequence 4, Appl
59	4	36.4	11	4	US-08-118-055-1	Sequence 1, Appl
60	4	36.4	11	4	US-08-287-145A-48	Sequence 48, Appl
61	4	36.4	11	4	US-08-863-813A-17	Sequence 17, Appl
62	4	36.4	11	4	US-08-863-813A-28	Sequence 28, Appl
63	4	36.4	11	4	US-08-288-061-2	Sequence 2, Appl
64	4	36.4	11	4	US-08-160-604-65	Sequence 65, Appl
65	4	36.4	11	4	US-08-160-604-66	Sequence 66, Appl
66	4	36.4	11	4	US-08-160-604-67	Sequence 67, Appl
67	4	36.4	11	4	US-08-160-604-68	Sequence 68, Appl
68	4	36.4	11	4	US-08-160-604-69	Sequence 69, Appl
69	4	36.4	11	4	US-08-160-604-70	Sequence 70, Appl
70	4	36.4	11	4	US-08-676-318A-17	Sequence 17, Appl
71	4	36.4	11	4	US-08-676-318A-28	Sequence 28, Appl
72	4	36.4	11	4	US-08-582-333A-87	Sequence 87, Appl
73	4	36.4	11	4	US-08-082-279B-815	Sequence 815, App
74	4	36.4	11	4	US-09-101-649-44	Sequence 44, Appl
75	4	36.4	11	4	US-09-366-103-5	Sequence 5, Appl
76	4	36.4	11	4	US-09-556-111-48	Sequence 48, Appl
77	4	36.4	11	4	US-08-466-163B-10	Sequence 10, Appl
78	4	36.4	11	4	US-08-466-163B-27	Sequence 27, Appl
79	4	36.4	11	4	US-08-723-661B-7	Sequence 7, Appl
80	4	36.4	11	4	US-09-315-304B-815	Sequence 815, App
81	4	36.4	11	4	US-09-305-923A-6	Sequence 1545, App
82	4	36.4	11	4	US-09-451-034-1	Sequence 1, Appl
83	4	36.4	11	4	US-08-255-208A-74	Sequence 74, Appl
84	4	36.4	11	4	US-08-988-843-38	Sequence 38, Appl
85	4	36.4	11	4	US-09-670-075A-1	Sequence 1, Appl
86	4	36.4	11	4	US-09-104-333A-467	Sequence 467, App
87	4	36.4	11	4	US-09-101-272G-42	Sequence 42, Appl
88	4	36.4	11	4	US-09-101-272G-45	Sequence 45, Appl
89	4	36.4	11	4	US-08-695-692B-15	Sequence 15, Appl
90	4	36.4	11	4	US-08-695-692B-16	Sequence 16, Appl
91	4	36.4	11	4	US-09-350-325-5	Sequence 5, Appl
92	4	36.4	11	4	US-09-367-777-75	Sequence 75, Appl
93	4	36.4	11	4	US-09-367-777-108	Sequence 108, App
94	4	36.4	11	4	US-09-834-784-815	Sequence 815, App
95	4	36.4	11	4	US-09-308-437A-1	Sequence 1, Appl
96	4	36.4	11	4	US-08-932-411A-28	Sequence 28, Appl
97	4	36.4	11	4	US-09-367-791A-83	Sequence 83, Appl
98	4	36.4	11	4	US-09-367-791A-83	Sequence 83, Appl
99	4	36.4	11	4	PCT US93-03985-4	Sequence 4, Appl
100	4	36.4	11	4	US-09-367-791A-83	Patent No. 5436138

101	3	27.3	8	6	54-01-18-15	Patient No. 5436138	174	3	27.3	9	3	US-08-723-425A-403	Sequence 403, App
102	3	27.3	8	6	5482-85-15	Patient No. 5482984	175	3	27.3	9	3	US-08-723-425A-404	Sequence 404, App
103	3	27.3	9	1	US-07-626-677A-2	Sequence 2, Appl	176	3	27.3	9	3	US-08-723-425A-405	Sequence 405, App
104	3	27.3	9	1	US-07-626-677A-3	Sequence 3, Appl	177	3	27.3	9	3	US-08-723-425A-406	Sequence 406, App
105	3	27.3	9	1	US-07-626-677A-4	Sequence 4, Appl	178	3	27.3	9	3	US-08-723-425A-407	Sequence 407, App
106	3	27.3	9	1	US-07-626-677A-5	Sequence 5, Appl	179	3	27.3	9	3	US-09-035-249A-13	Sequence 13, Appl
107	3	27.3	9	1	US-07-626-677A-6	Sequence 6, Appl	180	3	27.3	9	3	US-09-202-832-8	Sequence 8, Appl
108	3	27.3	9	1	US-07-626-677A-7	Sequence 7, Appl	181	3	27.3	9	3	US-08-960-780-67	Sequence 67, Appl
109	3	27.3	9	1	US-08-341-954-3	Sequence 3, Appl	182	3	27.3	9	3	US-09-112-206-180	Sequence 180, App
110	3	27.3	9	1	US-08-341-954-4	Sequence 4, Appl	183	3	27.3	9	3	US-09-112-206-181	Sequence 181, App
111	3	27.3	9	1	US-08-341-954-5	Sequence 5, Appl	184	3	27.3	9	3	US-09-112-206-182	Sequence 182, App
112	3	27.3	9	1	US-08-341-954-6	Sequence 6, Appl	185	3	27.3	9	3	US-09-112-206-183	Sequence 183, App
113	3	27.3	9	1	US-08-341-954-7	Sequence 7, Appl	186	3	27.3	9	3	US-09-112-206-184	Sequence 184, App
114	3	27.3	9	1	US-08-341-954-8	Sequence 8, Appl	187	3	27.3	9	3	US-09-112-206-185	Sequence 185, App
115	3	27.3	9	1	US-08-341-954-9	Sequence 9, Appl	188	3	27.3	9	3	US-09-112-206-186	Sequence 186, App
116	3	27.3	9	1	US-08-341-954-10	Sequence 10, Appl	189	3	27.3	9	3	US-09-112-206-190	Sequence 190, App
117	3	27.3	9	1	US-08-341-954-11	Sequence 11, Appl	190	3	27.3	9	3	US-09-112-206-191	Sequence 191, App
118	3	27.3	9	1	US-08-341-954-12	Sequence 12, Appl	191	3	27.3	9	3	US-09-112-206-192	Sequence 192, App
119	3	27.3	9	1	US-08-341-954-13	Sequence 13, Appl	192	3	27.3	9	3	US-09-112-206-233	Sequence 233, App
120	3	27.3	9	1	US-08-341-954-14	Sequence 14, Appl	193	3	27.3	9	3	US-09-112-206-234	Sequence 234, App
121	3	27.3	9	1	US-08-341-954-15	Sequence 15, Appl	194	3	27.3	9	3	US-09-112-206-235	Sequence 235, App
122	3	27.3	9	1	US-08-341-954-16	Sequence 16, Appl	195	3	27.3	9	3	US-09-112-206-236	Sequence 236, App
123	3	27.3	9	1	US-08-341-954-17	Sequence 17, Appl	196	3	27.3	9	3	US-09-112-206-237	Sequence 237, App
124	3	27.3	9	1	US-08-341-954-18	Sequence 18, Appl	197	3	27.3	9	3	US-09-112-206-238	Sequence 238, App
125	3	27.3	9	1	US-08-341-954-19	Sequence 19, Appl	198	3	27.3	9	3	US-09-112-206-239	Sequence 239, App
126	3	27.3	9	1	US-08-341-954-20	Sequence 20, Appl	199	3	27.3	9	3	US-09-112-206-401	Sequence 401, App
127	3	27.3	9	1	US-08-341-954-21	Sequence 21, Appl	200	3	27.3	9	3	US-09-112-206-402	Sequence 402, App
128	3	27.3	9	1	US-08-341-954-22	Sequence 22, Appl	201	3	27.3	9	3	US-09-112-206-403	Sequence 403, App
129	3	27.3	9	1	US-08-341-954-23	Sequence 23, Appl	202	3	27.3	9	3	US-09-112-206-404	Sequence 404, App
130	3	27.3	9	1	US-08-341-954-24	Sequence 24, Appl	203	3	27.3	9	3	US-09-112-206-405	Sequence 405, App
131	3	27.3	9	1	US-08-341-954-25	Sequence 25, Appl	204	3	27.3	9	3	US-09-112-206-406	Sequence 406, App
132	3	27.3	9	1	US-08-341-954-26	Sequence 26, Appl	205	3	27.3	9	3	US-09-112-206-407	Sequence 407, App
133	3	27.3	9	1	US-08-341-954-27	Sequence 27, Appl	206	3	27.3	9	3	US-09-073-898-67	Sequence 67, Appl
134	3	27.3	9	1	US-08-341-954-28	Sequence 28, Appl	207	3	27.3	9	3	US-09-082-279H-727	Sequence 727, App
135	3	27.3	9	1	US-08-341-954-29	Sequence 29, Appl	208	3	27.3	9	3	US-09-101-649-45	Sequence 45, Appl
136	3	27.3	9	1	US-08-341-954-30	Sequence 30, Appl	209	3	27.3	9	3	US-09-061-764A-8	Sequence 8, Appl
137	3	27.3	9	1	US-08-341-954-31	Sequence 31, Appl	210	3	27.3	9	3	US-09-459-956-18	Sequence 18, Appl
138	3	27.3	9	1	US-08-341-954-32	Sequence 32, Appl	211	3	27.3	9	3	US-09-315-304B-727	Sequence 727, App
139	3	27.3	9	1	US-08-341-954-33	Sequence 33, Appl	212	3	27.3	9	3	US-09-658-645A-11	Sequence 11, Appl
140	3	27.3	9	1	US-08-341-954-34	Sequence 34, Appl	213	3	27.3	9	3	US-08-255-208A-75	Sequence 75, Appl
141	3	27.3	9	1	US-08-341-954-35	Sequence 35, Appl	214	3	27.3	9	3	US-09-259-478A-5	Sequence 5, Appl
142	3	27.3	9	1	US-08-341-954-36	Sequence 36, Appl	215	3	27.3	9	3	US-09-259-478A-6	Sequence 6, Appl
143	3	27.3	9	1	US-08-341-954-37	Sequence 37, Appl	216	3	27.3	9	3	US-09-259-478A-7	Sequence 7, Appl
144	3	27.3	9	1	US-08-341-954-38	Sequence 38, Appl	217	3	27.3	9	3	US-09-259-478A-10	Sequence 10, Appl
145	3	27.3	9	1	US-08-341-954-39	Sequence 39, Appl	218	3	27.3	9	3	US-09-101-272G-41	Sequence 41, Appl
146	3	27.3	9	1	US-08-341-954-40	Sequence 40, Appl	219	3	27.3	9	3	US-09-101-272G-44	Sequence 44, Appl
147	3	27.3	9	1	US-08-341-954-41	Sequence 41, Appl	220	3	27.3	9	3	US-09-144-280-15	Sequence 15, Appl
148	3	27.3	9	1	US-08-341-954-42	Sequence 42, Appl	221	3	27.3	9	3	US-09-434-122-39	Sequence 39, Appl
149	3	27.3	9	1	US-08-341-954-43	Sequence 43, Appl	222	3	27.3	9	3	US-09-634-784-727	Sequence 727, App
150	3	27.3	9	1	US-08-341-954-44	Sequence 44, Appl	223	3	27.3	9	3	US-09-052-10068-19	Sequence 19, Appl
151	3	27.3	9	1	US-08-341-954-45	Sequence 45, Appl	224	3	27.3	9	3	US-07-656-719-14	Sequence 14, Appl
152	3	27.3	9	1	US-08-341-954-46	Sequence 46, Appl	225	3	27.3	9	3	US-07-968-781A-50	Sequence 50, Appl
153	3	27.3	9	1	US-08-341-954-47	Sequence 47, Appl	226	3	27.3	9	3	US-08-253-171-2	Sequence 2, Appl
154	3	27.3	9	1	US-08-341-954-48	Sequence 48, Appl	227	3	27.3	9	3	US-08-166-195A-9	Sequence 9, Appl
155	3	27.3	9	1	US-08-341-954-49	Sequence 49, Appl	228	3	27.3	9	3	US-08-166-195A-10	Sequence 10, Appl
156	3	27.3	9	1	US-08-341-954-50	Sequence 50, Appl	229	3	27.3	9	3	US-08-464-522-2	Sequence 2, Appl
157	3	27.3	9	1	US-08-341-954-51	Sequence 51, Appl	230	3	27.3	9	3	US-08-464-522-4	Sequence 4, Appl
158	3	27.3	9	1	US-08-341-954-52	Sequence 52, Appl	231	3	27.3	9	3	US-08-464-522-5	Sequence 5, Appl
159	3	27.3	9	1	US-08-341-954-53	Sequence 53, Appl	232	3	27.3	9	3	US-08-464-522-6	Sequence 6, Appl
160	3	27.3	9	1	US-08-341-954-54	Sequence 54, Appl	233	3	27.3	9	3	US-08-464-522-7	Sequence 7, Appl
161	3	27.3	9	1	US-08-341-954-55	Sequence 55, Appl	234	3	27.3	9	3	US-08-464-522-8	Sequence 8, Appl
162	3	27.3	9	1	US-08-341-954-56	Sequence 56, Appl	235	3	27.3	9	3	US-08-464-522-9	Sequence 9, Appl
163	3	27.3	9	1	US-08-341-954-57	Sequence 57, Appl	236	3	27.3	9	3	US-08-464-522-10	Sequence 10, Appl
164	3	27.3	9	1	US-08-341-954-58	Sequence 58, Appl	237	3	27.3	9	3	US-08-464-522-11	Sequence 11, Appl
165	3	27.3	9	1	US-08-341-954-59	Sequence 59, Appl	238	3	27.3	9	3	US-08-464-522-12	Sequence 12, Appl
166	3	27.3	9	1	US-08-341-954-60	Sequence 60, Appl	239	3	27.3	9	3	US-08-464-522-13	Sequence 13, Appl
167	3	27.3	9	1	US-08-341-954-61	Sequence 61, Appl	240	3	27.3	9	3	US-08-464-522-14	Sequence 14, Appl
168	3	27.3	9	1	US-08-341-954-62	Sequence 62, Appl	241	3	27.3	9	3	US-08-464-522-15	Sequence 15, Appl
169	3	27.3	9	1	US-08-341-954-63	Sequence 63, Appl	242	3	27.3	9	3	US-08-464-522-16	Sequence 16, Appl
170	3	27.3	9	1	US-08-341-954-64	Sequence 64, Appl	243	3	27.3	9	3	US-08-464-522-17	Sequence 17, Appl
171	3	27.3	9	1	US-08-341-954-65	Sequence 65, Appl	244	3	27.3	9	3	US-08-464-522-18	Sequence 18, Appl
172	3	27.3	9	1	US-08-341-954-66	Sequence 66, Appl	245	3	27.3	9	3	US-08-464-522-19	Sequence 19, Appl
173	3	27.3	9	1	US-08-341-954-67	Sequence 67, Appl	246	3	27.3	9	3	US-08-464-522-20	Sequence 20, Appl

247	3	27.3	16	2	US-08-436-322-79	Sequence 9, Appl	320	3	27.3	10	5	PCT-US94-02531-66	Sequence 66, Appl
248	3	27.3	10	2	US-08-436-322-79	Sequence 10, Appl	321	3	27.3	10	5	PCT-US95-03246-6	Sequence 6, Appl
249	3	27.3	10	2	US-08-436-322-79	Sequence 10, Appl	322	3	27.3	10	5	5168045-8	Patent No. 5168045
250	3	27.3	10	2	US-08-436-322-79	Sequence 9, Appl	323	3	27.3	10	5	5177189-10	Patent No. 5177189
251	3	27.3	10	2	US-08-436-322-79	Sequence 10, Appl	324	3	27.3	10	5	5182364-11	Patent No. 5182364
252	3	27.3	10	2	US-08-436-322-79	Sequence 4, Appl	325	3	27.3	10	5	US-07-851-941-11	Sequence 11, Appl
253	3	27.3	10	2	US-08-436-322-79	Sequence 6, Appl	326	3	27.3	10	5	US-07-851-941-18	Sequence 18, Appl
254	3	27.3	10	2	US-08-436-322-79	Sequence 7, Appl	327	3	27.3	10	5	US-08-185-448-5	Sequence 5, Appl
255	3	27.3	10	2	US-08-436-322-79	Sequence 17, Appl	328	3	27.3	10	5	US-08-480-505-1	Sequence 1, Appl
256	3	27.3	10	2	US-08-436-322-79	Sequence 17, Appl	329	3	27.3	10	5	US-08-428-488-17	Sequence 17, Appl
257	3	27.3	10	2	US-08-436-322-79	Sequence 25, Appl	330	3	27.3	10	5	US-08-256-773-27	Sequence 27, Appl
258	3	27.3	10	2	US-08-436-322-79	Sequence 6, Appl	331	3	27.3	10	5	US-08-445-745-122	Sequence 122, Appl
259	3	27.3	10	2	US-08-436-322-79	Sequence 11, Appl	332	3	27.3	10	5	US-08-615-181-84	Sequence 84, Appl
260	3	27.3	10	2	US-08-436-322-79	Sequence 7, Appl	333	3	27.3	10	5	US-08-191-338A-15	Sequence 15, Appl
261	3	27.3	10	2	US-08-436-322-79	Sequence 22, Appl	334	3	27.3	10	5	US-08-408-604A-33	Sequence 33, Appl
262	3	27.3	10	2	US-08-436-322-79	Sequence 22, Appl	335	3	27.3	10	5	US-08-408-604A-79	Sequence 79, Appl
263	3	27.3	10	2	US-08-436-322-79	Sequence 44, Appl	336	3	27.3	10	5	US-08-633-760-37	Sequence 37, Appl
264	3	27.3	10	2	US-08-436-322-79	Sequence 3, Appl	337	3	27.3	10	5	US-08-181-984-31	Sequence 31, Appl
265	3	27.3	10	2	US-08-436-322-79	Sequence 3, Appl	338	3	27.3	10	5	US-08-737-085A-12	Sequence 12, Appl
266	3	27.3	10	2	US-08-436-322-79	Sequence 15, Appl	339	3	27.3	10	5	US-07-737-371E-73	Sequence 73, Appl
267	3	27.3	10	2	US-08-436-322-79	Sequence 29, Appl	340	3	27.3	10	5	US-08-466-975A-3	Sequence 3, Appl
268	3	27.3	10	2	US-08-436-322-79	Sequence 1, Appl	341	3	27.3	10	5	US-08-391-671A-3	Sequence 3, Appl
269	3	27.3	10	2	US-08-436-322-79	Sequence 1, Appl	342	3	27.3	10	5	US-08-747-137-63	Sequence 63, Appl
270	3	27.3	10	2	US-08-436-322-79	Sequence 102B, Appl	343	3	27.3	10	5	US-08-482-228-200	Sequence 200, Appl
271	3	27.3	10	2	US-08-436-322-79	Sequence 6, Appl	344	3	27.3	10	5	US-08-751-767A-29	Sequence 29, Appl
272	3	27.3	10	2	US-08-436-322-79	Sequence 7, Appl	345	3	27.3	10	5	US-08-115-209-74	Sequence 74, Appl
273	3	27.3	10	2	US-08-436-322-79	Sequence 8, Appl	346	3	27.3	10	5	US-08-467-902A-3	Sequence 3, Appl
274	3	27.3	10	2	US-08-436-322-79	Sequence 9, Appl	347	3	27.3	10	5	US-08-482-258-200	Sequence 200, Appl
275	3	27.3	10	2	US-08-436-322-79	Sequence 13, Appl	348	3	27.3	10	5	US-08-246-258-12	Sequence 12, Appl
276	3	27.3	10	2	US-08-436-322-79	Sequence 11, Appl	349	3	27.3	10	5	US-08-444-818-105	Sequence 105, Appl
277	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	350	3	27.3	10	5	US-08-392-542-4	Sequence 4, Appl
278	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	351	3	27.3	10	5	US-08-392-542-13	Sequence 13, Appl
279	3	27.3	10	2	US-08-436-322-79	Sequence 65, Appl	352	3	27.3	10	5	US-08-602-999A-283	Sequence 283, Appl
280	3	27.3	10	2	US-08-436-322-79	Sequence 75, Appl	353	3	27.3	10	5	US-08-652-877-73	Sequence 73, Appl
281	3	27.3	10	2	US-08-436-322-79	Sequence 31, Appl	354	3	27.3	10	5	US-09-208-966-3	Sequence 3, Appl
282	3	27.3	10	2	US-08-436-322-79	Sequence 213, Appl	355	3	27.3	10	5	US-08-647-405B-3	Sequence 3, Appl
283	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	356	3	27.3	10	5	US-08-647-405B-4	Sequence 4, Appl
284	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	357	3	27.3	10	5	US-08-647-405B-6	Sequence 5, Appl
285	3	27.3	10	2	US-08-436-322-79	Sequence 1, Appl	358	3	27.3	10	5	US-09-177-249-253	Sequence 253, Appl
286	3	27.3	10	2	US-08-436-322-79	Sequence 11, Appl	359	3	27.3	10	5	US-08-476-515A-73	Sequence 73, Appl
287	3	27.3	10	2	US-08-436-322-79	Sequence 4, Appl	360	3	27.3	10	5	US-08-894-327-4	Sequence 4, Appl
288	3	27.3	10	2	US-08-436-322-79	Sequence 4, Appl	361	3	27.3	10	5	US-08-894-327-14	Sequence 14, Appl
289	3	27.3	10	2	US-08-436-322-79	Sequence 4, Appl	362	3	27.3	10	5	US-09-532-106-12	Sequence 12, Appl
290	3	27.3	10	2	US-08-436-322-79	Sequence 4, Appl	363	3	27.3	10	5	US-09-275-265-3	Sequence 3, Appl
291	3	27.3	10	2	US-08-436-322-79	Sequence 11, Appl	364	3	27.3	10	5	US-08-456-466-100	Sequence 100, Appl
292	3	27.3	10	2	US-08-436-322-79	Sequence 14, Appl	365	3	27.3	10	5	US-09-311-626B-30	Sequence 30, Appl
293	3	27.3	10	2	US-08-436-322-79	Sequence 8, Appl	366	3	27.3	10	5	US-09-685-027-4	Sequence 4, Appl
294	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	367	3	27.3	10	5	US-09-585-027-13	Sequence 13, Appl
295	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	368	3	27.3	10	5	US-08-255-208A-77	Sequence 77, Appl
296	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	369	3	27.3	10	5	US-08-255-208A-77	Sequence 77, Appl
297	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	370	3	27.3	10	5	US-08-255-208A-77	Sequence 77, Appl
298	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	371	3	27.3	10	5	US-08-255-208A-77	Sequence 77, Appl
299	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	372	3	27.3	10	5	US-08-255-208A-77	Sequence 77, Appl
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301	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	374	3	27.3	10	5	US-08-255-208A-77	Sequence 77, Appl
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306	3	27.3	10	2	US-08-436-322-79	Sequence 2, Appl	379	3	27.3	10	5	US-08-255-208A-77	Sequence 77, Appl
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455	1	27.3	1	US-08-042-137-75	Sequence 45, Appl	458	1	27.3	1	US-09-329-350-27	Sequence 27, Appl
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460	1	27.3	1	US-08-042-137-75	Sequence 45, Appl	463	1	27.3	1	US-09-058-459-15	Sequence 15, Appl
461	1	27.3	1	US-08-042-137-75	Sequence 45, Appl	464	1	27.3	1	US-09-058-459-16	Sequence 16, Appl
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## ALIGNMENTS

RESULT 1  
 US-08-462-040-14  
 Sequence 9, Application US-08-462-040-14  
 Patent No. 5739409  
 GENERAL INFORMATION:  
 APPLICANT: FISHER, ROBERT  
 APPLICANT: KIM, SUNG-P  
 APPLICANT: CHOI, JUNG-M  
 APPLICANT: PENNAPOLIT, LISA  
 APPLICANT: GIOVANNINI, JAMES  
 TITLE OF INVENTION: KIM, PASCAL  
 TITLE OF INVENTION: ENOUGH USLY SWEETENED TRANSGENIC PLANT  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: MORRISON & PIERSON  
 STREET: 2270 PENNSYLVANIA AVENUE, NW  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 REF: 200001812  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: EATON-10 Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-08-462-040-14  
 FILING DATE: 07/20/1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFO: KIM, SUNG-P  
 REGISTRATION NUMBER: 29, 259

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REFERENCE/POCKET NUMBER: 2000-9501110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
FLEX: 90 4030 MRSNFORSKSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-418-856A-4
Query Match: 36.4%, Score 4, DB 2, Length 8;
Best Local Similarity: 100.0%, Pct. No. 2.5e-05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSK 6
1111
2 2 KSK 5

RESULT 3
US-08-418-856A-4
Sequence 4, Application: US/0811856A
Patent No. 5972451
GENERAL INFORMATION:
APPLICANT: ADRIAN V. S. HILL, et al.
TITLE OF INVENTION: CLASSIFIED PLASMODIUM MHC CLASS I*
TITLE OF INVENTION: RESTRICTED CELL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAG
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodstock, Lind & Penack, L.L.P.
STREET: 233 K Street, N.W., Suite 900
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418-856A
FILING DATE: October 3, 1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GP 92 08 068.8
FILING DATE: April 4, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GP 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,549
REFERENCE/POCKET NUMBER: 264 PPIR157705
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MEDIUM TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-418-856A-4
Query Match: 36.4%, Score 4, DB 2, Length 8;
Best Local Similarity: 100.0%, Pct. No. 2.5e-05;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KSK 11
1111
26 1 KSK 4

RESULT 4
US-09-105-849D-25
Sequence 25, Application: US/09/05839D
Patent No. 6287556
GENERAL INFORMATION:
APPLICANT: Tarelli, et al.
APPLICANT: Chen, Yoo-Tsooq
APPLICANT: Sakai, Ugor
APPLICANT: Goto, Ali

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```

: APPLICANT: Old, Lloyd J
: APPLICANT: Freundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
: TITLE OF INVENTION: Expression of an SSX gene
: FILE REFERENCE: LUD 5556
: CURRENT APPLICATION NUMBER: US/09/105,8390
: CURRENT FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 08/851,130
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 72
: SEQ ID NO 25
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-105-8390-25

Query Match 36.4% Score 4: DB 3: Length 8;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 KKK 8
LD 1 1 1
3 KKK 5

RESULT 5
US-09-105-8390-40
: Sequence 40: Application US/09/105,8390
: Patent No. 6287756
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Chen, Yao-Tsong
: APPLICANT: Sahin, Ugur
: APPLICANT: Gure, Ali
: APPLICANT: Old, Lloyd J
: APPLICANT: Freundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
: TITLE OF INVENTION: Expression of an SSX gene
: FILE REFERENCE: LUD 5556
: CURRENT APPLICATION NUMBER: US/09/105,8390
: CURRENT FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 08/851,130
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 72
: SEQ ID NO 40
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-105-8390-40

Query Match 36.4% Score 4: DB 3: Length 8;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 KKK 8
LD 1 1 1
3 KKK 5

RESULT 6
US-09-105-8390-57
: Sequence 57: Application US/09/105,8390
: Patent No. 6287756
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Chen, Yao-Tsong
: APPLICANT: Sahin, Ugur
: APPLICANT: Gure, Ali
: APPLICANT: Old, Lloyd J
: APPLICANT: Freundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
: TITLE OF INVENTION: Expression of an SSX gene
: FILE REFERENCE: LUD 5556

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: CURRENT APPLICATION NUMBER: US/09/105,8390
: CURRENT FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 08/851,130
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 72
: SEQ ID NO 57
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-105-8390-57

Query Match 36.4% Score 4: DB 3: Length 8;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 KKK 8
LD 1 1 1
3 KKK 6

RESULT 7
US-09-105-8390-69
: Sequence 69: Application US/09/105,8390
: Patent No. 6287756
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Chen, Yao-Tsong
: APPLICANT: Sahin, Ugur
: APPLICANT: Gure, Ali
: APPLICANT: Old, Lloyd J
: APPLICANT: Freundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Dete
: TITLE OF INVENTION: Expression of an SSX gene
: FILE REFERENCE: LUD 5556
: CURRENT APPLICATION NUMBER: US/09/105,8390
: CURRENT FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 08/851,130
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 72
: SEQ ID NO 69
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-105-8390-69

Query Match 36.4% Score 4: DB 3: Length 8;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 KKK 8
LD 1 1 1
3 KKK 6

RESULT 8
US-09-105-8390-18
: Sequence 18: Application US/08/197484
: Patent No. 641593
: GENERAL INFORMATION:
: APPLICANT: Vitello, Maria A.
: APPLICANT: CHESTNET, Robert W.
: APPLICANT: SETTE, Alessandro D.
: APPLICANT: CELIS, Esteban
: APPLICANT: GRAY, Howard
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
: TITLE OF INVENTION: CTL IMMUNITY
: NUMBER OF SEQUENCES: 153
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Koorie and Crew
: STREET: Stewart Street Tower, One Market Plaza
: CITY: San Francisco
: STATE: California
: COUNTRY: US

```

1 ZIPS: 94105-1493  
 2 COMPILER READABLE FORM:  
 3 MEDIUM TYPE: Floppy disk  
 4 OPERATING SYSTEM: PC-DOS/MS-DOS  
 5 SOFTWARE: Patent In Release #10, Version #1.2  
 6 CURRENT APPLICATION DATA:  
 7 APPLICATION NUMBER: US/09/147,404  
 8 FILING DATE: 16-FEB-1994  
 9 CLASSIFICATION: 424  
 10 PRIOR APPLICATION DATA:  
 11 APPLICATION NUMBER: US 07/945,831  
 12 FILING DATE: 26-AUG-1992  
 13 PRIOR APPLICATION DATA:  
 14 APPLICATION NUMBER: US 07/974,491  
 15 FILING DATE: 27-APR-1992  
 16 PRIOR APPLICATION DATA:  
 17 APPLICATION NUMBER: US 07/827,062  
 18 FILING DATE: 29-JAN-1992  
 19 PRIOR APPLICATION DATA:  
 20 APPLICATION NUMBER: US 07/774,565  
 21 FILING DATE: 26-AUG-1991  
 22 ATTORNEY/AGENT INFORMATION:  
 23 NAME: Parmelee, Steven W.  
 24 REGISTRATION NUMBER: 31,955  
 25 REFERENCE/DOCKET NUMBER: 14187-27-4  
 26 TELECOMMUNICATION INFORMATION:  
 27 TELEPHONE: (206) 467-9609  
 28 TELEFAX: (206) 624-6793  
 29 INFORMATION FOR SEQ ID NO: 1:  
 30 SEQUENCE CHARACTERISTICS:  
 31 LENGTH: 8 amino acids  
 32 TYPE: amino acid  
 33 STRANDEDNESS: unknown  
 34 TOPOLGY: unknown  
 35 N-TERMINUS TYPE: peptido  
 36 US 08-137 484 B

Query Match 36.4% Score 4: DB 4: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 KSKD 1:  
 DB 1111  
 3 KSKD 4

RESULT 1:  
 1 US-09-344-040C-91  
 2 Sequence 9: Application US/09-443-40C  
 3 Patent No. 6548564  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Tureci, Ozlem  
 6 APPLICANT: Sahin, Ugur  
 7 APPLICANT: Pfreundschuh, Michael  
 8 APPLICANT: Ramensee, Hans Georg  
 9 APPLICANT: Stivanovic, Stefan  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Detecting Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof  
 11 TITLE OF INVENTION: Gene, and Uses Thereof  
 12 FILE REFERENCE: LUD 5556.1  
 13 CURRENT APPLICATION NUMBER: US/09/144,040C  
 14 CURRENT FILING DATE: 1999-06-25  
 15 PRIOR APPLICATION NUMBER: US 09/105,839  
 16 PRIOR FILING DATE: 1998-06-26  
 17 PRIOR APPLICATION NUMBER: US 06/851,130  
 18 PRIOR FILING DATE: 1997-05-05  
 19 NUMBER OF SEQ ID NOS: 132  
 20 SEQ ID NO 39  
 21 LENGTH: 8  
 22 TYPE: PRI  
 23 ORGANISM: Homo sapiens  
 24 US 09-344 040C-91

Query Match 36.4% Score 4: DB 4: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
 QY 5 KRPK 8  
 DB 1111  
 3 KRPK 6  
 RESULT 1:  
 1 US-09-344-040C-91  
 2 Sequence 9: Application US/09-443-40C  
 3 Patent No. 6548564  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Tureci, Ozlem  
 6 APPLICANT: Sahin, Ugur  
 7 APPLICANT: Pfreundschuh, Michael  
 8 APPLICANT: Ramensee, Hans Georg  
 9 APPLICANT: Stivanovic, Stefan  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Detecting Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof  
 11 TITLE OF INVENTION: Gene, and Uses Thereof  
 12 FILE REFERENCE: LUD 5556.1  
 13 CURRENT APPLICATION NUMBER: US/09/144,040C  
 14 CURRENT FILING DATE: 1999-06-25  
 15 PRIOR APPLICATION NUMBER: US 09/105,839  
 16 PRIOR FILING DATE: 1998-06-26  
 17 PRIOR APPLICATION NUMBER: US 06/851,130  
 18 PRIOR FILING DATE: 1997-05-05  
 19 NUMBER OF SEQ ID NOS: 132  
 20 SEQ ID NO 64  
 21 LENGTH: 8  
 22 TYPE: PRI  
 23 ORGANISM: Homo sapiens  
 24 US 09-344-040C-91

Query Match 36.4% Score 4: DB 4: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 KRPK 8  
 DB 1111  
 3 KRPK 6

RESULT 1:  
 1 US-09-344-040C-91  
 2 Sequence 9: Application US/09-443-40C  
 3 Patent No. 6548564  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Tureci, Ozlem  
 6 APPLICANT: Sahin, Ugur  
 7 APPLICANT: Pfreundschuh, Michael  
 8 APPLICANT: Ramensee, Hans Georg  
 9 APPLICANT: Stivanovic, Stefan  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Detecting Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof  
 11 TITLE OF INVENTION: Gene, and Uses Thereof  
 12 FILE REFERENCE: LUD 5556.1  
 13 CURRENT APPLICATION NUMBER: US/09/144,040C  
 14 CURRENT FILING DATE: 1999-06-25  
 15 PRIOR APPLICATION NUMBER: US 09/105,839  
 16 PRIOR FILING DATE: 1998-06-26  
 17 PRIOR APPLICATION NUMBER: US 06/851,130  
 18 PRIOR FILING DATE: 1997-05-05  
 19 NUMBER OF SEQ ID NOS: 132  
 20 SEQ ID NO 91  
 21 LENGTH: 8  
 22 TYPE: PRI  
 23 ORGANISM: Homo sapiens  
 24 US-09-344-040C-91

Query Match 36.4% Score 4; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8  
 ID 111  
 3 REK 6

RESULT 12  
 US 09-44 0400-111  
 : Sequence 111, Application US/09-4404-1  
 : Patent No. 6548064  
 : GENERAL INFORMATION:  
 : APPLICANT: Durell, Ozlem  
 : APPLICANT: Sahler, Ogar  
 : APPLICANT: Pfrendschuh, Michael  
 : APPLICANT: Ramonsee, Hans Georg  
 : APPLICANT: Stevanovic, Stefan  
 : TITLE OF INVENTION: Expression of an SSX gene isolated from Solid SSX gene  
 : TITLE OF INVENTION: Method for detecting presence of tumor in a sample by detecting  
 : TITLE OF INVENTION: Gene, and Uses Thereof  
 : FILE REFERENCE: IUD 5536.1  
 : CURRENT APPLICATION NUMBER: US/09-44-0100  
 : CURRENT FILING DATE: 1999-06-25  
 : PRIOR APPLICATION NUMBER: US 09/05-800  
 : PRIOR FILING DATE: 1998-06-26  
 : PRIOR APPLICATION NUMBER: US 08/951-100  
 : PRIOR FILING DATE: 1997-05-09  
 : NUMBER OF SEQ ID NOS: 132  
 : SEQ ID NO: 111  
 : LENGTH: 8  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : US 09-44 0400-111

Query Match 36.4% Score 4; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 REK 8  
 ID 111  
 3 REK 6

RESULT 13  
 US 09-44 0400-111  
 : Sequence 111, Application US/09-4404-1  
 : Patent No. 6548064  
 : GENERAL INFORMATION:  
 : APPLICANT: Durell, Ozlem  
 : APPLICANT: Sahler, Ogar  
 : APPLICANT: Pfrendschuh, Michael  
 : APPLICANT: Ramonsee, Hans Georg  
 : APPLICANT: Stevanovic, Stefan  
 : TITLE OF INVENTION: Expression of an SSX gene isolated from Solid SSX gene  
 : TITLE OF INVENTION: Method for detecting presence of tumor in a sample by detecting  
 : TITLE OF INVENTION: Gene, and Uses Thereof  
 : FILE REFERENCE: IUD 5536.1  
 : CURRENT APPLICATION NUMBER: US/09-44-0100  
 : CURRENT FILING DATE: 1999-06-25  
 : PRIOR APPLICATION NUMBER: US 09/05-800  
 : PRIOR FILING DATE: 1998-06-26  
 : PRIOR APPLICATION NUMBER: US 08/951-100  
 : PRIOR FILING DATE: 1997-05-09  
 : NUMBER OF SEQ ID NOS: 132  
 : SEQ ID NO: 111  
 : LENGTH: 8  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 : US 09-44 0400-111

Query Match 36.4% Score 4; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KSKD 11  
 ID 111  
 3 KSKD 4

RESULT 14  
 5487983-7  
 : Patent No. 5487983  
 : APPLICANT: KIM, SUNG-HO; CHOI, JUNG-M  
 : TITLE OF INVENTION: EXPRESSION SYSTEMS FOR MAKING  
 : SINGLE-CHAIN MONOCLINAL ANTIBODIES  
 : NUMBER OF SEQUENCES: 46  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09-146-426  
 : FILING DATE: 02-MAY-1999  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 502,257  
 : FILING DATE: 12-MAY-1990  
 : APPLICATION NUMBER: 455,585  
 : FILING DATE: 14-JAN-1990  
 : APPLICATION NUMBER: 117,124  
 : FILING DATE: 04-NOV-1987  
 : APPLICATION NUMBER: 44,441  
 : FILING DATE: 19-JUN-1987  
 : APPLICATION NUMBER: 64,443  
 : FILING DATE: 13-JUN-1986  
 : SEQ ID NO: 7  
 : LENGTH: 8  
 : 5487983-7

Query Match 36.4% Score 4; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KIR 6  
 ID 111  
 2 KIR 6

RESULT 15  
 US-08-648-1288-10  
 : Sequence 10, Application US/86081288  
 : Patent No. 5840568  
 : GENERAL INFORMATION:  
 : APPLICANT: Pfrendschuh, Michael  
 : TITLE OF INVENTION: Rodkin's Disease Associated Molecules And  
 : TITLE OF INVENTION: Uses Thereof  
 : NUMBER OF SEQUENCES: 14  
 : CURRENT INVENTION ADDRESS:

ADDRESSEE: Folie & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York City  
 STATE: New York  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 60 kb storage  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/479,426  
 FILING DATE: 21-JUNE-1996  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/479,426  
 FILING DATE: 10 MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hanson, No. 584056, Sean D.  
 REGISTRATION NUMBER: 30,946  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 638-3884  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 US-08 bkr 128B 12

Query Match: 96.4%, Score: 4, DB 2: Length 9:  
 Best Local Similarity: 100.0%, Pred. No. 2, Set 05:  
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 5 REK 8  
 LB 11  
 11  
 5 REK 5

RESULT 14  
 US-08 965,443-10  
 Sequence 9: Application US/08/443-11A  
 Patent No. 6140454  
 GENERAL INFORMATION:  
 APPLICANT: Pfeleidschuh, Michael  
 TITLE OF INVENTION: Method for Identifying or Isolating A Molecule  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Folie & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York City  
 STATE: New York  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 60 kb storage  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/479,426  
 FILING DATE: 21-JUNE-1996  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/479,426  
 FILING DATE: 10 MAY-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hanson, No. 584056, Sean D.  
 REGISTRATION NUMBER: 30,946  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 638-3884  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 US-08 bkr 128B 12

APPLICATION NUMBER: US/044,116  
 FILING DATE: 10-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/580,480  
 FILING DATE: 03 JANUARY 1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/479,426  
 FILING DATE: 07-JUNE-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hanson, No. 649401, Sean D.  
 REGISTRATION NUMBER: 30,946  
 REFERENCE/DOCKET NUMBER: LID 5441  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 638-3884  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 US-08-905-445-10

Query Match: 96.4%, Score: 4, DB 2: Length 9:  
 Best Local Similarity: 100.0%, Pred. No. 2, Set 05:  
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 5 REK 8  
 LB 11  
 11  
 5 REK 5

RESULT 17  
 US-08 544-116A-9  
 Sequence 9: Application US/0444116A  
 Patent No. 6140454  
 GENERAL INFORMATION:  
 APPLICANT: Pfeleidschuh, Michael; Ramnensee, Hans-Georg  
 TITLE OF INVENTION: Method for Identifying or Isolating A Molecule  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Folie & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York City  
 STATE: New York  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.5 inch, 60 kb storage  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/044,116A  
 FILING DATE: 10-MAY-1996  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/580,480  
 FILING DATE: 03-JANUARY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/479,426  
 FILING DATE: 07-JUNE-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hanson, No. 614046, Sean D.  
 REGISTRATION NUMBER: 30,946  
 REFERENCE/DOCKET NUMBER: LID 5410.2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 638-3884  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear

US-09-787-443-14-A 9

Query Match 36.4% Score 4: DB 3: Length 9;  
 Best Local Similarity 100.0%; Prod. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 29  
 US-09-105-8390-51  
 1 Sequence 51: Application: US/09/105-8390-51  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tseng  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Dete  
 11 TITLE OF INVENTION: Expression of an SSX gene  
 12 FILE REFERENCE: L00 5556  
 13 CURRENT APPLICATION NUMBER: US/09/105-8390  
 14 PRIOR FILING DATE: 1998-06-26  
 15 PRIOR APPLICATION NUMBER: US 08/851,140  
 16 NUMBER OF SEQ ID NOS: 72  
 17 SEQ ID NO 27  
 18 LENGTH: 9  
 19 TYPE: PRT  
 20 ORGANISM: Homo sapiens  
 21 US-09-105-8390-51

Query Match 36.4% Score 4: DB 3: Length 9;  
 Best Local Similarity 100.0%; Prod. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 29  
 US-09-105-8390-44  
 1 Sequence 44: Application: US/09/105-8390-44  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tseng  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Dete  
 11 TITLE OF INVENTION: Expression of an SSX gene  
 12 FILE REFERENCE: L00 5556  
 13 CURRENT APPLICATION NUMBER: US/09/105-8390  
 14 PRIOR FILING DATE: 1998-06-26  
 15 PRIOR APPLICATION NUMBER: US 08/851,140  
 16 NUMBER OF SEQ ID NOS: 72  
 17 SEQ ID NO 44  
 18 LENGTH: 9  
 19 TYPE: PRT  
 20 ORGANISM: Homo sapiens  
 21 US-09-105-8390-44

Query Match 36.4% Score 4: DB 3: Length 9;  
 Best Local Similarity 100.0%; Prod. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 29  
 US-09-105-8390-51  
 1 Sequence 51: Application: US/09/105-8390-51  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tseng  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Dete  
 11 TITLE OF INVENTION: Expression of an SSX gene  
 12 FILE REFERENCE: L00 5556  
 13 CURRENT APPLICATION NUMBER: US/09/105-8390  
 14 PRIOR FILING DATE: 1998-06-26  
 15 PRIOR APPLICATION NUMBER: US 08/851,140  
 16 NUMBER OF SEQ ID NOS: 72  
 17 SEQ ID NO 51  
 18 LENGTH: 9  
 19 TYPE: PRT  
 20 ORGANISM: Homo sapiens  
 21 US-09-105-8390-51

Query Match 36.4% Score 4: DB 3: Length 9;  
 Best Local Similarity 100.0%; Prod. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

5 KERR B  
 11  
 3 KERR 4

RESULT 21  
 US-09-105-8390-60  
 1 Sequence 60: Application: US/09/105-8390-60  
 2 Patent No. 6287756  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Tureci, Ozlem  
 5 APPLICANT: Chen, Yao-Tseng  
 6 APPLICANT: Sahin, Gaur  
 7 APPLICANT: Gure, Ali  
 8 APPLICANT: Old, Lloyd J  
 9 APPLICANT: Friendschuh, Michael  
 10 TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Dete  
 11 TITLE OF INVENTION: Expression of an SSX gene  
 12 FILE REFERENCE: L00 5556  
 13 CURRENT APPLICATION NUMBER: US/09/105-8390  
 14 PRIOR FILING DATE: 1998-06-26  
 15 PRIOR APPLICATION NUMBER: US 08/851,140  
 16 NUMBER OF SEQ ID NOS: 72  
 17 SEQ ID NO 60  
 18 LENGTH: 9  
 19 TYPE: PRT  
 20 ORGANISM: Homo sapiens  
 21 US-09-105-8390-60

Query Match 36.4% Score 4: DB 3: Length 9;  
 Best Local Similarity 100.0%; Prod. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

5 KERR B  
 11  
 3 KERR 4

```

RESULT 22
US 09-165-8350-70
: Sequence 70, Application US/091658350
: Patent No. 6287756
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Chen, Yao-Tsung
: APPLICANT: Sahin, Ugur
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Gure, Ali
: APPLICANT: Gid, Ilyed J
: APPLICANT: Pfreundschuh, Michael
: TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Detecting
: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
: FILE REFERENCE: L30 5556
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 72
: SEQ ID NO 70
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-165-8350-70

Query Match 36.4%, Score 4, DB 4, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 1 PERK 4

RESULT 23
US 09-344-0400-75
: Sequence 75, Application US/093440400
: Patent No. 6548064
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Sahin, Ugur
: APPLICANT: Pfreundschuh, Michael
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Stevanovic, Stefan
: TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Detecting
: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
: FILE REFERENCE: L30 5556.1
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 132
: SEQ ID NO 4
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-344-0400-75

Query Match 36.4%, Score 4, DB 4, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 1 PERK 4

RESULT 24
US 09-344-0400-75
: Sequence 75, Application US/093440400
: Patent No. 6548064
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Sahin, Ugur
: APPLICANT: Pfreundschuh, Michael
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Stevanovic, Stefan
: TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Detecting
: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
: FILE REFERENCE: L30 5556.1
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 132
: SEQ ID NO 4
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-344-0400-75

Query Match 36.4%, Score 4, DB 4, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 1 PERK 4

RESULT 25
US 09-344-0400-75
: Sequence 75, Application US/093440400
: Patent No. 6548064
: GENERAL INFORMATION:
: APPLICANT: Tureci, Ozlem
: APPLICANT: Sahin, Ugur
: APPLICANT: Pfreundschuh, Michael
: APPLICANT: Ramonsee, Hans Georg
: APPLICANT: Stevanovic, Stefan
: TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Detecting
: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
: FILE REFERENCE: L30 5556.1
: CURRENT FILING DATE: 1999-06-25
: PRIOR FILING DATE: 1998-06-26
: PRIOR APPLICATION NUMBER: US 09/105,839
: PRIOR FILING DATE: 1997-05-05
: NUMBER OF SEQ ID NOS: 132
: SEQ ID NO 75
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09-344-0400-75

Query Match 36.4%, Score 4, DB 4, Length 9,
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 PERK 8
DB 3 PERK 6

RESULT 26
US 09-344-0400-94
: Sequence 94, Application US/093440400

```



```
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Jurek, Ozlem
APPLICANT: Sahin, Jigar
APPLICANT: Priemdschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stelzer, Stefan
TITLE OF INVENTION: Method for determining presence of a protein in a sample by Western blotting
TITLE OF INVENTION: Expression of an SXX gene, peptides derived from said SXX gene and uses thereof
FILE REFERENCE: LBG 5556.1
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US/09/444,043
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US/97/05,869
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 94
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US 09-444-0406-94

Query Match: 36.4%; Score 4; DH 4; Length 9;
Best Local Similarity: 100.0%; Pred. No. 1 SeqID;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERK 8
ID 1
1 ERK 4

RESULT 27
US 09-444-0406-112
Sequence 112, Application US/09/444,043
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Jurek, Ozlem
APPLICANT: Sahin, Jigar
APPLICANT: Priemdschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stelzer, Stefan
TITLE OF INVENTION: Method for determining presence of a protein in a sample by Western blotting
TITLE OF INVENTION: Expression of an SXX gene, peptides derived from said SXX gene and uses thereof
FILE REFERENCE: LBG 5556.1
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US/09/444,043
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US/97/05,869
PRIOR FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 112
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US 09-444-0406-112

Query Match: 36.4%; Score 4; DH 4; Length 9;
Best Local Similarity: 100.0%; Pred. No. 2 SeqID;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERK 8
ID 1
1 ERK 4

RESULT 28
US 09-444-0406-277A-43
Sequence 43, Application US/98/06,277A
Patent No. 599B374
GENERAL INFORMATION:
APPLICANT: Jurek, Robert L.
APPLICANT: Lee, In-Hye
APPLICANT: Zhao, Chengquan
TITLE OF INVENTION: GLYASPIRINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARRISON & FORSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1086
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/608,277A
FILING DATE: 2000-04-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DRCKET NUMBER: 220002657300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 887-1500
TELEFAX: 202-822-9168
TELEX:
INFORMATION FOR SEQ ID NO: 43
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-608-277A-43

Query Match: 40.4%; Score 4; DH 2; Length 10;
Best Local Similarity: 100.0%; Pred. No. 1 SeqID;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERK 9
ID 1
1 ERK 6

RESULT 29
US 09-444-0406-222-1
Sequence 1, Application US/09/265,222
Patent No. 6579082
GENERAL INFORMATION:
APPLICANT: Innerarity, Thomas
APPLICANT: Borek, Jan
TITLE OF INVENTION: METHODS AND TOOLS FOR IDENTIFYING
TITLE OF INVENTION: COMPOUNDS WHICH MODULATE ATHEROSCLEROSIS BY IMPACTING
TITLE OF INVENTION: LDI-PROTEOGLYCAN BINDING
FILE REFERENCE: 220002059700
CURRENT APPLICATION NUMBER: US/09/265,222
CURRENT FILING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: US 60/077,618
PRIOR FILING DATE: 1998-03-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: MURASHIGE
```

1 LOCATION: 1  
2 OTHER INFORMATION: Missense mutation  
US-09-787-443-14

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERKS 7  
1111  
DB 4 ERKS 7

RESULT 41  
US-08-746-006-16  
1 Sequence 50; Application US/08/746-160  
2 Patent No. 6150500  
3 GENERAL INFORMATION:  
4 APPLICANT: Leherer, Robert E.  
5 APPLICANT: Harwig, Sylvia L.  
6 APPLICANT: Zhao, Chongquan  
7 APPLICANT: Lee, In-Hee  
8 TITLE OF INVENTION: CLAVANINS  
9 NUMBER OF SEQUENCES: 51  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: MORRISON & FORSTER  
12 STREET: 2000 Pennsylvania Avenue, NW, Suite 5000  
13 CITY: Washington  
14 STATE: DC  
15 COUNTRY: USA  
16 ZIP: 20004-1886  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Diskette  
19 COMPUTER: IBM compatible  
20 OPERATING SYSTEM: DOS  
21 SOFTWARE: FASTSEQ for Windows Version 1.0  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/08/746-160  
24 FILING DATE: 06-NOV-1996  
25 CLASSIFICATION: 510  
26 PRIOR APPLICATION DATA:  
27 APPLICATION NUMBER:  
28 FILING DATE:  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: Morrison, Kate B.  
31 REGISTRATION NUMBER: 24,900  
32 REFERENCE/DOCKET NUMBER: 22-000-2000-0000  
33 TELECOMMUNICATION INFORMATION:  
34 TELEPHONE: 202-887-3500  
35 TELEFAX: 202-822-0168  
36 INDEX:  
37 INFORMATION FOR SEQ ID NO: 51:  
38 SEQUENCE CHARACTERISTICS:  
39 LENGTH: 11 amino acids  
40 TYPE: amino acid  
41 STRANDEDNESS: single  
42 TOPOLOGY: linear  
43 US-08-746-006-16

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERKS 9  
1111  
DB 4 ERKS 7

RESULT 41  
US-08-746-006-16  
1 Sequence 40; Application US/08/746-160  
2 Patent No. 6150500  
3 GENERAL INFORMATION:  
4 APPLICANT: Leherer, Robert E.  
5 APPLICANT: Harwig, Sylvia L.  
6 APPLICANT: Zhao, Chongquan  
7 APPLICANT: Lee, In-Hee  
8 TITLE OF INVENTION: CLAVANINS  
9 NUMBER OF SEQUENCES: 51  
10 CORRESPONDENCE ADDRESS:  
11 ADDRESSEE: MORRISON & FORSTER  
12 STREET: 2000 Pennsylvania Avenue, NW, Suite 5000  
13 CITY: Washington  
14 STATE: DC  
15 COUNTRY: USA  
16 ZIP: 20004-1886  
17 COMPUTER READABLE FORM:  
18 MEDIUM TYPE: Diskette  
19 COMPUTER: IBM compatible  
20 OPERATING SYSTEM: DOS  
21 SOFTWARE: FASTSEQ for Windows Version 1.0  
22 CURRENT APPLICATION DATA:  
23 APPLICATION NUMBER: US/08/746-160  
24 FILING DATE: 06-NOV-1996  
25 CLASSIFICATION: 510  
26 PRIOR APPLICATION DATA:  
27 APPLICATION NUMBER:  
28 FILING DATE:  
29 ATTORNEY/AGENT INFORMATION:  
30 NAME: Morrison, Kate B.  
31 REGISTRATION NUMBER: 24,900  
32 REFERENCE/DOCKET NUMBER: 22-000-2000-0000  
33 TELECOMMUNICATION INFORMATION:  
34 TELEPHONE: 202-887-3500  
35 TELEFAX: 202-822-0168  
36 INDEX:  
37 INFORMATION FOR SEQ ID NO: 51:  
38 SEQUENCE CHARACTERISTICS:  
39 LENGTH: 11 amino acids  
40 TYPE: amino acid  
41 STRANDEDNESS: single  
42 TOPOLOGY: linear  
43 US-08-746-006-16

1 APPLICANT: Leherer, Robert E.  
2 APPLICANT: Zhao, Chongquan  
3 APPLICANT: Lee, In-Hee  
4 APPLICANT: Harwig, Sylvia L.  
5 TITLE OF INVENTION: CLAVANINS  
6 FILE REFERENCE: 22000-20563-20  
7 CURRENT APPLICATION NUMBER: US/08/746-160  
8 CURRENT FILING DATE: 1997-02-28  
9 EARLIER APPLICATION NUMBER: 08/746-160  
10 EARLIER FILING DATE: 1996-11-06  
11 NUMBER OF SEQ ID NOS: 52  
12 SOFTWARE: PatentIn Ver. 2.0  
13 SEQ ID NO: 46  
14 LENGTH: 11  
15 TYPE: PRI  
16 ORGANISM: Stylota clava  
US-08-746-006-16

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERKS 9  
1111  
DB 4 ERKS 7

RESULT 42  
US-08-679-006-16  
1 Sequence 10; Application US/08/746-006  
2 Patent No. 6150500  
3 GENERAL INFORMATION:  
4 APPLICANT: Salernio, John C.  
5 TITLE OF INVENTION: APPLICATIONS FOR REGULATORY REGION OF  
6 TITLE OF INVENTION: NGS ISOFORMS  
7 NUMBER OF SEQUENCES: 45  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
10 STREET: Two Millia Drive  
11 CITY: Lexington  
12 STATE: Massachusetts  
13 COUNTRY: USA  
14 ZIP: 02175  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: floppy disk  
17 COMPUTER: IBM PC compatible  
18 OPERATING SYSTEM: DOS/MS-DOS  
19 SOFTWARE: PatentIn Release #1.0, Version #1.30  
20 CURRENT APPLICATION DATA:  
21 APPLICATION NUMBER: US/08/679-006  
22 FILING DATE: 12-JUL-1996  
23 CLASSIFICATION: 514  
24 ATTORNEY/AGENT INFORMATION:  
25 NAME: Brook, David E.  
26 REGISTRATION NUMBER: 24,592  
27 REFERENCE/DOCKET NUMBER: JCS96-01  
28 TELECOMMUNICATION INFORMATION:  
29 TELEPHONE: (617) 861-6240  
30 TELEFAX: (617) 861-9540  
31 INFORMATION FOR SEQ ID NO: 16:  
32 SEQUENCE CHARACTERISTICS:  
33 LENGTH: 11 amino acids  
34 TYPE: amino acid  
35 STRANDEDNESS:  
36 TOPOLOGY: linear  
37 MOLECULE TYPE: peptide  
US-08-679-006-16

Query Match 36.4% Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERKS 9

14. 111  
5 PARS 6

RESULT 34  
US-09-147-592A-41  
Sequence 41: Application US/09/147-592A  
Patent No. 6096543  
GENERAL INFORMATION:  
APPLICANT: BELL, GRAEF  
APPLICANT: BELLS, GRABER  
APPLICANT: BELLS, GRABER  
TITLE OF INVENTION: COMPOSITIONS AND METHODS  
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARTHUR, WHITE & DUCKER  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TEXAS  
COUNTRY: United States of America  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/147-592A

FILING DATE: 05 Nov 1993

CLASSIFICATION: 435

APPLICATION NUMBER: 08/100,694

FILING DATE: 30 Jul 1993

CLASSIFICATION: 435

FILING DATE: 20 May 1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARK B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: ARD 143/WIR

TELEPHONE: (512) 418 3000

TELEFAX: (512) 474 7577

TELEX: N/A

INFORMATION FOR SEQ ID NO: 41

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids

TYPE: amino acid

FUNCTION: linear

MOLECULE TYPE: protein

US-09-147-592A-41

Quality Match: 66.4% Score: 41 DP: 41 Length: 143

Best Local Similarity: 100.0% Pval: No. 1 9e-02

Mismatches: 41 Conservative: 0 Indels: 0 Gaps: 0

US-09-292-694A-41

Sequence 41: Application US/09/292-694A

Patent No. 6096543

GENERAL INFORMATION:  
APPLICANT: BELL, GRAEF

APPLICANT: BELLS, GRABER

APPLICANT: BELLS, GRABER

APPLICANT: YASUDA, KAZUKI

TITLE OF INVENTION: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARTHUR, WHITE & DUCKER

STREET: P.O. Box 4433

CITY: Houston

STATE: TEXAS

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/292-694A

FILING DATE: August 19, 1994

CLASSIFICATION: 435

APPLICATION NUMBER: 08/050,296

FILING DATE: 20 May 1994

CLASSIFICATION: 435

APPLICATION NUMBER: 08/100,694

FILING DATE: 30 Jul 1993

CLASSIFICATION: 435

FILING DATE: 08/147,592

CLASSIFICATION: 435

APPLICATION NUMBER: PCT/US94/35747

FILING DATE: 20 May 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: MARK B. WILSON

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: ARD 143/WIR

TELEPHONE: (512) 418 3000

TELEFAX: (512) 789 2679

TELEX: 79 0924

INFORMATION FOR SEQ ID NO: 41

SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids

TYPE: amino acid

FUNCTION: linear

MOLECULE TYPE: protein

US-09-292-694A-41

Quality Match: 66.4% Score: 41 DP: 41 Length: 143

Best Local Similarity: 100.0% Pval: No. 1 9e-02

Mismatches: 41 Conservative: 0 Indels: 0 Gaps: 0

US-09-292-694A-41

Sequence 46: Application US/09/292-694A

Patent No. 6096543

GENERAL INFORMATION:  
APPLICANT: BELL, GRAEF

APPLICANT: BELLS, GRABER

APPLICANT: BELLS, GRABER

APPLICANT: YASUDA, KAZUKI

TITLE OF INVENTION: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARTHUR, WHITE & DUCKER

STREET: P.O. Box 4433

CITY: Houston

STATE: TEXAS

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

```

1  COMPUTER: IBM PC COMPATIBLE
2  OPERATING SYSTEM: PC-DOS/MS-DOS/OS/2
3  SOFTWARE: Patent Release #1.0, Version #1.0
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/09/292,694A
6  FILING DATE: August 19, 1994
7  CLASSIFICATION: 435
8  PRIORITY APPLICATION DATA:
9  APPLICATION NUMBER: 08/796,295
10 FILING DATE: 20 May 1994
11 CLASSIFICATION: 435
12 APPLICATION NUMBER: 08/796,295
13 FILING DATE: 20 May 1994
14 CLASSIFICATION: 435
15 APPLICATION NUMBER: 08/796,295
16 FILING DATE: 20 May 1994
17 CLASSIFICATION: 435
18 APPLICATION NUMBER: 08/796,295
19 FILING DATE: 20 May 1994
20 CLASSIFICATION: 435
21 ATTORNEY/AGENT INFORMATION:
22 NAME: MARK A. WILLSON
23 REGISTRATION NUMBER: 47,254
24 REFERENCE/DOCKET NUMBER: AR/0111/0039
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (512) 478-3000
27 TELEFAX: (512) 789-2679
28 COUNTRY: USA
29 ZIP: 78702
30 MEDIUM TYPE: DISKETTE, 3 1/2 inch, 5.25 MB
31 OPERATING SYSTEM: WINDOWS 95 WORKGROUP
32 SOFTWARE: WORDPERFECT 5.1
33 CURRENT APPLICATION DATA:
34 APPLICATION NUMBER: US/09/443-14
35 FILING DATE: October 29, 1994
36 CLASSIFICATION: 436
37 PRIORITY APPLICATION DATA:
38 APPLICATION NUMBER: 08/796,295
39 FILING DATE: October 29, 1994

```

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1  PRIORITY APPLICATION DATA:
2  APPLICATION NUMBER: 07/745,484
3  FILING DATE: August 14, 1991
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Jane Massey Licata
6  REGISTRATION NUMBER: 42,257
7  REFERENCE/DOCKET NUMBER: PENN-0142
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: (609) 779-2400
10 TELEFAX: (609) 779-8486
11 INFORMATION FOR SEQ ID NO: 1:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 14
14 TYPE: Amino Acid
15 POLYMER: Linear
16 US-09-495-128 2
17
18 Quality Match: 27.4%, Score 41, DB 1, Length 14;
19 Best Local Similarity: 100.0%, Pred. No. 2e+02;
20 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
21
22 QY 8 KSKD 11
23 DE 1111
24 3 KSKD 6
25
26 RESLI 47
27 US-09-652-648 1
28 Sequence 1, Application US/09/652,648
29 Patent No. 526454
30 GENERAL INFORMATION:
31 APPLICANT: Barstad, Paul A.
32 APPLICANT: Iverson, Gilbert M.
33 TITLE OF INVENTION: A Composition for Inducing Humoral
34 TITLE OF INVENTION: Ability to an Immunogen Comprising a T Cell
35 TITLE OF INVENTION: Epitope-Delicient Analog of the Immunogen Conjugated
36 TITLE OF INVENTION: to a No. 5268454 Immunogenic Carrier
37 NUMBER OF SEQUENCES: 1
38 CORRESPONDENCE ADDRESS:
39 ADDRESSER: Ivell & Marcella
40 STREET: 545 Midland Road, Suite 200
41 CITY: Menlo Park
42 STATE: CA
43 COUNTRY: USA
44 ZIP: 94025
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: Floppy disk
47 COMPUTER: IBM PC COMPATIBLE
48 OPERATING SYSTEM: PC-DOS/MS-DOS
49 SOFTWARE: Patent Release #1.0, Version #1.25
50 CURRENT APPLICATION DATA:
51 APPLICATION NUMBER: US/07/652,648
52 FILING DATE: 19910209
53 CLASSIFICATION: 424
54 ATTORNEY/AGENT INFORMATION:
55 NAME: Clotell, Thomas E.
56 REGISTRATION NUMBER: 21,013
57 REFERENCE/DOCKET NUMBER: 5211-0060
58 TELECOMMUNICATION INFORMATION:
59 TELEPHONE: (415) 327-7250
60 TELEFAX: (415) 327-2951
61 TELEX: 766141
62 INFORMATION FOR SEQ ID NO: 1:
63 SEQUENCE CHARACTERISTICS:
64 LENGTH: 8 amino acids
65 TYPE: AMINO ACID
66 STRANDEDNESS: Single
67 TOPOLOGY: Linear
68 US-07-652-648-1
69
70 Quality Match: 27.4%, Score 41, DB 1, Length 8;
71 Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
72 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

```

```

QY      8 KSK 10
      1
      4 KSK 5
RESULT 0
US 08 249 087 5
Sequence 5, Application US/08249087
Patent No. 5770409
GENERAL INFORMATION:
APPLICANT: BOCHILLA, MORRIS
INVENTOR: KRECH, EDWIN
TITLE OF INVENTION: ASSAY FOR PATENT SPECIFICITY OF ANTIBODIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 1100 Peachtree Street, Suite 2600
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309 4510
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,087
FILING DATE:
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 415
REFERENCE/DOCKET NUMBER: 415
TELEPHONE: (404) 815-6555
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDNESS: single
Topology: linear
MEDIUM TYPE: peptide
HYDROPHETAL: NO
ANTISENSE: NO
FRAGMENT TYPE: internal
US 08 249 087 5
Query Match: 27 %, Score 5, ID 1, Length 8
Best Local Similarity: 100 %, Pred. No. 2.5e-05
Matches: 3, Conservative 0, Mismatches 0, Gaps 0
QY      8 KSK 10
      1
      4 KSK 5
RESULT 0
US 08 249 087 5
Sequence 5, Application US/08249087
Patent No. 5770409
GENERAL INFORMATION:
APPLICANT: BOCHILLA, MORRIS
INVENTOR: KRECH, EDWIN
TITLE OF INVENTION: ASSAY FOR PATENT SPECIFICITY OF ANTIBODIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 1100 Peachtree Street, Suite 2600
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309 4510
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,087
FILING DATE:
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 415
REFERENCE/DOCKET NUMBER: 415
TELEPHONE: (404) 815-6555
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDNESS: single
Topology: linear
MEDIUM TYPE: peptide
HYDROPHETAL: NO
ANTISENSE: NO
FRAGMENT TYPE: internal
US 08 249 087 5

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QY      8 KSK 10
      1
      4 KSK 5
RESULT 0
US 08 249 087 5
Sequence 5, Application US/08249087
Patent No. 5770409
GENERAL INFORMATION:
APPLICANT: BOCHILLA, MORRIS
INVENTOR: KRECH, EDWIN
TITLE OF INVENTION: ASSAY FOR PATENT SPECIFICITY OF ANTIBODIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 1100 Peachtree Street, Suite 2600
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309 4510
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,087
FILING DATE:
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 415
REFERENCE/DOCKET NUMBER: 415
TELEPHONE: (404) 815-6555
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDNESS: single
Topology: linear
MEDIUM TYPE: peptide
HYDROPHETAL: NO
ANTISENSE: NO
FRAGMENT TYPE: internal
US 08 249 087 5
Query Match: 27 %, Score 5, ID 1, Length 8
Best Local Similarity: 100 %, Pred. No. 2.5e-05
Matches: 3, Conservative 0, Mismatches 0, Gaps 0
QY      8 KSK 10
      1
      4 KSK 5
RESULT 0
US 08 249 087 5
Sequence 5, Application US/08249087
Patent No. 5770409
GENERAL INFORMATION:
APPLICANT: BOCHILLA, MORRIS
INVENTOR: KRECH, EDWIN
TITLE OF INVENTION: ASSAY FOR PATENT SPECIFICITY OF ANTIBODIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 1100 Peachtree Street, Suite 2600
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309 4510
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,087
FILING DATE:
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 415
REFERENCE/DOCKET NUMBER: 415
TELEPHONE: (404) 815-6555
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDNESS: single
Topology: linear
MEDIUM TYPE: peptide
HYDROPHETAL: NO
ANTISENSE: NO
FRAGMENT TYPE: internal
US 08 249 087 5

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TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 33  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
RECORD TYPE: peptide  
US-09-616-855

Query Match: 27.4% Score 3: DB 2: Length 8:  
Best Local Similarity: 100.0%: Pred No: 2.5e+05:  
Matches: 3: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 7 EKS 9  
DL 6 EKS 8

RESULT 4:  
US-09-259-550A-35  
Sequence 35: Application US/0826550A  
Patent No. 5775892  
GENERAL INFORMATION:  
APPLICANT: GENTS, David E.  
TITLE OF INVENTION: Anticellulimatory peptides  
NUMBER OF SEQUENCES: 91  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & RUMBLE  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10046-2711  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patent Release #1.0, Version #1.05  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/259-550A  
FILING DATE: 16-JUN-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MISTOCK, S. Leslie  
REGISTRATION NUMBER: 38,872  
REFERENCE/DOCKET NUMBER: 714-01  
TELEPHONE: (212) 750-9099  
TELEFAX: (212) 669-8864/994  
TELEX: 66141 PENNIS  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
RECORD TYPE: peptide  
HYPERTHREAD: NO  
ANTI-SENSE: NO  
US-09-259-550A-35

Query Match: 27.4% Score 3: DB 2: Length 8:  
Best Local Similarity: 100.0%: Pred No: 2.5e+05:  
Matches: 3: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 5 EKS 7  
DL 4 EKS 9

RESULT 4:  
US-09-452-724A-38

Sequence 38: Application US/08452724A  
Patent No. 583680  
GENERAL INFORMATION:  
APPLICANT: Cited, Robert G.  
TITLE OF INVENTION: Walk-Through Mutagenesis  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.  
STREET: 2 Millis Drive  
CITY: Lexington  
STATE: MA  
COUNTRY: USA  
ZIP: 02174  
COMPUTER: READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,724A  
FILING DATE: 10-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/930,600  
FILING DATE: 05-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02362  
FILING DATE: 05-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/505,314  
FILING DATE: 05-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOK ESQ., David E.  
REGISTRATION NUMBER: 22,542  
REFERENCE/DOCKET NUMBER: R090 01A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
US-09-452-724A-38

Query Match: 27.4% Score 3: DB 2: Length 8:  
Best Local Similarity: 100.0%: Pred No: 2.5e+05:  
Matches: 3: Conservative: 0: Mismatches: 0: Indels: 0: Gaps: 0:

QY 4 TRE 6  
DL 5 TRE 7

RESULT 4:  
US-09-373-190-48  
Sequence 48: Application US/08473190  
Patent No. 5851829  
GENERAL INFORMATION:  
APPLICANT: MASASCO, WAYNE  
TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRODSKIN, ROBERTS & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MA  
COUNTRY: US  
ZIP: 02119  
COMPUTER: READABLE FORM:  
MEDIUM TYPE: Diskette

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1  COME-JIKKE: IBM Compatible
2  OPERATING SYSTEM: DOS
3  SOFTWARE: FASTSEQ Version 1.5
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/08/4374-14
6  FILING DATE: 17-JAN-1995
7  CLASSIFICATION: 435
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: PCT/US94/0166
10 FILING DATE: 16-JUL-1994
11 ATTORNEY/AGENT INFORMATION:
12 NAME: RESNICK, DAVID S.
13 REGISTRATION NUMBER: 44245
14 REFERENCE/DCKET NUMBER: 43966-05-05
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: 617-523-3400
17 TELEFAX: 617-523-6446
18 TELEX: SURE UR 2092
19 INFORMATION FOR SEQ ID NO: 435
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 8 amino acids
22 TYPE: amino acid
23 STRANDEDNESS: single
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 HYDROPHOBIC: NO
27 ANTI SENSE: NO
28 FRAGMENT TYPE: N-terminal
29 ORIGINAL SOURCE:
30 US 08 437 43-48
31
32 Query Match: 27.4% Score 4; DB 2; Length 8;
33 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
34 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
35
36 47 8 KSK 10
37 11
38 4 KSK 6
39
40 RESULT 44
41 US 08-443-4474-17
42 Sequence 17, Application US/08443474
43 Patent No. 5983748
44 GENERAL INFORMATION:
45 APPLICANT: TEN CLIKE, Peter
46 APPLICANT: HELDIN, Carl Henrik
47 APPLICANT: MIYAZONO, Robert
48 APPLICANT: SAMPATH, Robert
49 TITLE OF INVENTION: MGP-Induced T-Cell Death Ind. Act
50 TITLE OF INVENTION: Surface Receptors and Gene Expression
51 NUMBER OF SEQUENCES: 18
52 CORRESPONDENCE ADDRESS:
53 ADDRESSEE: Testa, Hurwitz & Thibault
54 STREET: 125 High St.
55 CITY: Boston
56 STATE: MA
57 COUNTRY: USA
58 ZIP: 02110
59 COMPUTER READABLE FORM:
60 MEDIUM TYPE: Floppy disk
61 COMPUTER: IBM PC compatible
62 OPERATING SYSTEM: PC-DOS/MS-DOS
63 SOFTWARE: PatentIn Release 3.1.0, Version 3.1.0
64 CURRENT APPLICATION DATA:
65 APPLICATION NUMBER: US/08/443474
66 FILING DATE: 02-JUN-1995
67 CLASSIFICATION: 435
68 ATTORNEY/AGENT INFORMATION:
69 NAME: MEYERS, Thomas G.
70 REGISTRATION NUMBER: 36,389
71 REFERENCE/DCKET NUMBER: 43966-05-14
72 TELECOMMUNICATION INFORMATION:

```

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1  TELEPHONE: (617) 248-7000
2  TELEFAX: (617) 248-7100
3  INFORMATION FOR SEQ ID NO: 17:
4  SEQUENCE CHARACTERISTICS:
5  LENGTH: 8 amino acids
6  TYPE: amino acid
7  STRANDEDNESS:
8  TOPOLOGY: linear
9  MOLECULE TYPE: peptide
10 US-08-443-4474-17
11
12 Query Match: 27.4% Score 4; DB 2; Length 8;
13 Best Local Similarity: 100.0%; Prod. No. 2.5e+05;
14 Matches: 3; Conservative: 0; Mismatches: 0; Indels: 0;
15
16 49 8 KSK 10
17 11
18 5 KSK 7
19
20 RESULT 45
21 US-08-147-777-4
22 Sequence 4, Application US/08:47777
23 Patent No. 5914265
24 GENERAL INFORMATION:
25 APPLICANT: Koop, Dennis R.
26 APPLICANT: Rothmann, Joseph A.
27 APPLICANT: Greenhalgh, David A.
28 APPLICANT: Yuspa, Stuart H.
29 TITLE OF INVENTION: KERATIN KI EXPRESSION VECTORS
30 TITLE OF INVENTION: AND METHODS OF USE
31 NUMBER OF SEQUENCES: 5
32 CORRESPONDENCE ADDRESS:
33 ADDRESSEE: LYON & LYON
34 STREET: 511 West Sixth Street
35 CITY: Los Angeles
36 STATE: California
37 COUNTRY: U.S.A.
38 ZIP: 90017
39 COMPUTER READABLE FORM:
40 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
41 COMPUTER: IBM PC compatible
42 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
43 SOFTWARE: WordPerfect (Version 5.1)
44 CURRENT APPLICATION DATA:
45 APPLICATION NUMBER: US/08/147,777
46 FILING DATE:
47 CLASSIFICATION: 800
48 PRIOR APPLICATION DATA:
49 PRIOR APPLICATION DATA: including application
50 PRIOR APPLICATION DATA: described below:
51 APPLICATION NUMBER: 07/876,289
52 FILING DATE: April 30, 1992
53 APPLICATION NUMBER: Unassigned (204/144)
54 FILING DATE: October 29, 1993
55 ATTORNEY/AGENT INFORMATION:
56 NAME: Warburg, Richard J.
57 REGISTRATION NUMBER: 32,327
58 REFERENCE/DCKET NUMBER: 204/153
59 TELECOMMUNICATION INFORMATION:
60 TELEPHONE: (213) 489-1600
61 TELEFAX: (213) 955-0440
62 TELEX: 67 9510
63 INFORMATION FOR SEQ ID NO: 4:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH: 8 amino acids
66 TYPE: amino acid
67 STRANDEDNESS: single
68 TOPOLOGY: linear
69 MOLECULE TYPE: peptide
70 US-08-147-777-4
71
72 Query Match: 27.4% Score 4; DB 2; Length 8;

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Best Local Similarity 100.0% Score 41 Mismatches 0 Gaps 0
Matches 0 Conservative 0 Mismatches 0 Gaps 0

CY 7 KIR 9
   1 1
   5 KIR 5

RESULT 46
US 08 463-216 7
Sequence 7: Application US/08/463-216
Patent No. 596883
GENERAL INFORMATION:
APPLICANT: S&W, A.D.
TITLE OF INVENTION: ANIMAL MODELS & HUMAN ARMY MODELS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Christensen, O'Connell, Johnson, and Kinross
STREET: 1420 Fifth Avenue, Suite 2500
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101 2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 1.2MB Storage
COMPUTER: IBM PC/86 Compatible
OPERATING SYSTEM: MS DOS 4.01
SOFTWARE: Word for Windows 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411 216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,744
FILING DATE: October 23, 1992
APPLICATION NUMBER: 07/950,417
FILING DATE: September 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Goodrick, Thomas F.
REGISTRATION NUMBER: 31,177
REFERENCE/ROCKET NUMBER: JFW 1 92 7
TELEPHONE: 1-206-682-8100; 1-206-224-9100 (1 line)
FLEX: 1-206-224-2779
FLEX: 4948023
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDNESS: Single
POLARITY: linear
MUTATOR TYPE: peptide
DESCRIPTION: APP(324 381) 443-41 000-6 10
US 08 463-216 7

Query Match:
Best Local Similarity 100.0% Score 41 Mismatches 0 Gaps 0
Matches 0 Conservative 0 Mismatches 0 Gaps 0

CY 6 KIR 7
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RESULT 47
US 08 450-260A 467
Sequence 47: Application US/08/450-260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
ADDRESS: Griffiths, Andrew Edward
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Samuel Edward
APPLICANT: Waterhouse, Robert

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1  APPLICANT: BASELINE, WILLIAM
2  TITLE OF INVENTION: METHOD OF INCREASING THE PURITY OF
3  TITLE OF INVENTION: PROTEINS
4  NUMBER OF SEQUENCES: 78
5  CURRENT NAME ADDRESS:
6  ADDRESS: LAMAR, 1000 N. 10TH ST., SUITE 100, DENVER, CO 80202
7  ADDRESS: CUSHMAN
8  STREET: 100 WATER STREET
9  CITY: BOSTON
10 STATE: MASSACHUSETTS
11 COUNTRY: US
12 ZIP: 02109
13 MODER READABLE FORM:
14 MEDIUM TYPE: floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.0
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/438,196A
20 FILING DATE:
21 CLASSIFICATION: 435
22 ATTORNEY/AGENT INFORMATION:
23 NAME: EISENSTEIN, RONALD L.
24 REGISTRATION NUMBER: 50628
25 REFERENCE/DOCKET NUMBER: 41993
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (617) 523-3400
28 TELEFAX: (617) 523-6443
29 INFORMATION FOR SEQ ID NO: 48:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 8 amino acids
32 TYPE: amino acid
33 SUBPOLYMER: linear
34 US 09-438,196A 48
35
36 Query Match: 27.0% Score 48 DB 2 Length 8:
37 Best Local Similarity: 100.0% Prod. No. 2.5e-05
38 Matches: 3 Conserved: 0 Mismatches: 0 Indels: 0
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Search completed: September 23, 2003 11:26 AM  
JLE:line 116 9157 SCS

Gene2go version 5.0.1  
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One protein - protein search, using sw method

Run on: September 30, 2003, 11:06:52, Search time 21.56 seconds  
(excluding alignment)

US-09-787-443-14  
Perfect score: 11  
Sequence: 1 AKTKERKSKD 11

Scoring table: 60x60

Searches: 506494 seqs, 151467094 residues

Word size: 0

Total number of hits satisfying chosen parameters: 13887

Minimum hit seq length: 8

Maximum hit seq length: 15

Post processing: listing first 500 summaries

Database: Published\_Applications\_AA.\*

- 1: /cqn2\_6/ptodata/2/pubaa/US07\_PUBAA\_Ms.pep.\*
- 2: /cqn2\_6/ptodata/2/pubaa/PT\_NEW\_PUB.pep.\*
- 3: /cqn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cqn2\_6/ptodata/2/pubaa/US06\_PUB\_Ms.pep.\*
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- 18: /cqn2\_6/ptodata/2/pubaa/US09\_PUB\_Ms.pep.\*

Note: N is the number of results found, which may be larger than or equal to the sum of the results found, and is derived by analysis of the data range distribution.

#### SUMMARY

Result No.	Query	Score	Match	Length	DB ID	Description
1	5	45.5	8	12	US-09-945-384-322	Sequence 122, App
2	5	45.5	9	11	US-09-945-384-326	Sequence 126, App
3	5	45.5	10	11	US-09-945-384-416	Sequence 416, App
4	5	45.5	10	11	US-09-945-384-527	Sequence 527, App
5	5	45.5	10	12	US-09-945-384-610	Sequence 610, App
6	4	36.4	8	12	US-09-945-384-692	Sequence 692, App
7	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
8	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
9	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
10	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
11	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
12	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
13	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
14	4	36.4	8	12	US-09-945-384-780	Sequence 780, App
15	4	36.4	8	12	US-09-945-384-780	Sequence 780, App

89	3	27.3	8	12	US-09-809-638-438	Sequence 304, App	162	3	27.3	9	11	US-09-809-638-438	Sequence 438, App
90	3	27.3	8	12	US-09-809-638-438	Sequence 516, App	163	3	27.3	9	11	US-09-809-638-438	Sequence 516, App
91	3	27.3	8	12	US-09-809-638-438	Sequence 204, App	164	3	27.3	9	11	US-09-809-638-438	Sequence 204, App
92	3	27.3	8	12	US-09-809-638-438	Sequence 379, App	165	3	27.3	9	11	US-09-809-638-438	Sequence 379, App
93	3	27.3	8	12	US-09-809-638-438	Sequence 467, App	166	3	27.3	9	11	US-09-809-638-438	Sequence 467, App
94	3	27.3	8	12	US-09-809-638-438	Sequence 596, App	167	3	27.3	9	11	US-09-809-638-438	Sequence 596, App
95	3	27.3	8	12	US-09-809-638-438	Sequence 67, App	168	3	27.3	9	11	US-09-809-638-438	Sequence 67, App
96	3	27.3	8	12	US-09-809-638-438	Sequence 411, App	169	3	27.3	9	11	US-09-809-638-438	Sequence 411, App
97	3	27.3	8	12	US-09-809-638-438	Sequence 48, App	170	3	27.3	9	11	US-09-809-638-438	Sequence 48, App
98	3	27.3	8	12	US-09-809-638-438	Sequence 444, App	171	3	27.3	9	11	US-09-809-638-438	Sequence 444, App
99	3	27.3	8	12	US-09-809-638-438	Sequence 605, App	172	3	27.3	9	11	US-09-809-638-438	Sequence 605, App
100	3	27.3	8	12	US-09-809-638-438	Sequence 622, App	173	3	27.3	9	11	US-09-809-638-438	Sequence 622, App
101	3	27.3	8	12	US-09-809-638-438	Sequence 1036, App	174	3	27.3	9	11	US-09-809-638-438	Sequence 1036, App
102	3	27.3	8	12	US-09-809-638-438	Sequence 9, App	175	3	27.3	9	11	US-09-809-638-438	Sequence 9, App
103	3	27.3	8	12	US-09-809-638-438	Sequence 6, App	176	3	27.3	9	11	US-09-809-638-438	Sequence 6, App
104	3	27.3	8	12	US-09-809-638-438	Sequence 528, App	177	3	27.3	9	11	US-09-809-638-438	Sequence 528, App
105	3	27.3	8	12	US-09-809-638-438	Sequence 21, App	178	3	27.3	9	11	US-09-809-638-438	Sequence 21, App
106	3	27.3	8	12	US-09-809-638-438	Sequence 22, App	179	3	27.3	9	11	US-09-809-638-438	Sequence 22, App
107	3	27.3	8	12	US-09-809-638-438	Sequence 23, App	180	3	27.3	9	11	US-09-809-638-438	Sequence 23, App
108	3	27.3	8	12	US-09-809-638-438	Sequence 26, App	181	3	27.3	9	11	US-09-809-638-438	Sequence 26, App
109	3	27.3	8	12	US-09-809-638-438	Sequence 11, App	182	3	27.3	9	11	US-09-809-638-438	Sequence 11, App
110	3	27.3	8	12	US-09-809-638-438	Sequence 317, App	183	3	27.3	9	11	US-09-809-638-438	Sequence 317, App
111	3	27.3	8	12	US-09-809-638-438	Sequence 324, App	184	3	27.3	9	11	US-09-809-638-438	Sequence 324, App
112	3	27.3	8	12	US-09-809-638-438	Sequence 607, App	185	3	27.3	9	11	US-09-809-638-438	Sequence 607, App
113	3	27.3	8	12	US-09-809-638-438	Sequence 2185, App	186	3	27.3	9	11	US-09-809-638-438	Sequence 2185, App
114	3	27.3	8	12	US-09-809-638-438	Sequence 2186, App	187	3	27.3	9	11	US-09-809-638-438	Sequence 2186, App
115	3	27.3	8	12	US-09-809-638-438	Sequence 2187, App	188	3	27.3	9	11	US-09-809-638-438	Sequence 2187, App
116	3	27.3	8	12	US-09-809-638-438	Sequence 6, App	189	3	27.3	9	11	US-09-809-638-438	Sequence 6, App
117	3	27.3	8	12	US-09-809-638-438	Sequence 429, App	190	3	27.3	9	11	US-09-809-638-438	Sequence 429, App
118	3	27.3	8	12	US-09-809-638-438	Sequence 110, App	191	3	27.3	9	11	US-09-809-638-438	Sequence 110, App
119	3	27.3	8	12	US-09-809-638-438	Sequence 120, App	192	3	27.3	9	11	US-09-809-638-438	Sequence 120, App
120	3	27.3	8	12	US-09-809-638-438	Sequence 80, App	193	3	27.3	9	11	US-09-809-638-438	Sequence 80, App
121	3	27.3	8	12	US-09-809-638-438	Sequence 104, App	194	3	27.3	9	11	US-09-809-638-438	Sequence 104, App
122	3	27.3	8	12	US-09-809-638-438	Sequence 6, App	195	3	27.3	9	11	US-09-809-638-438	Sequence 6, App
123	3	27.3	8	12	US-09-809-638-438	Sequence 23, App	196	3	27.3	9	11	US-09-809-638-438	Sequence 23, App
124	3	27.3	8	12	US-09-809-638-438	Sequence 284, App	197	3	27.3	9	11	US-09-809-638-438	Sequence 284, App
125	3	27.3	8	12	US-09-809-638-438	Sequence 401, App	198	3	27.3	9	11	US-09-809-638-438	Sequence 401, App
126	3	27.3	8	12	US-09-809-638-438	Sequence 601, App	199	3	27.3	9	11	US-09-809-638-438	Sequence 601, App
127	3	27.3	8	12	US-09-809-638-438	Sequence 658, App	200	3	27.3	9	11	US-09-809-638-438	Sequence 658, App
128	3	27.3	8	12	US-09-809-638-438	Sequence 695, App	201	3	27.3	9	11	US-09-809-638-438	Sequence 695, App
129	3	27.3	8	12	US-09-809-638-438	Sequence 1064, App	202	3	27.3	9	11	US-09-809-638-438	Sequence 1064, App
130	3	27.3	8	12	US-09-809-638-438	Sequence 1073, App	203	3	27.3	9	11	US-09-809-638-438	Sequence 1073, App
131	3	27.3	8	12	US-09-809-638-438	Sequence 1283, App	204	3	27.3	9	11	US-09-809-638-438	Sequence 1283, App
132	3	27.3	8	12	US-09-809-638-438	Sequence 1460, App	205	3	27.3	9	11	US-09-809-638-438	Sequence 1460, App
133	3	27.3	8	12	US-09-809-638-438	Sequence 1546, App	206	3	27.3	9	11	US-09-809-638-438	Sequence 1546, App
134	3	27.3	8	12	US-09-809-638-438	Sequence 1585, App	207	3	27.3	9	11	US-09-809-638-438	Sequence 1585, App
135	3	27.3	8	12	US-09-809-638-438	Sequence 1590, App	208	3	27.3	9	11	US-09-809-638-438	Sequence 1590, App
136	3	27.3	8	12	US-09-809-638-438	Sequence 1669, App	209	3	27.3	9	11	US-09-809-638-438	Sequence 1669, App
137	3	27.3	8	12	US-09-809-638-438	Sequence 1677, App	210	3	27.3	9	11	US-09-809-638-438	Sequence 1677, App
138	3	27.3	8	12	US-09-809-638-438	Sequence 1896, App	211	3	27.3	9	11	US-09-809-638-438	Sequence 1896, App
139	3	27.3	8	12	US-09-809-638-438	Sequence 2014, App	212	3	27.3	9	11	US-09-809-638-438	Sequence 2014, App
140	3	27.3	8	12	US-09-809-638-438	Sequence 37, App	213	3	27.3	9	11	US-09-809-638-438	Sequence 37, App
141	3	27.3	8	12	US-09-809-638-438	Sequence 39, App	214	3	27.3	9	11	US-09-809-638-438	Sequence 39, App
142	3	27.3	8	12	US-09-809-638-438	Sequence 27, App	215	3	27.3	9	11	US-09-809-638-438	Sequence 27, App
143	3	27.3	8	12	US-09-809-638-438	Sequence 111, App	216	3	27.3	9	11	US-09-809-638-438	Sequence 111, App
144	3	27.3	8	12	US-09-809-638-438	Sequence 187, App	217	3	27.3	9	11	US-09-809-638-438	Sequence 187, App
145	3	27.3	8	12	US-09-809-638-438	Sequence 271, App	218	3	27.3	9	11	US-09-809-638-438	Sequence 271, App
146	3	27.3	8	12	US-09-809-638-438	Sequence 50, App	219	3	27.3	9	11	US-09-809-638-438	Sequence 50, App

[illegible]



1 PRIOR FILING DATE: 2000-08-17  
2 NUMBER OF SEQ ID NOS: 1508  
3 SOFTWARE: Patent In Ver. 2.1  
4 SEQ ID NO 1442  
5 LENGTH: 8  
6 TYPE: PRT  
7 ORGANISM: Artificial Sequence  
8 FEATURE:  
9 OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US 09-572-404B-214

Query Match: 45.5%, Score 5; DB 11; Length 10;  
Best Local Similarity: 100.0%; Pref. No. 44;  
Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 7 RESKS 11  
LB 1 RESKS 5

RESULT 2  
US-09-572-404B-214  
1 Sequence 456, Application US/09/572404B  
2 Publication No. US20030072794A1  
3 GENERAL INFORMATION:  
4 APPLICANT: BOEHRINGER-INGHELBACH  
5 TITLE OF INVENTION: ENCAPSULATION OF GLASSIONIC DNA (COPOLYMERS TM) AND THERAPEUTIC  
6 TITLE OF INVENTION: AGENTS WITH NEURAL DIFFERENTIATION SIGNAL/FOUSGENIC PEPTIDE  
7 FILE REFERENCE: TB-2002-00  
8 CURRENT APPLICATION NUMBER: US/09/572-404B  
9 PRIOR FILING DATE: 2001-06-08  
10 PRIOR APPLICATION NUMBER: US 66/210,942  
11 PRIOR FILING DATE: 2000-06-09  
12 NUMBER OF SEQ ID NOS: 629  
13 SOFTWARE: Patent In Ver. 2.1  
14 SEQ ID NO 465  
15 LENGTH: 7  
16 TYPE: PRT  
17 ORGANISM: Unknown Organism  
18 FEATURE:  
19 OTHER INFORMATION: Description of Unknown Organism: Rat, mouse, human, dog, cat  
US-09-572-404B-214

Query Match: 45.5%, Score 5; DB 11; Length 10;  
Best Local Similarity: 100.0%; Pref. No. 44;  
Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 6 RESKS 10  
LB 4 RESKS 8

RESULT 3  
US-09-572-404B-214  
1 Sequence 214, Application US/09/572404B  
2 Publication No. US20030072794A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
6 FILE REFERENCE: Human patent  
7 CURRENT APPLICATION NUMBER: US/09/572-404B  
8 PRIOR FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 4203  
10 SOFTWARE: Patent In Ver. 2.1  
11 SEQ ID NO 214  
12 LENGTH: 10  
13 TYPE: PRT  
14 ORGANISM: Homo Sapiens  
15 FEATURE:  
16 OTHER INFORMATION: Sequence located in ARAF1 at 419-428 and may interact with S  
US-09-572-404B-214

Query Match: 45.5%, Score 5; DB 11; Length 10;  
Best Local Similarity: 100.0%; Pref. No. 44;  
Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 6 RESKS 10  
LB 4 RESKS 8

RESULT 4  
US-09-572-404B-214  
1 Sequence 216, Application US/09/572404B  
2 Publication No. US20030072794A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Complementary peptide ligands from the human genome  
6 FILE REFERENCE: Human patent  
7 CURRENT APPLICATION NUMBER: US/09/572-404B  
8 PRIOR FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 4203  
10 SOFTWARE: Patent In Ver. 2.1  
11 SEQ ID NO 216  
12 LENGTH: 10  
13 TYPE: PRT  
14 ORGANISM: Homo Sapiens  
15 FEATURE:  
16 OTHER INFORMATION: Sequence located in ARAF1 at 418-427 and may interact with S  
US-09-572-404B-216

Query Match: 45.5%, Score 5; DB 11; Length 10;  
Best Local Similarity: 100.0%; Pref. No. 44;  
Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 RESKS 9  
LB 6 RESKS 12

RESULT 5  
US-09-572-404B-216  
1 Sequence 135, Application US/09/572404B  
2 Publication No. US20030072794A1  
3 GENERAL INFORMATION:  
4 APPLICANT: RALPH, ARTHUR  
5 APPLICANT: CHALLITA-ELI, PIA M.  
6 APPLICANT: FARIS, MARY  
7 APPLICANT: SAPPAN, DOUGLAS  
8 APPLICANT: APAR, DANIEL  
9 APPLICANT: LEVIN, ELANA  
10 APPLICANT: ROBERT, RENE  
11 APPLICANT: GU, WANGMAO  
12 APPLICANT: JAKOBOWITZ, AVA  
13 TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
14 TITLE OF INVENTION: 83P283 AND CATT22E11 USEFUL IN TREATMENT AND  
15 FILE REFERENCE: DETECTION OF CANCER  
16 FILE REFERENCE: 51158-200-4.00  
17 CURRENT APPLICATION NUMBER: US/09/572-404B  
18 PRIOR FILING DATE: 2001-08-17  
19 PRIOR APPLICATION NUMBER: 60/226,329  
20 PRIOR FILING DATE: 2000-08-17  
21 NUMBER OF SEQ ID NOS: 1508  
22 SOFTWARE: Patent In Ver. 2.1  
23 SEQ ID NO 1305  
24 LENGTH: 10  
25 TYPE: PRT  
26 ORGANISM: Artificial Sequence  
27 FEATURE:  
28 OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-572-404B-216





DE 3 REK 6

RESULT 10

US-09-043-059-111

Sequence 54, Application US/09/043-059

Publication No. US2000175963A1

GENERAL INFORMATION:

APPLICANT: Iureci, Ozlem

APPLICANT: Sahin, Bgnt

APPLICANT: Pfrendtschub, Michael

TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof

FILE REFERENCE: LUD 5622.1

CURRENT APPLICATION NUMBER: US/09/043-059

PRIOR FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: US/09/043-059

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: US/09/043-059

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: US/09/043-059

PRIOR FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: US/08/051-129

PRIOR FILING DATE: 1997-05-05

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 101

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

US-09-043-059-111

Query Match: 46.4% Score 4: 0; DB 14: Length 8;

Best Local Similarity: 100.0%; Pct. No. Seqs: 0;

Matches: 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE 3 REK 6

RESULT 11

US-10-014-465A-54

Sequence 54, Application US/10/014-465A

Publication No. US2002016864A1

GENERAL INFORMATION:

APPLICANT: Cell Signaling Technology, Inc.

APPLICANT: CHANG, Michael J.

APPLICANT: ZHANG, Hui

APPLICANT: TAN, Yi

TITLE OF INVENTION: PROTECTION OF MOLECULAR SEQUENCES AND COMPLEX INDEPENDENT ANTIBODIES

FILE REFERENCE: CSI-138 CIP2

CURRENT APPLICATION NUMBER: US/10/014-465A

PRIOR FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: US/09/148-712

PRIOR FILING DATE: 1998-09-04

PRIOR APPLICATION NUMBER: US/09/535-364

PRIOR FILING DATE: 2000-04-24

NUMBER OF SEQ ID NOS: 145

SEQ ID NO 54

LENGTH: 8

TYPE: PRT

ORGANISM: Homo sapiens

FEATURES:

NAME/KEY: M00-RES

LOCATION: (6)...(6)

OTHER INFORMATION: PROSPEROXYLATION: threonine at position 6 is phosphorylated

US-10-014-465A-54

Query Match: 46.4% Score 4: 0; DB 14: Length 8;

Best Local Similarity: 100.0%; Pct. No. Seqs: 0;

Matches: 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE 3 REK 4

RESULT 12

US-10-174-105A-54

Sequence 54, Application US/10/174-105A

Publication No. US20030093652A1

GENERAL INFORMATION:

APPLICANT: Cell Signaling Technology, Inc.

APPLICANT: ZHANG, Hui

APPLICANT: CHANG, Michael J.

APPLICANT: TAN, Yi

TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPEC

FILE REFERENCE: CSI-138 CIP4

CURRENT APPLICATION NUMBER: US/10/174-105A

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US/09/148-712

PRIOR FILING DATE: 1998-09-04

PRIOR APPLICATION NUMBER: US/09/535-364

PRIOR FILING DATE: 2000-04-24

NUMBER OF SEQ ID NOS: 193

SOFTWARE: PatentIn version 3.1

SEQ ID NO 54

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES:

NAME/KEY: M00-RES

LOCATION: (6)...(6)

OTHER INFORMATION: PHOSPHORYLATION: threonine at position 6 is phosphorylated

US-10-174-105A-54

Query Match: 46.4% Score 4: 0; DB 15: Length 8;

Best Local Similarity: 100.0%; Pct. No. Seqs: 0;

Matches: 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE 3 REK 4

RESULT 13

US-10-125-71-14

Sequence 18, Application US/20/24711

Publication No. US20030099634A1

GENERAL INFORMATION:

APPLICANT: VITELLO, Maria A.

APPLICANT: CHESTNUT, Robert W.

APPLICANT: SETTE, Alessandro D.

APPLICANT: CELIS, Esteban

APPLICANT: GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING

NUMBER OF SEQ ID NOS: 153

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend Kourie and Crew

STREET: Stewart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105-1494

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

1. APPLICATION NUMBER: US/09/124,384  
 2. FILING DATE: 22 APR 1992  
 3. CLASSIFICATION: Unknown  
 4. PRIOR APPLICATION DATA:  
 5. APPLICATION NUMBER: US/09/124,384  
 6. FILING DATE: 15 FEB 1994  
 7. APPLICATION NUMBER: US/09/124,384  
 8. FILING DATE: 26 APR 1992  
 9. APPLICATION NUMBER: US/09/124,384  
 10. FILING DATE: 27 APR 1992  
 11. APPLICATION NUMBER: US/09/124,384  
 12. FILING DATE: 29 JAN 1992  
 13. APPLICATION NUMBER: US/09/124,384  
 14. FILING DATE: 26 APR 1991  
 15. NAME: Parmelee, Steven W  
 16. REGISTRATION NUMBER: 41900  
 17. REFERENCE/Docket NUMBER: 41900  
 18. TELECOMMUNICATION INFORMATION:  
 19. TELEPHONE: (206) 467-6600  
 20. TELEFAX: (206) 467-6794  
 21. INFORMATION FOR SEQ ID NO: 18:  
 22. SEQUENCE CHARACTERISTICS:  
 23. LENGTH: 8 amino acids  
 24. TYPE: amino acid  
 25. STANDARD: unknown  
 26. ORIGIN: unknown  
 27. SEQUENCE TYPE: peptide  
 28. SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
 29. 128-711-18

Query Match 46.4% Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pos. No. 50-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 100 1 KSKK 4

1. APPLICATION NUMBER: US/09/124,384  
 2. FILING DATE: 22 APR 1992  
 3. CLASSIFICATION: Unknown  
 4. PRIOR APPLICATION DATA:  
 5. APPLICATION NUMBER: US/09/124,384  
 6. FILING DATE: 15 FEB 1994  
 7. APPLICATION NUMBER: US/09/124,384  
 8. FILING DATE: 26 APR 1992  
 9. APPLICATION NUMBER: US/09/124,384  
 10. FILING DATE: 27 APR 1992  
 11. APPLICATION NUMBER: US/09/124,384  
 12. FILING DATE: 29 JAN 1992  
 13. APPLICATION NUMBER: US/09/124,384  
 14. FILING DATE: 26 APR 1991  
 15. NAME: Parmelee, Steven W  
 16. REGISTRATION NUMBER: 41900  
 17. REFERENCE/Docket NUMBER: 41900  
 18. TELECOMMUNICATION INFORMATION:  
 19. TELEPHONE: (206) 467-6600  
 20. TELEFAX: (206) 467-6794  
 21. INFORMATION FOR SEQ ID NO: 18:  
 22. SEQUENCE CHARACTERISTICS:  
 23. LENGTH: 8 amino acids  
 24. TYPE: amino acid  
 25. STANDARD: unknown  
 26. ORIGIN: unknown  
 27. SEQUENCE TYPE: peptide  
 28. SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
 29. 128-711-18

Query Match 46.4% Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pos. No. 50-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

29 7 KSKK 10  
 30 11  
 31 6 KSKK 9  
 32 1 KSKK 4  
 33 1 KSKK 4  
 34 1 KSKK 4  
 35 1 KSKK 4  
 36 1 KSKK 4  
 37 1 KSKK 4  
 38 1 KSKK 4  
 39 1 KSKK 4  
 40 1 KSKK 4  
 41 1 KSKK 4  
 42 1 KSKK 4  
 43 1 KSKK 4  
 44 1 KSKK 4  
 45 1 KSKK 4  
 46 1 KSKK 4  
 47 1 KSKK 4  
 48 1 KSKK 4  
 49 1 KSKK 4  
 50 1 KSKK 4  
 51 1 KSKK 4  
 52 1 KSKK 4  
 53 1 KSKK 4  
 54 1 KSKK 4  
 55 1 KSKK 4  
 56 1 KSKK 4  
 57 1 KSKK 4  
 58 1 KSKK 4  
 59 1 KSKK 4  
 60 1 KSKK 4  
 61 1 KSKK 4  
 62 1 KSKK 4  
 63 1 KSKK 4  
 64 1 KSKK 4  
 65 1 KSKK 4  
 66 1 KSKK 4  
 67 1 KSKK 4  
 68 1 KSKK 4  
 69 1 KSKK 4  
 70 1 KSKK 4  
 71 1 KSKK 4  
 72 1 KSKK 4  
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 75 1 KSKK 4  
 76 1 KSKK 4  
 77 1 KSKK 4  
 78 1 KSKK 4  
 79 1 KSKK 4  
 80 1 KSKK 4  
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 85 1 KSKK 4  
 86 1 KSKK 4  
 87 1 KSKK 4  
 88 1 KSKK 4  
 89 1 KSKK 4  
 90 1 KSKK 4  
 91 1 KSKK 4  
 92 1 KSKK 4  
 93 1 KSKK 4  
 94 1 KSKK 4  
 95 1 KSKK 4  
 96 1 KSKK 4  
 97 1 KSKK 4  
 98 1 KSKK 4  
 99 1 KSKK 4  
 100 1 KSKK 4

Best Local Similarity: 100.0%; Score: 4; DB: 12; Length: 9;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q7 7 RSKK 10  
11  
14 4 RSKK 7

RESULT 17  
US-09-935-484-416  
Sequence 426, Application US/99/935,384  
Publication No. US2000/0166525A1  
GENERAL INFORMATION:  
APPLICANT: CHALLITA-ELD, PIA  
APPLICANT: HUBERT, RENE  
APPLICANT: RATTANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: PARIS, MARY  
APPLICANT: GE, WANGMAO  
APPLICANT: JAKBOVITZ, AYA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-2003-00  
CURRENT APPLICATION NUMBER: US/99/935,384  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 66/227,096  
NUMBER OF SEQ ID NOS: 783  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 426  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-935-484-416

Query Match: 36.4%; Score: 4; DB: 12; Length: 9;  
Best Local Similarity: 100.0%; Prod. No. 50-05;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q7 7 RSKK 10  
11  
14 4 RSKK 7

RESULT 18  
US-09-935-484-416  
Sequence 426, Application US/99/935,384  
Publication No. US2000/0166525A1  
GENERAL INFORMATION:  
APPLICANT: CHALLITA-ELD, PIA  
APPLICANT: HUBERT, RENE  
APPLICANT: RATTANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: PARIS, MARY  
APPLICANT: GE, WANGMAO  
APPLICANT: JAKBOVITZ, AYA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-2003-00  
CURRENT APPLICATION NUMBER: US/99/935,384  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 66/227,096  
NUMBER OF SEQ ID NOS: 783  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 426  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-935-484-416

Query Match: 36.4%; Score: 4; DB: 12; Length: 9;  
Best Local Similarity: 100.0%; Prod. No. 50-05;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q7 7 RSKK 10  
11  
14 4 RSKK 7

RESULT 19  
US-09-935-484-416  
Sequence 426, Application US/99/935,384  
Publication No. US2000/0166525A1  
GENERAL INFORMATION:  
APPLICANT: CHALLITA-ELD, PIA  
APPLICANT: HUBERT, RENE  
APPLICANT: RATTANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: PARIS, MARY  
APPLICANT: GE, WANGMAO  
APPLICANT: JAKBOVITZ, AYA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-2003-00  
CURRENT APPLICATION NUMBER: US/99/935,384  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 66/227,096  
NUMBER OF SEQ ID NOS: 783  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 426  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-935-484-416

Query Match: 36.4%; Score: 4; DB: 12; Length: 9;  
Best Local Similarity: 100.0%; Prod. No. 50-05;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Q7 7 RSKK 10  
11  
14 4 RSKK 7

RESULT 20  
US-09-935-484-416  
Sequence 426, Application US/99/935,384  
Publication No. US2000/0166525A1  
GENERAL INFORMATION:  
APPLICANT: CHALLITA-ELD, PIA  
APPLICANT: HUBERT, RENE  
APPLICANT: RATTANO, ARTHUR  
APPLICANT: AFAR, DANIEL  
APPLICANT: LEVIN, ELANA  
APPLICANT: PARIS, MARY  
APPLICANT: GE, WANGMAO  
APPLICANT: JAKBOVITZ, AYA  
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
TITLE OF INVENTION: OTHER CANCERS  
FILE REFERENCE: 51158-2003-00  
CURRENT APPLICATION NUMBER: US/99/935,384  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 66/227,096  
NUMBER OF SEQ ID NOS: 783  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 426  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-935-484-416

```

1  LENGTH: 9
2  TYPE: PRT
3  ORGANISM: Homo Sapiens
4  US 09 833 039 68

Query Match:          36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod No. 5006001
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 7 8SKK 10
   1 1
   1 8SKK 6

RESULT 21
US 09 833 039 41
1  Sequence 75, Application US/09/833039
2  Publication No. US20030175960A1
3  GENERAL INFORMATION:
4  APPLICANT: Tumor, Ozlem
5  APPLICANT: Sahin, Dilar
6  APPLICANT: Friedmann, Michael
7  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8  FILE REFERENCE: LID 5622.1
9  CURRENT APPLICATION NUMBER: US/09/833039
10  PRIOR FILING DATE: 2001-04-12
11  PRIOR APPLICATION NUMBER: US 09/409,455
12  PRIOR FILING DATE: 1999-09-30
13  PRIOR APPLICATION NUMBER: US 09/444,040
14  PRIOR FILING DATE: 1999-06-25
15  PRIOR APPLICATION NUMBER: US 09/105,849
16  PRIOR FILING DATE: 1998-06-26
17  PRIOR APPLICATION NUMBER: US 08/451,140
18  PRIOR FILING DATE: 1997-05-05
19  NUMBER OF SEQ ID NOS: 129
20  SEQ ID NO: 41
21  LENGTH: 9
22  TYPE: PRT
23  ORGANISM: Homo Sapiens
24  US 09 833 039 41

Query Match:          36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod No. 5006001
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 7 8SKK 6
   1 1
   1 8SKK 4

RESULT 22
US 09 833 039 68
1  Sequence 94, Application US/09/833039
2  Publication No. US20030175960A1
3  GENERAL INFORMATION:
4  APPLICANT: Tumor, Ozlem
5  APPLICANT: Sahin, Dilar
6  APPLICANT: Friedmann, Michael
7  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8  FILE REFERENCE: LID 5622.1
9  CURRENT APPLICATION NUMBER: US/09/833039
10  PRIOR FILING DATE: 2001-04-12
11  PRIOR APPLICATION NUMBER: US 09/409,455
12  PRIOR FILING DATE: 1999-09-30
13  PRIOR APPLICATION NUMBER: US 09/444,040
14  PRIOR FILING DATE: 1999-06-25
15  PRIOR APPLICATION NUMBER: US 09/105,849
16  PRIOR FILING DATE: 1998-06-26
17  PRIOR APPLICATION NUMBER: US 08/451,140
18  PRIOR FILING DATE: 1997-05-05
19  NUMBER OF SEQ ID NOS: 129
20  SEQ ID NO: 49
21  LENGTH: 9
22  TYPE: PRT

```

```

1  TYPE: PRT
2  ORGANISM: Homo Sapiens
3  US 09 833 039 68

Query Match:          36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod No. 5006001
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 7 8SKK 8
   1 1
   1 8SKK 4

RESULT 23
US 09 833 039 75
1  Sequence 75, Application US/09/833039
2  Publication No. US20030175960A1
3  GENERAL INFORMATION:
4  APPLICANT: Tumor, Ozlem
5  APPLICANT: Sahin, Dilar
6  APPLICANT: Friedmann, Michael
7  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8  FILE REFERENCE: LID 5622.1
9  CURRENT APPLICATION NUMBER: US/09/833039
10  PRIOR FILING DATE: 2001-04-12
11  PRIOR APPLICATION NUMBER: US 09/409,455
12  PRIOR FILING DATE: 1999-09-30
13  PRIOR APPLICATION NUMBER: US 09/444,040
14  PRIOR FILING DATE: 1999-06-25
15  PRIOR APPLICATION NUMBER: US 09/105,849
16  PRIOR FILING DATE: 1998-06-26
17  PRIOR APPLICATION NUMBER: US 08/451,140
18  PRIOR FILING DATE: 1997-05-05
19  NUMBER OF SEQ ID NOS: 129
20  SEQ ID NO: 75
21  LENGTH: 9
22  TYPE: PRT
23  ORGANISM: Homo Sapiens
24  US 09 833 039 75

Query Match:          36.4%, Score 41, DP 121, Length 9,
Best Local Similarity: 100.0%, Prod No. 5006001
Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 7 8SKK 8
   1 1
   1 8SKK 4

RESULT 24
US 09 833 039 94
1  Sequence 94, Application US/09/833039
2  Publication No. US20030175960A1
3  GENERAL INFORMATION:
4  APPLICANT: Tumor, Ozlem
5  APPLICANT: Sahin, Dilar
6  APPLICANT: Friedmann, Michael
7  TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
8  FILE REFERENCE: LID 5622.1
9  CURRENT APPLICATION NUMBER: US/09/833039
10  PRIOR FILING DATE: 2001-04-12
11  PRIOR APPLICATION NUMBER: US 09/409,455
12  PRIOR FILING DATE: 1999-09-30
13  PRIOR APPLICATION NUMBER: US 09/444,040
14  PRIOR FILING DATE: 1999-06-25
15  PRIOR APPLICATION NUMBER: US 09/105,849
16  PRIOR FILING DATE: 1998-06-26
17  PRIOR APPLICATION NUMBER: US 08/451,140
18  PRIOR FILING DATE: 1997-05-05
19  NUMBER OF SEQ ID NOS: 129
20  SEQ ID NO: 94
21  LENGTH: 9
22  TYPE: PRT

```

ORGANISM: Homo sapiens  
US-09-833-039-94

Query Match: 36.4%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 REK 8  
DE 1 REK 4

RESULT 25

US-09-833-039-122  
Sequence 122, Application US/09/430-09  
Publication No. US20030175960A1  
GENERAL INFORMATION:  
APPLICANT: Tarek, Ozlem  
APPLICANT: Sebun, Ugur  
APPLICANT: Pfundschud, Michael  
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof  
FILE REFERENCE: LED 5622.1  
CURRENT APPLICATION NUMBER: US/09/833-039  
PRIOR FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: US/09/430-09  
PRIOR FILING DATE: 1999-09-30  
PRIOR APPLICATION NUMBER: US/09/444-140  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: US/09/405-844  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: US/08/451-100  
PRIOR FILING DATE: 1997-05-05  
NUMBER OF SEQ ID NOS: 129  
SEQ ID NO 112  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-833-039-112

Query Match: 36.4%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 REK 8  
DE 1 REK 4

RESULT 26

US-10-259-31A-195  
Sequence 195, Application US/10259-31A  
Publication No. US20030175295A1  
GENERAL INFORMATION:  
APPLICANT: KINGDER - HAMOUR, Christine  
APPLICANT: CORVAIA, Nathalie  
APPLICANT: BRCK, Alain  
APPLICANT: GOETSCH, Liliane  
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING A ITS  
TITLE OF INVENTION: N-TERMINAL A GLUCAMIC ACID OR A GLUTAMINE IN THE FORM  
TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACTIVE STRONG ACID  
FILE REFERENCE: 343 727 - US  
CURRENT APPLICATION NUMBER: US/10/259-31A  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: FR 00/04711  
PRIOR FILING DATE: 2000-03-23  
PRIOR APPLICATION NUMBER: PCT 01/70772  
PRIOR FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 697  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 195  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Influenza virus

US-10-259-313A-195

Query Match: 36.4%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 REK 5  
DE 6 REK 9

RESULT 27

US-09-894-912A-21  
Sequence 21, Application US/09894912A  
Publication No. US20030044792A1  
GENERAL INFORMATION:  
APPLICANT: Gao et al.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL STEM CELL GROWTH  
TITLE OF INVENTION: FACTOR-LIKE POLYPEPTIDES AND POLYNUCLEOTIDES  
FILE REFERENCE: 28110/37260A  
CURRENT APPLICATION NUMBER: US/09/894-912A  
CURRENT FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: To be assigned  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: 60/265,614  
PRIOR FILING DATE: 2001-02-05  
PRIOR APPLICATION NUMBER: 60/415,734  
PRIOR FILING DATE: 2000-06-28  
PRIOR APPLICATION NUMBER: 09/757,562  
PRIOR FILING DATE: 2001-01-09  
PRIOR APPLICATION NUMBER: 09/543,274  
PRIOR FILING DATE: 2000-04-05  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 21  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-894-912A-21

Query Match: 36.4%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 REK 8  
DE 4 REK 7

RESULT 28

US-09-876-904A-391  
Sequence 391, Application US/09876904A  
Publication No. US2003007294A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: COMBUNATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876-904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 391  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
FEATURE:  
OTHER INFORMATION: C. elegans Sdc 3 protein (sex-determining protein)  
US-09-876-904A-391

Query Match 36.4% Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 RSKS 10  
111  
DB 2 RSKS 5

RESULT 29  
US-09-922-256-09  
1 Sequence 69, Application US/09/922-29  
2 Publication No. US20030134784A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Zhao, Yi  
5 APPLICANT: Huoher, Scott M.  
6 APPLICANT: Xiao, Jia Bao  
7 APPLICANT: Kasali, Jyotirmoy  
8 APPLICANT: Chandrasekhar, Roshantha A  
9 TITLE OF INVENTION: Methods of Screening for Compounds that  
10 TITLE OF INVENTION: Modulate Bacterial Motility  
11 FILE REFERENCE: P-AK 4081  
12 CURRENT APPLICATION NUMBER: US/09/922-226  
13 PRIOR FILING DATE: 2002-01-09  
14 PRIOR APPLICATION NUMBER: US 60/284,397  
15 NUMBER OF SEQ ID NOS: 19;  
16 SOFTWARE: FastSeq for Windows Version 4.0  
17 SEQ ID NO 69  
18 LENGTH: 10  
19 TYPE: PRT  
20 ORGANISM: Artificial Sequence  
21 FEATURE:  
22 OTHER INFORMATION: Synthetic peptide  
US-09-922-226-09

Query Match 36.4% Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 RSKS 10  
111  
DB 4 RSKS 5

RESULT 30  
US-09-932-165-780  
1 Sequence 265, Application US/09/932-165  
2 Publication No. US20030134784A1  
3 GENERAL INFORMATION:  
4 APPLICANT: RATTANOL, ARTHUR  
5 APPLICANT: CHALLITA-ELD, PIA M.  
6 APPLICANT: FARIS, MARY  
7 APPLICANT: SAFERAN, DOUGLAS  
8 APPLICANT: AFAR, DANIEL  
9 APPLICANT: LEVIN, ELANA  
10 APPLICANT: HUBERT, RENE  
11 APPLICANT: GE, WANGMAO  
12 APPLICANT: JAKOBOWITZ, AYA  
13 TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
14 TITLE OF INVENTION: DETECTION OF CANCER  
15 FILE REFERENCE: 51158-20014-00  
16 CURRENT APPLICATION NUMBER: US/09/932-165  
17 PRIOR FILING DATE: 2003-08-17  
18 PRIOR APPLICATION NUMBER: 60/226,129  
19 PRIOR FILING DATE: 2000-08-17  
20 NUMBER OF SEQ ID NOS: 1508  
21 SOFTWARE: PatentIn Ver. 2.1  
22 SEQ ID NO 780  
23 LENGTH: 10  
24 TYPE: PRT  
25 ORGANISM: Artificial Sequence

FEATURE:  
1 OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-780

Query Match 36.4% Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RSKS 10  
111  
DB 7 RSKS 10

RESULT 31  
US-09-932-165-1416  
1 Sequence 1416, Application US/09/932-165  
2 Publication No. US20030134784A1  
3 GENERAL INFORMATION:  
4 APPLICANT: RATTANOL, ARTHUR  
5 APPLICANT: CHALLITA-ELD, PIA M.  
6 APPLICANT: FARIS, MARY  
7 APPLICANT: SAFERAN, DOUGLAS  
8 APPLICANT: AFAR, DANIEL  
9 APPLICANT: LEVIN, ELANA  
10 APPLICANT: HUBERT, RENE  
11 APPLICANT: GE, WANGMAO  
12 APPLICANT: JAKOBOWITZ, AYA  
13 TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED  
14 TITLE OF INVENTION: BAP2H3 AND CatF2E11 USEFUL IN TREATMENT AND  
15 TITLE OF INVENTION: DETECTION OF CANCER  
16 FILE REFERENCE: 51158-20014-00  
17 CURRENT APPLICATION NUMBER: US/09/932-165  
18 PRIOR APPLICATION NUMBER: 60/226,129  
19 PRIOR FILING DATE: 2003-08-17  
20 NUMBER OF SEQ ID NOS: 1508  
21 SOFTWARE: PatentIn Ver. 2.1  
22 SEQ ID NO 1416  
23 LENGTH: 10  
24 TYPE: PRT  
25 ORGANISM: Artificial Sequence  
26 FEATURE:  
27 OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-932-165-1416

Query Match 36.4% Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4; 4e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RSKS 11  
111  
DB 1 RSKS 4

RESULT 32  
US-09-572-270A-554  
1 Sequence 654, Application US/09/572-270A  
2 Publication No. US20030148458A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Proteom Ltd  
5 TITLE OF INVENTION: Inter- complementary peptide listing  
6 FILE REFERENCE:  
7 CURRENT APPLICATION NUMBER: US/09/572,270A  
8 CURRENT FILING DATE: 2000-05-17  
9 NUMBER OF SEQ ID NOS: 1144  
10 SOFTWARE: ProPatent version 1.0  
11 SEQ ID NO 654  
12 LENGTH: 10  
13 TYPE: PRT  
14 ORGANISM: Arabidopsis thaliana  
15 OTHER INFORMATION: Sequence located in Gaps OR f3f17.8. at 199-208 and may  
US-09-572-270A-554

Query Match 36.4% Score 4: DB 12: Length 10:  
 Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 7 PKSK 10

## RESULT 44

US-09-945 484-10

Sequence 97: Application US/09/945 604

Publication No. US20030166526A1

GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA

APPLICANT: HUBERT, RENE

APPLICANT: RAITANO, ARTHUR

APPLICANT: AFAR, DANIEL

APPLICANT: LEVIN, ELANA

APPLICANT: FARIS, MARY

APPLICANT: GE, WANGMAO

APPLICANT: JAKOBOWITZ, AYA

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P114

TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

TITLE OF INVENTION: OTHER CANCERS

FILE REFERENCE: 51158-2003-00

CURRENT APPLICATION NUMBER: US/09/945 604

CURRENT FILING DATE: 2003 09 22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2000 08 22

NUMBER OF SEQ ID NOS: 783

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 97

LENGTH 10

TYPE: PRT

ORGANISM: Homo sapiens

US-09-945 484-10

## Query Match

Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 7 PKSK 10

## RESULT 41

US-09-945 484-10

Sequence 161: Application US/09/945 604

Publication No. US20030166526A1

GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA

APPLICANT: HUBERT, RENE

APPLICANT: RAITANO, ARTHUR

APPLICANT: AFAR, DANIEL

APPLICANT: LEVIN, ELANA

APPLICANT: FARIS, MARY

APPLICANT: GE, WANGMAO

APPLICANT: JAKOBOWITZ, AYA

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P114

TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

TITLE OF INVENTION: OTHER CANCERS

FILE REFERENCE: 51158-2003-00

CURRENT APPLICATION NUMBER: US/09/945 604

CURRENT FILING DATE: 2003 09 22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2000 08 22

NUMBER OF SEQ ID NOS: 783

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 10

LENGTH 10

TYPE: PRT

ORGANISM: Homo sapiens  
 US-09-945 484-10

Query Match 36.4% Score 4: DB 12: Length 10:  
 Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 4 PKSK 7

## RESULT 45

US-09-945 484-275

Sequence 275: Application US/09/945 384

Publication No. US20030166526A1

GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA

APPLICANT: HUBERT, RENE

APPLICANT: RAITANO, ARTHUR

APPLICANT: AFAR, DANIEL

APPLICANT: LEVIN, ELANA

APPLICANT: FARIS, MARY

APPLICANT: GE, WANGMAO

APPLICANT: JAKOBOWITZ, AYA

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P114

TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

TITLE OF INVENTION: OTHER CANCERS

FILE REFERENCE: 51158-2003-00

CURRENT APPLICATION NUMBER: US/09/945 384

CURRENT FILING DATE: 2003 08 22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2000 08 22

NUMBER OF SEQ ID NOS: 783

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 275

LENGTH 10

TYPE: PRT

ORGANISM: Homo sapiens

US-09-945 484-275

## Query Match

Best Local Similarity 100.0% Prod. No. 4.3e+02:  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 PKSK 10  
 111  
 10 4 PKSK 7

## RESULT 46

US-09-945 484-072

Sequence 372: Application US/09/945 384

Publication No. US20030166526A1

GENERAL INFORMATION:

APPLICANT: CHALLITA-EID, PIA

APPLICANT: HUBERT, RENE

APPLICANT: RAITANO, ARTHUR

APPLICANT: AFAR, DANIEL

APPLICANT: LEVIN, ELANA

APPLICANT: FARIS, MARY

APPLICANT: GE, WANGMAO

APPLICANT: JAKOBOWITZ, AYA

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P114

TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

TITLE OF INVENTION: OTHER CANCERS

FILE REFERENCE: 51158-2003-00

CURRENT APPLICATION NUMBER: US/09/945 384

CURRENT FILING DATE: 2003 08 22

PRIOR APPLICATION NUMBER: 60/227,098

PRIOR FILING DATE: 2000 08 22

NUMBER OF SEQ ID NOS: 783

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 72

LENGTH 10

TYPE: PRT





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: STATE: New York
: COUNTRY: United States of America
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: DISKETTE, 5.25, 360 KB, 5 1/4"
: COMPUTER: COMPAQ, PROLIMA MI 4700
: OPERATING SYSTEM: DOS 5.0
: SOFTWARE: WORD PERFECT 5.2
: CURRENT APPLICATION NUMBER: US/09/096-246
: FILING DATE: 14-Mar-2002
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/99/119,044
: FILING DATE: 10-Sep-1999
: ATTORNEY/AGENT INFORMATION:
: NAME: Adja C. Gouffier, Esq.
: REGISTRATION NUMBER: 29,734
: REFERENCE/DOCKET NUMBER: 5999/119,044 US
: TELEPHONE: (212) 527-7700
: TELEFAX: (212) 753-5257
: TELEX: 246687
: INFORMATION FOR SEQ ID NO: 27:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: COMPOSITION: unknown
: OTHER INFORMATION: DESCRIPTION: SEQ ID NO: 27.
US 10 096-246 27
:
: Query Match 36.4% Score 4: DB 11: Length 11:
: Best Local Similarity 100.0% Pident No. 4 4.7e-02:
: Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 5 REK 8
: ID 111
: DB 1 REK 11
:
: RESULT 44
: US 10 039-645 3
: Sequence 3: Application US/10049645
: Publication No. US2002047170A1
: GENERAL INFORMATION:
: APPLICANT: Kopin, Alan S.
: TITLE OF INVENTION: Constitutively Active, Hypersensitive,
: FILE REFERENCE: 60496/51002
: CURRENT APPLICATION NUMBER: US/10/039,645
: CURRENT FILING DATE: 2001-10-25
: PRIOR APPLICATION NUMBER: US 60/243,550
: PRIOR FILING DATE: 2000-11-25
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 11
: TYPE: PKT
: ORGANISM: Homo sapiens
: US 10 039-645 4
:
: Query Match 36.4% Score 4: DB 14: Length 11:
: Best Local Similarity 100.0% Pident No. 4 4.7e-02:
: Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 5 REK 8
: ID 111
: DB 1 REK 4
:
: RESULT 44
: US 10 139-084 4
: Sequence 1: Application US/13149084
: Publication No. US2003087313A1
: GENERAL INFORMATION:
: APPLICANT: Kopin, Alan S.
: TITLE OF INVENTION: Base Response-Based Methods for
: TITLE OF INVENTION: Identifying Receptors Having Alterations in Signaling
: FILE REFERENCE: 60494/51502
: CURRENT APPLICATION NUMBER: US/10/139,084
:
: Query Match 36.6% Score 4: DB 1: Length 11:
: Best Local Similarity 100.0% Pident No. 4 4.7e-02:
: Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 5 REK 8
: ID 111
: DB 1 REK 4
:
: RESULT 44
: US 09 576-904A-239
: Sequence 3: Application US/09576904A
: Publication No. US2003007279A1
: GENERAL INFORMATION:
: APPLICANT: BEULIKAS, JENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMIID DNA (LIPIDGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSIOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
: FILE REFERENCE: 16 2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 65/219,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 239
: LENGTH: 11
: TYPE: PKT
: ORGANISM: Unknown organism
: FEATURES:
: OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein
US 09 576-904A-239

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1 CURRENT FILING DATE: 2002-12-23  
 2 PRIOR APPLICATION NUMBER: US 69/288,547  
 3 PRIOR FILING DATE: 2001-05-03  
 4 NUMBER OF SEQ ID NOS: 74  
 5 SOFTWARE: FASTSEQ for Windows Version 4.0  
 6 SEQ ID NO: 4  
 7 LENGTH: 11  
 8 TYPE: PPT  
 9 ORGANISM: Homo sapiens  
 10 US 10-075-884-14

Quality Match: 46.4%; Score 4; Dk 15; Length 11;  
 Best Local Similarity: 100.0%; Pred. No. 5e+02;  
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 5 RRSK 8  
 1111  
 10 1 RRSK 4

RESULT 45  
 US 10 093-958-1  
 1 Sequence 1; Application US/1009358  
 2 Publication No. US2003064442A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Gillies, Stephen  
 5 APPLICANT: Jeffrey, Way  
 6 TITLE OF INVENTION: Expression Test-to-Body for Proteins Containing a Hybrid Isotype At  
 7 FILE REFERENCE: MO1074  
 8 CURRENT APPLICATION NUMBER: US/10/093-958  
 9 PRIOR FILING DATE: 2002-04-07  
 10 PRIOR APPLICATION NUMBER: US 60/274,196  
 11 PRIOR FILING DATE: 2001-04-07  
 12 NUMBER OF SEQ ID NOS: 50  
 13 SOFTWARE: Patent In Ver. 2.1  
 14 SEQ ID NO: 1  
 15 LENGTH: 12  
 16 TYPE: PPT  
 17 ORGANISM: artificial sequence  
 18 FEATURE:  
 19 OTHER INFORMATION: IgG2 hinge sequence  
 20 US 10 093-958-1

Quality Match: 46.4%; Score 4; Dk 15; Length 12;  
 Best Local Similarity: 100.0%; Pred. No. 5e+02;  
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 6 RRSK 9  
 1111  
 10 1 RRSK 4

RESULT 46  
 US 10 075-884-10  
 1 Sequence 12; Application US/1007589  
 2 Publication No. US20030104622A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Robbins, Paul E.  
 5 APPLICANT: Mi, Zhibao  
 6 APPLICANT: Filizelli, Raymond  
 7 APPLICANT: Giortoso, Joseph C.  
 8 APPLICANT: Gambuto, Andrea  
 9 TITLE OF INVENTION: IDENTIFICATION OF PROTEIN-INDUCED  
 10 TITLE OF INVENTION: FACILITATE DECAE AND EYE PLACED ANALYSE AND/OR NDT-TEAR TRANSFER  
 11 FILE REFERENCE: OF PROTEINS, DNA AND VIRUSES  
 12 FILE REFERENCE: AP32573-AAA 072496-0-37  
 13 CURRENT APPLICATION NUMBER: US/10/075-889  
 14 CURRENT FILING DATE: 2002-02-24  
 15 PRIOR APPLICATION NUMBER: 60/151,980  
 16 PRIOR FILING DATE: 1999-09-01  
 17 PRIOR APPLICATION NUMBER: 60/288,444  
 18 PRIOR FILING DATE: 2000-03-14

1 NUMBER OF SEQ ID NOS: 99  
 2 SOFTWARE: FASTSEQ for Windows Version 4.0  
 3 SEQ ID NO: 10  
 4 LENGTH: 12  
 5 TYPE: PPT  
 6 ORGANISM: Artificial Sequence  
 7 FEATURE:  
 8 OTHER INFORMATION: Random peptide library  
 9 US 10 075-889-10

Quality Match: 46.4%; Score 4; Dk 15; Length 12;  
 Best Local Similarity: 100.0%; Pred. No. 5e+02;  
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 7 RRSK 10  
 1111  
 10 4 RRSK 7

RESULT 47  
 US 09 876-904A-79  
 1 Sequence 79; Application US/09876904A  
 2 Publication No. US20030672794A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: BOULIKAS, TENI  
 5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
 6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
 7 FILE REFERENCE: TH-2002-06  
 8 CURRENT APPLICATION NUMBER: US/09/876,904A  
 9 CURRENT FILING DATE: 2001-06-08  
 10 PRIOR APPLICATION NUMBER: US 60/210,925  
 11 PRIOR FILING DATE: 2000-06-09  
 12 NUMBER OF SEQ ID NOS: 629  
 13 SOFTWARE: Patent In Ver. 2.1  
 14 SEQ ID NO: 79  
 15 LENGTH: 13  
 16 TYPE: PPT  
 17 ORGANISM: Artificial Sequence  
 18 FEATURE:  
 19 OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide crossli  
 20 OTHER INFORMATION: to bovine serum albumin  
 21 US 09 876 904A-79

Quality Match: 46.4%; Score 4; Dk 11; Length 13;  
 Best Local Similarity: 100.0%; Pred. No. 5.4e+02;  
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ARRS 4  
 1111  
 10 5 ARRS 8

RESULT 48  
 US 09 876-904A-179  
 1 Sequence 196; Application US/09876904A  
 2 Publication No. US20030672794A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: BOULIKAS, TENI  
 5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
 6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
 7 FILE REFERENCE: TH-2002-06  
 8 CURRENT APPLICATION NUMBER: US/09/876,904A  
 9 CURRENT FILING DATE: 2001-06-08  
 10 PRIOR APPLICATION NUMBER: US 60/210,925  
 11 PRIOR FILING DATE: 2000-06-09  
 12 NUMBER OF SEQ ID NOS: 629  
 13 SOFTWARE: Patent In Ver. 2.1  
 14 SEQ ID NO: 179  
 15 LENGTH: 13  
 16 TYPE: PPT  
 17 ORGANISM: Artificial Sequence

1 FEATURE:  
2 OTHER INFORMATION: Karyophilic peptide  
3 US-09-876-904A-19b

Query Match 36.4% Score 47 DB 11 Length 15  
Best Local Similarity 100.0% Prod No. 60729  
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KSK 5  
II  
DB 5 KSK 8

RESULT 49

US-09-876-904A-454  
1 Sequence 454 Application: US/09870904A  
2 Publication No. US20030072794A1

3 GENERAL INFORMATION:

4 APPLICANT: BOEYKAS, TENJ

5 TITLE OF INVENTION: ENCAPSULATION OF PLASMINOGEN ACTIVATOR (EC-GENES TM) AND THERAPEUTIC

6 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/PUS-AGENT PEPTIDE

7 TITLE OF INVENTION: CONJUGATES AND TARGETED LIPID-SOME COMPLEXES

8 FILE REFERENCE: TB-2002-00

9 CURRENT APPLICATION NUMBER: US/09/876-904A

10 CURRENT FILING DATE: 2001-06-08

11 PRIOR APPLICATION NUMBER: US 60/216,925

12 PRIOR FILING DATE: 2000-06-09

13 NUMBER OF SEQ ID NOS: 629

14 SOFTWARE: PatentIn Ver. 2.1

15 SEQ ID NO: 454

16 LENGTH: 14

17 TYPE: PRT

18 ORGANISM: Unknown organism

19 FEATURE:

20 OTHER INFORMATION: Description of Unknown organism: Mergo and human CR

21 OTHER INFORMATION: (glucocorticoid receptor)

US-09-876-904A-454

Query Match 36.4% Score 47 DB 11 Length 15  
Best Local Similarity 100.0% Prod No. 60729  
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 ASK 4  
II  
DB 2 ASK 6

RESULT 50

US-09-158-100A-42

1 Sequence 42 Application: US/0108100A

2 Publication No. US20030059805A1

3 GENERAL INFORMATION:

4 APPLICANT: RAPPOLD-HOERBRAND, GUILTON

5 APPLICANT: RAO, PROCOLE

6 TITLE OF INVENTION: HUMAN GROWTH GENE AND SEBT STRUCTURE GENE REGION

7 FILE REFERENCE: 108351-00004

8 CURRENT APPLICATION NUMBER: US/09/158-100A

9 CURRENT FILING DATE: 2002-08-23

10 PRIOR APPLICATION NUMBER: 09/147,699

11 PRIOR FILING DATE: 1999-06-24

12 PRIOR APPLICATION NUMBER: PCT/EP97/09,036

13 PRIOR FILING DATE: 1997-09-29

14 PRIOR APPLICATION NUMBER: 60/027,645

15 PRIOR FILING DATE: 1996-10-01

16 PRIOR APPLICATION NUMBER: EP/97100583.0

17 PRIOR FILING DATE: 1997-01-16

18 NUMBER OF SEQ ID NOS: 55

19 SOFTWARE: PatentIn Ver. 2.1

20 SEQ ID NO: 42

21 LENGTH: 15

22 TYPE: PRT

23 ORGANISM: Artificial Sequence

24 FEATURE:

1 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
2 OTHER INFORMATION: peptide  
3 US-10-158-160A-42

Query Match 36.4% Score 47 DB 15 Length 15  
Best Local Similarity 100.0% Prod No. 60729  
Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KSK 11  
II  
DB 2 KSK 11

Search completed: September 30, 2003, 15:33:01  
Job time: 22.5 secs

GenCore version 5.1.4  
Copyright (c) 1993 - 2003 CompuGen Ltd.

100 proteins - protein search, using sw model

Run on: September 30, 2003, 10:11:03 - Search time 21.5 seconds  
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77,413 million cell updates/sec

Title: US-09-787-443-15

Perfect score: 11

Sequence: 1 ASQAKKKGPR 11

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

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Word size: 0

Total number of hits satisfying chosen parameters: 6687

Minimum hit seq length: 8

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Post processing: Listing first 500 summaries

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18: /cgn2\_6/ptodata/2/pubaa/US09A\_P1B.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	5	45.5	13	10	US-09-746-170-2	Sequence 2, Appl
2	5	45.5	13	10	US-09-746-170-5	Sequence 5, Appl
3	5	45.5	13	10	US-09-746-170-8	Sequence 6, Appl
4	5	45.5	13	10	US-09-746-170-11	Sequence 11, Appl
5	5	45.5	13	10	US-09-746-170-14	Sequence 14, Appl
6	5	45.5	13	10	US-09-746-170-17	Sequence 17, Appl
7	5	45.5	13	10	US-09-746-170-20	Sequence 20, Appl
8	5	45.5	13	10	US-09-746-170-23	Sequence 23, Appl
9	5	45.5	13	10	US-09-746-170-26	Sequence 26, Appl
10	5	45.5	13	10	US-09-746-170-29	Sequence 29, Appl
11	5	45.5	13	10	US-09-746-170-32	Sequence 32, Appl
12	5	45.5	13	10	US-09-746-170-35	Sequence 35, Appl
13	5	45.5	13	10	US-09-746-170-38	Sequence 38, Appl
14	5	45.5	13	10	US-09-746-170-41	Sequence 41, Appl
15	4	36.4	8	9	US-09-243-079-43	Sequence 43, Appl
16	4	36.4	8	9	US-09-243-079-44	Sequence 44, Appl
17	4	36.4	8	9	US-09-243-079-45	Sequence 45, Appl

16	4	36.4	8	9	US-09-243-079-46	Sequence 46, Appl
17	4	36.4	8	9	US-09-243-079-47	Sequence 47, Appl
18	4	36.4	8	11	US-09-726-470A-28	Sequence 28, Appl
19	4	36.4	8	11	US-09-726-470A-35	Sequence 35, Appl
20	4	36.4	8	11	US-09-726-470A-37	Sequence 37, Appl
21	4	36.4	8	11	US-09-726-470A-40	Sequence 40, Appl
22	4	36.4	8	11	US-09-726-470A-42	Sequence 42, Appl
23	4	36.4	8	11	US-09-726-470A-43	Sequence 43, Appl
24	4	36.4	8	11	US-09-726-470A-44	Sequence 44, Appl
25	4	36.4	8	11	US-09-726-470A-45	Sequence 45, Appl
26	4	36.4	8	11	US-09-726-470A-46	Sequence 46, Appl
27	4	36.4	8	11	US-09-726-470A-55	Sequence 55, Appl
28	4	36.4	8	11	US-09-726-470A-75	Sequence 75, Appl
29	4	36.4	8	11	US-09-726-470A-76	Sequence 76, Appl
30	4	36.4	8	11	US-09-726-470A-77	Sequence 77, Appl
31	4	36.4	8	11	US-09-726-470A-78	Sequence 78, Appl
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33	4	36.4	8	11	US-09-726-470A-80	Sequence 80, Appl
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39	4	36.4	8	11	US-09-726-470A-86	Sequence 86, Appl
40	4	36.4	8	11	US-09-726-470A-87	Sequence 87, Appl
41	4	36.4	8	11	US-09-726-470A-88	Sequence 88, Appl
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45	4	36.4	8	11	US-09-726-470A-92	Sequence 92, Appl
46	4	36.4	8	11	US-09-726-470A-94	Sequence 94, Appl
47	4	36.4	8	11	US-09-726-470A-95	Sequence 95, Appl
48	4	36.4	8	11	US-09-726-470A-96	Sequence 96, Appl
49	4	36.4	8	11	US-09-726-470A-97	Sequence 97, Appl
50	4	36.4	8	11	US-09-726-470A-98	Sequence 98, Appl
51	4	36.4	8	11	US-09-726-470A-99	Sequence 99, Appl
52	4	36.4	8	11	US-09-726-470A-100	Sequence 100, Appl
53	4	36.4	8	11	US-09-726-470A-101	Sequence 101, Appl
54	4	36.4	8	11	US-09-726-470A-102	Sequence 102, Appl
55	4	36.4	8	11	US-09-726-470A-103	Sequence 103, Appl
56	4	36.4	8	11	US-09-726-470A-104	Sequence 104, Appl
57	4	36.4	8	11	US-09-726-470A-105	Sequence 105, Appl
58	4	36.4	8	11	US-09-726-470A-106	Sequence 106, Appl
59	4	36.4	8	11	US-09-726-470A-107	Sequence 107, Appl
60	4	36.4	8	11	US-09-726-470A-110	Sequence 110, Appl
61	4	36.4	8	11	US-09-726-470A-111	Sequence 111, Appl
62	4	36.4	8	11	US-09-726-470A-114	Sequence 114, Appl
63	4	36.4	8	11	US-09-726-470A-116	Sequence 116, Appl
64	4	36.4	8	11	US-09-726-470A-119	Sequence 119, Appl
65	4	36.4	8	11	US-09-726-470A-121	Sequence 121, Appl
66	4	36.4	8	11	US-09-726-470A-124	Sequence 124, Appl
67	4	36.4	8	11	US-09-726-470A-125	Sequence 125, Appl
68	4	36.4	8	11	US-09-726-470A-135	Sequence 135, Appl
69	4	36.4	8	11	US-09-726-470A-136	Sequence 136, Appl
70	4	36.4	8	11	US-09-726-470A-137	Sequence 137, Appl
71	4	36.4	8	11	US-09-726-470A-138	Sequence 138, Appl
72	4	36.4	8	11	US-09-726-470A-139	Sequence 139, Appl
73	4	36.4	8	11	US-09-726-470A-140	Sequence 140, Appl
74	4	36.4	8	11	US-09-726-470A-141	Sequence 141, Appl
75	4	36.4	8	11	US-09-726-470A-142	Sequence 142, Appl
76	4	36.4	8	11	US-09-726-470A-143	Sequence 143, Appl
77	4	36.4	8	11	US-09-726-470A-144	Sequence 144, Appl
78	4	36.4	8	11	US-09-726-470A-145	Sequence 145, Appl
79	4	36.4	8	11	US-09-726-470A-146	Sequence 146, Appl
80	4	36.4	8	11	US-09-726-470A-147	Sequence 147, Appl
81	4	36.4	8	11	US-09-726-470A-148	Sequence 148, Appl
82	4	36.4	8	11	US-09-726-470A-149	Sequence 149, Appl
83	4	36.4	8	11	US-09-726-470A-150	Sequence 150, Appl
84	4	36.4	8	11	US-09-726-470A-151	Sequence 151, Appl
85	4	36.4	8	11	US-09-726-470A-152	Sequence 152, Appl
86	4	36.4	8	11	US-09-726-470A-153	Sequence 153, Appl
87	4	36.4	8	11	US-09-726-470A-154	Sequence 154, Appl
88	4	36.4	8	11	US-09-726-470A-155	Sequence 155, Appl







```

Query Match 45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKG 9
DB 11 1
7 KKKKG 11

RESULT 2
US-09-746-170-6
: Sequence 5, Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 5
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-5
Query Match 45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKG 9
DB 11 1
7 KKKKG 11

RESULT 3
US-09-746-170-8
: Sequence 8, Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 8
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-7
Query Match 45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKG 9
DB 11 1
7 KKKKG 11

RESULT 4
US-09-746-170-11
: Sequence 11, Application US/09746170
: Patent No. US20020127543A1

```

```

: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 11
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-11
Query Match 45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKG 9
DB 11 1
7 KKKKG 11

RESULT 5
US-09-746-170-14
: Sequence 14, Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 14
: LENGTH: 13
: TYPE: PKT
: ORGANISM: Hepatitis C virus
US-09-746-170-14
Query Match 45.5%; Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKG 9
DB 11 1
7 KKKKG 11

RESULT 6
US-09-746-170-17
: Sequence 17, Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karn, Jonathan
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
: FILE REFERENCE: 22620/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 17
: LENGTH: 13

```



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1  TYPE: Pst
2  ORGANISM: Hepatitis C Virus
US-09-746-170-17

Query Match 45.5% Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

CY 5 KRRKG 9
DB 7 KRRKG 11

RESULT 7
US-09-746-170-20
1 Sequence 20; Application US/09746170
2 Patent No. US20020127543A1
3 GENERAL INFORMATION:
4 APPLICANT: Karn, Jonathan
5 TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
6 FILE REFERENCE: 22620/1280
7 CURRENT APPLICATION NUMBER: US/09/746,170
8 CURRENT FILING DATE: 2000-12-22
9 PRIOR APPLICATION NUMBER: 60/171,804
10 PRIOR FILING DATE: 1999-12-22
11 NUMBER OF SEQ ID NOS: 48
12 SOFTWARE: PatentIn version 3.0
13 SEQ ID NO 20
14 LENGTH: 13
15 TYPE: PRT
16 ORGANISM: Hepatitis C Virus
US-09-746-170-20

Query Match 45.5% Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

CY 5 KRRKG 9
DB 7 KRRKG 11

RESULT 10
US-09-746-170-30
1 Sequence 30; Application US/09746170
2 Patent No. US20020127543A1
3 GENERAL INFORMATION:
4 APPLICANT: Karn, Jonathan
5 TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
6 FILE REFERENCE: 22620/1280
7 CURRENT APPLICATION NUMBER: US/09/746,170
8 CURRENT FILING DATE: 2000-12-22
9 PRIOR APPLICATION NUMBER: 60/171,804
10 PRIOR FILING DATE: 1999-12-22
11 NUMBER OF SEQ ID NOS: 48
12 SOFTWARE: PatentIn version 3.0
13 SEQ ID NO 30
14 LENGTH: 13
15 TYPE: PRT
16 ORGANISM: Hepatitis C Virus
US-09-746-170-30

Query Match 45.5% Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

CY 5 KRRKG 9
DB 7 KRRKG 11

RESULT 11
US-09-746-170-43
1 Sequence 33; Application US/09746170
2 Patent No. US20020127543A1
3 GENERAL INFORMATION:
4 APPLICANT: Karn, Jonathan
5 TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
6 FILE REFERENCE: 22620/1280
7 CURRENT APPLICATION NUMBER: US/09/746,170
8 CURRENT FILING DATE: 2000-12-22
9 PRIOR APPLICATION NUMBER: 60/171,804
10 PRIOR FILING DATE: 1999-12-22
11 NUMBER OF SEQ ID NOS: 48
12 SOFTWARE: PatentIn version 3.0
13 SEQ ID NO 25
14 LENGTH: 13
15 TYPE: PRT
16 ORGANISM: Hepatitis C Virus
US-09-746-170-25

Query Match 45.5% Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

CY 5 KRRKG 9
DB 7 KRRKG 11

RESULT 26
US-09-746-170-26
1 Sequence 26; Application US/09746170
2 Patent No. US20020127543A1
3 GENERAL INFORMATION:
4 APPLICANT: Karn, Jonathan
5 TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecules
6 FILE REFERENCE: 22620/1280
7 CURRENT APPLICATION NUMBER: US/09/746,170
8 CURRENT FILING DATE: 2000-12-22
9 PRIOR APPLICATION NUMBER: 60/171,804
10 PRIOR FILING DATE: 1999-12-22
11 NUMBER OF SEQ ID NOS: 48
12 SOFTWARE: PatentIn version 3.0
13 SEQ ID NO 25
14 LENGTH: 13
15 TYPE: PRT
16 ORGANISM: Hepatitis C Virus
US-09-746-170-25

Query Match 45.5% Score 5; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

CY 5 KRRKG 9
DB 7 KRRKG 11
```

1 NUMBER OF SEQ ID NOS: 49  
 2 SOFTWARE: PatentIn version 3.0  
 3 SEQ ID NO 43  
 4 LENGTH: 13  
 5 TYPE: PRT  
 6 ORGANISM: Hepatitis C virus  
 7 US-09-746-170 43

Query Match 45.5% Score 61 DB 10 Length 13  
 Best Local Similarity 100.0% Pred. No. 0  
 Matches 5: Conservative 0: Mismatches 0: Gaps 0:

QY 5 KRRK 9  
 DB 7 KRRK 12

RESULT 12

1 US-09-746-170 46  
 2 Sequence 46: Application US/09746170  
 3 Patent No. US20020127543A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Bernat, Alberto  
 6 TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY  
 7 FILE REFERENCE: 29928-PCT-USA 1  
 8 CURRENT FILING DATE: 1999-02-02  
 9 PRIOR APPLICATION NUMBER: US/09/243,079  
 10 PRIOR FILING DATE: 1994-11-10  
 11 PRIOR APPLICATION NUMBER: PCT/179/00049  
 12 PRIOR FILING DATE: 1993-05-10  
 13 NUMBER OF SEQ ID NOS: 48  
 14 SOFTWARE: PatentIn version 3.0  
 15 SEQ ID NO 46  
 16 LENGTH: 13  
 17 TYPE: PRT  
 18 ORGANISM: Human Immunodeficiency Virus  
 19 US-09-746-170 46

Query Match 45.5% Score 61 DB 10 Length 13  
 Best Local Similarity 100.0% Pred. No. 0  
 Matches 5: Conservative 0: Mismatches 0: Gaps 0:

QY 5 KRRK 9  
 DB 7 KRRK 12

RESULT 14

1 US-09-243-079 45  
 2 Sequence 45: Application US/09243079  
 3 Patent No. US2002081566A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Bernat, Alberto  
 6 TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY  
 7 FILE REFERENCE: 29928-PCT-USA 1  
 8 CURRENT FILING DATE: 1999-02-02  
 9 PRIOR APPLICATION NUMBER: US/09/243,079  
 10 PRIOR FILING DATE: 1994-11-10  
 11 PRIOR APPLICATION NUMBER: PCT/179/00049  
 12 PRIOR FILING DATE: 1993-05-10  
 13 NUMBER OF SEQ ID NOS: 89  
 14 SOFTWARE: FastSeq for Windows Version 3.0  
 15 SEQ ID NO 45  
 16 LENGTH: 8  
 17 TYPE: PRT  
 18 ORGANISM: Human Immunodeficiency Virus  
 19 US-09-243-079 45

Query Match 45.4% Score 61 DB 10 Length 13

Best Local Similarity 100.0% Pred. No. 50057  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 4 AKRR 7  
 DB 5 AKRR 8

RESULT 14

1 US-09-243-079 44  
 2 Sequence 44: Application US/09243079  
 3 Patent No. US2002081566A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Bernat, Alberto  
 6 TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY  
 7 FILE REFERENCE: 29928-PCT-USA 1  
 8 CURRENT FILING DATE: 1999-02-02  
 9 PRIOR APPLICATION NUMBER: US/09/243,079  
 10 PRIOR FILING DATE: 1994-11-10  
 11 PRIOR APPLICATION NUMBER: PCT/179/00049  
 12 PRIOR FILING DATE: 1993-05-10  
 13 PRIOR APPLICATION NUMBER: PCT/179/00049  
 14 PRIOR FILING DATE: 1993-05-10  
 15 NUMBER OF SEQ ID NOS: 69  
 16 SOFTWARE: FastSeq for Windows Version 3.0  
 17 SEQ ID NO 44  
 18 LENGTH: 8  
 19 TYPE: PRT  
 20 ORGANISM: Human Immunodeficiency Virus  
 21 US-09-243-079 44

Query Match 45.4% Score 47 DB 9 Length 8  
 Best Local Similarity 100.0% Pred. No. 50057  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 4 AKRR 7  
 DB 4 AKRR 7

RESULT 15

1 US-09-243-079 45  
 2 Sequence 45: Application US/09243079  
 3 Patent No. US2002081566A1  
 4 GENERAL INFORMATION:  
 5 APPLICANT: Bernat, Alberto  
 6 TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY  
 7 FILE REFERENCE: 29928-PCT-USA 1  
 8 CURRENT FILING DATE: 1999-02-02  
 9 PRIOR APPLICATION NUMBER: US/09/243,079  
 10 PRIOR FILING DATE: 1994-11-10  
 11 PRIOR APPLICATION NUMBER: PCT/179/00049  
 12 PRIOR FILING DATE: 1993-05-10  
 13 PRIOR APPLICATION NUMBER: PCT/179/00049  
 14 PRIOR FILING DATE: 1993-05-10  
 15 NUMBER OF SEQ ID NOS: 89  
 16 SOFTWARE: FastSeq for Windows Version 3.0  
 17 SEQ ID NO 45  
 18 LENGTH: 8  
 19 TYPE: PRT  
 20 ORGANISM: Human Immunodeficiency Virus  
 21 US-09-243-079 45

Query Match 45.4% Score 47 DB 9 Length 8  
 Best Local Similarity 100.0% Pred. No. 50057  
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 4 AKRR 7  
 DB 4 AKRR 7



```

RESULT 21
US-09-726-470A-43
1 Sequence 43, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GC1-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 PRIOR FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 43
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence
22 FEATURES:
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived
24 OTHER INFORMATION: peptide
US-09-726-470A 37

```

```

Query Match 36.4% Score 47 DB 11 Length 8
Post Local Similarity 100.0% Pred No. 5e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

RESULT 21
US-09-726-470A-43
1 Sequence 40, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GC1-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 PRIOR FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 40
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence
22 FEATURES:
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived
24 OTHER INFORMATION: peptide
25 OTHER INFORMATION: Synthesised with free amino terminus and as the
26 OTHER INFORMATION: C-terminal carboxamide
US-09-726-470A 40

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```

Query Match 36.4% Score 47 DB 11 Length 8
Post Local Similarity 100.0% Pred No. 5e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

US-09-726-470A-42
1 Sequence 42, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GC1-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 PRIOR FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 42
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence
22 FEATURES:
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived
24 OTHER INFORMATION: peptide
25 OTHER INFORMATION: Synthesised with free amino terminus and as the
26 OTHER INFORMATION: C-terminal carboxamide
US-09-726-470A-42

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```

Query Match 36.4% Score 47 DB 11 Length 8
Post Local Similarity 100.0% Pred No. 5e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

RESULT 21
US-09-726-470A-43
1 Sequence 43, Application: US/09726470A
2 Publication No.: US20030036628A1
3 GENERAL INFORMATION:
4 APPLICANT: Zheleva, Daniela I
5 APPLICANT: Fischer, Peter M
6 APPLICANT: McInnes, Campbell
7 APPLICANT: Andrews, Martin J
8 APPLICANT: Chan, Weng C
9 APPLICANT: Atkinson, Gail E
10 TITLE OF INVENTION: p21 Peptides
11 FILE REFERENCE: GC1-014
12 CURRENT APPLICATION NUMBER: US/09/726,470A
13 PRIOR FILING DATE: 2000-11-29
14 PRIOR APPLICATION NUMBER: GB 9928423.6
15 PRIOR FILING DATE: 1999-11-30
16 NUMBER OF SEQ ID NOS: 275
17 SOFTWARE: Patent In Ver. 2.1
18 SEQ ID NO 43
19 LENGTH: 8
20 TYPE: PRI
21 ORGANISM: Artificial Sequence

```

1 FEATURE:  
 2 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 3 FEATURE:  
 4 OTHER INFORMATION: peptide  
 5 FEATURE:  
 6 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 7 OTHER INFORMATION: C-terminal carboxamide  
 8 FEATURE:  
 9 NAME/KEY: SITE  
 10 LOCATION: (1)  
 11 OTHER INFORMATION: Xaa - 2 Thionylalanine  
 12 US-09-726-470A-43

Query Match 36.4% Score 41 bp 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 4 AKRR 7  
 III  
 2 AKRR 5

RESULT 24  
 US-09-726-470A-44  
 1 Sequence 44: Application US/09/21470A  
 2 Publication No. US20030046628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela I  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McIntus, Campbell  
 7 APPLICANT: Andrews, Martin J  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 FILE REFERENCE: p21 Peptides  
 11 CURRENT APPLICATION NUMBER: US/09/21470A  
 12 PRIOR FILING DATE: 2000-11-29  
 13 PRIOR FILING DATE: 1999-11-30  
 14 NUMBER OF SEQ ID NOS: 275  
 15 SOFTWARE: Patent In Ver. 2.1  
 16 SEQ ID NO 44  
 17 LENGTH: 8  
 18 TYPE: PRT  
 19 ORGANISM: Artificial Sequence  
 20 FEATURE:  
 21 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 22 OTHER INFORMATION: peptide  
 23 FEATURE:  
 24 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 25 OTHER INFORMATION: C-terminal carboxamide  
 26 NAME/KEY: SITE  
 27 LOCATION: (1)  
 28 OTHER INFORMATION: Xaa - Histosethine  
 29 US-09-726-470A-44

Query Match 36.4% Score 41 bp 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 4 AKRR 7  
 III  
 2 AKRR 5

RESULT 25  
 US-09-726-470A-45  
 1 Sequence 45: Application US/09/21470A  
 2 Publication No. US20030046628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela I  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McIntus, Campbell

1 APPLICANT: Andrews, Martin J  
 2 APPLICANT: Chan, Weng C  
 3 APPLICANT: Atkinson, Gail E  
 4 FILE REFERENCE: p21 Peptides  
 5 FILE REFERENCE: CCI-014  
 6 CURRENT APPLICATION NUMBER: US/09/226-470A  
 7 PRIOR FILING DATE: 2000-11-29  
 8 PRIOR FILING DATE: 1999-11-30  
 9 NUMBER OF SEQ ID NOS: 275  
 10 SOFTWARE: Patent In Ver. 2.1  
 11 SEQ ID NO 45  
 12 LENGTH: 8  
 13 TYPE: PRT  
 14 ORGANISM: Artificial Sequence  
 15 FEATURE:  
 16 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 17 OTHER INFORMATION: peptide  
 18 FEATURE:  
 19 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 20 OTHER INFORMATION: C-terminal carboxamide  
 21 US-09-726-470A-45

Query Match 36.4% Score 41 bp 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 4 AKRR 7  
 III  
 2 AKRR 5

RESULT 26  
 US-09-726-470A-46  
 1 Sequence 46: Application US/09/26470A  
 2 Publication No. US20030046628A1  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Zheleva, Daniela I  
 5 APPLICANT: Fischer, Peter M  
 6 APPLICANT: McIntus, Campbell  
 7 APPLICANT: Andrews, Martin J  
 8 APPLICANT: Chan, Weng C  
 9 APPLICANT: Atkinson, Gail E  
 10 FILE REFERENCE: p21 Peptides  
 11 FILE REFERENCE: CCI-014  
 12 CURRENT APPLICATION NUMBER: US/09/226-470A  
 13 PRIOR FILING DATE: 2000-11-29  
 14 PRIOR FILING DATE: 1999-11-30  
 15 NUMBER OF SEQ ID NOS: 275  
 16 SOFTWARE: Patent In Ver. 2.1  
 17 SEQ ID NO 46  
 18 LENGTH: 8  
 19 TYPE: PRT  
 20 ORGANISM: Artificial Sequence  
 21 FEATURE:  
 22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 23 OTHER INFORMATION: peptide  
 24 FEATURE:  
 25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 26 OTHER INFORMATION: C-terminal carboxamide  
 27 NAME/KEY: SITE  
 28 LOCATION: (1)  
 29 OTHER INFORMATION: Xaa - L-L-Glutamyl-L-proline acid  
 30 US-09-726-470A-46

Query Match 36.4% Score 41 bp 11 Length 8  
 Best Local Similarity 100.0% Pred. No. 5e-05  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 4 AKRR 7  
 III

DB 2 AKRR 5

RESULT 27  
US 09-726-470A-55  
; Sequence 75, Application US/09726475A  
; Publication No. US20030036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; TITLE OF INVENTION: p21 Peptides  
; FILE REFERENCE: CCI-014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: GR 9928323.6  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 55  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; FEATURE:  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09-726-470A-55

Query Match 36.4% Score 4: DB 11: Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 AKRR 7  
DB 2 AKRR 5

RESULT 28 US 09-726-470A-75  
; Sequence 75, Application US/09726475A  
; Publication No. US20030036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; TITLE OF INVENTION: p21 Peptides  
; FILE REFERENCE: CCI-014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: GR 9928323.6  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 75  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; FEATURE:  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09-726-470A-75

Query Match 36.4% Score 4: DB 11: Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 AKRR 7  
DB 2 AKRR 5

RESULT 29 US 09-726-470A-76  
; Sequence 76, Application US/09726476A  
; Publication No. US20030036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; TITLE OF INVENTION: p21 Peptides  
; FILE REFERENCE: CCI-014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: GR 9928323.6  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 76  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; FEATURE:  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09-726-470A-76

Query Match 36.4% Score 4: DB 11: Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 AKRR 7  
DB 2 AKRR 5

RESULT 30 US 09-726-470A-77  
; Sequence 77, Application US/09726477A  
; Publication No. US20030036628A1  
; GENERAL INFORMATION:  
; APPLICANT: Zheleva, Daniela I  
; APPLICANT: Fischer, Peter M  
; APPLICANT: McInnes, Campbell  
; APPLICANT: Andrews, Martin JI  
; APPLICANT: Chan, Weng C  
; APPLICANT: Atkinson, Gail E  
; TITLE OF INVENTION: p21 Peptides  
; FILE REFERENCE: CCI-014  
; CURRENT APPLICATION NUMBER: US/09/726,470A  
; PRIOR FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: GR 9928323.6  
; PRIOR FILING DATE: 1999-11-30  
; NUMBER OF SEQ ID NOS: 275  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 77  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
; OTHER INFORMATION: peptide  
; FEATURE:  
; OTHER INFORMATION: Synthesised with free amino terminus and as the  
; OTHER INFORMATION: C-terminal carbamide  
US 09-726-470A-77

1 FEATURE:  
2 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
3 OTHER INFORMATION: peptide  
4 FEATURE:  
5 OTHER INFORMATION: Synthesised with free amino terminus and as the  
6 OTHER INFORMATION: C-terminal carboxamide  
7 FEATURE:  
8 NAME/KEY: SITE  
9 LOCATION: (6)  
10 OTHER INFORMATION: Xaa - D Leu  
11 US-09-726-470A-77

Query Match: 36.4% Score 47 DB 11 Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
DB 1  
2 AKKR 5

RESULT 43  
US-09-726-470A-78  
1 Sequence 78, Application US/09726470A  
2 Publication No. US2003036628A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Zheleva, Daniela I  
5 APPLICANT: Fischer, Peter M  
6 APPLICANT: McInnes, Campbell  
7 APPLICANT: Andrews, Martin JI  
8 APPLICANT: Chan, Weng C  
9 APPLICANT: Atkinson, Gail E  
10 TITLE OF INVENTION: p21 Peptides  
11 FILE REFERENCE: C01-014  
12 CURRENT APPLICATION NUMBER: US/09726470A  
13 PRIOR FILING DATE: 2000-11-29  
14 PRIOR APPLICATION NUMBER: GB 9928323.5  
15 NUMBER OF SEQ ID NOS: 275  
16 SOFTWARE: Patent In Ver. 2.1  
17 SEQ ID NO 78  
18 LENGTH: 8  
19 TYPE: PRI  
20 ORGANISM: Artificial Sequence  
21 FEATURE:  
22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
23 OTHER INFORMATION: peptide  
24 FEATURE:  
25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
26 OTHER INFORMATION: C-terminal carboxamide  
27 NAME/KEY: MQLSES  
28 LOCATION: (6)  
29 OTHER INFORMATION: Nle  
30 US-09-726-470A-78

Query Match: 36.4% Score 47 DB 11 Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
DB 1  
2 AKKR 5

RESULT 43  
US-09-726-470A-79  
1 Sequence 79, Application US/09726470A  
2 Publication No. US2003036628A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Zheleva, Daniela I  
5 APPLICANT: Fischer, Peter M  
6 APPLICANT: McInnes, Campbell  
7 APPLICANT: Andrews, Martin JI  
8 APPLICANT: Chan, Weng C  
9 APPLICANT: Atkinson, Gail E  
10 TITLE OF INVENTION: p21 Peptides  
11 FILE REFERENCE: C01-014  
12 CURRENT APPLICATION NUMBER: US/09726470A  
13 PRIOR FILING DATE: 2000-11-29  
14 PRIOR APPLICATION NUMBER: GB 9928323.5  
15 NUMBER OF SEQ ID NOS: 275  
16 SOFTWARE: Patent In Ver. 2.1  
17 SEQ ID NO 79  
18 LENGTH: 8  
19 TYPE: PRI  
20 ORGANISM: Artificial Sequence  
21 FEATURE:  
22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
23 OTHER INFORMATION: peptide  
24 FEATURE:  
25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
26 OTHER INFORMATION: C-terminal carboxamide  
27 NAME/KEY: MQLSES  
28 LOCATION: (6)  
29 OTHER INFORMATION: Nle  
30 US-09-726-470A-79

Query Match: 36.4% Score 47 DB 11 Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
DB 1  
2 AKKR 5

1 FILE REFERENCE: C01-014  
2 CURRENT APPLICATION NUMBER: US/09726470A  
3 CURRENT FILING DATE: 2000-11-29  
4 PRIOR APPLICATION NUMBER: GB 9928323.5  
5 PRIOR FILING DATE: 1999-11-30  
6 NUMBER OF SEQ ID NOS: 275  
7 SOFTWARE: Patent In Ver. 2.1  
8 SEQ ID NO 79  
9 LENGTH: 8  
10 TYPE: PRI  
11 ORGANISM: Artificial Sequence  
12 FEATURE:  
13 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
14 OTHER INFORMATION: peptide  
15 FEATURE:  
16 OTHER INFORMATION: Synthesised with free amino terminus and as the  
17 OTHER INFORMATION: C-terminal carboxamide  
18 NAME/KEY: MQLSES  
19 LOCATION: (6)  
20 OTHER INFORMATION: Nle  
21 US-09-726-470A-79

Query Match: 36.4% Score 47 DB 11 Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
DB 1  
2 AKKR 5

RESULT 43  
US-09-726-470A-80  
1 Sequence 80, Application US/09726470A  
2 Publication No. US2003036628A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Zheleva, Daniela I  
5 APPLICANT: Fischer, Peter M  
6 APPLICANT: McInnes, Campbell  
7 APPLICANT: Andrews, Martin JI  
8 APPLICANT: Chan, Weng C  
9 APPLICANT: Atkinson, Gail E  
10 TITLE OF INVENTION: p21 Peptides  
11 FILE REFERENCE: C01-014  
12 CURRENT APPLICATION NUMBER: US/09726470A  
13 CURRENT FILING DATE: 2000-11-29  
14 PRIOR APPLICATION NUMBER: GB 9928323.5  
15 PRIOR FILING DATE: 1999-11-30  
16 NUMBER OF SEQ ID NOS: 275  
17 SOFTWARE: Patent In Ver. 2.1  
18 SEQ ID NO 80  
19 LENGTH: 8  
20 TYPE: PRI  
21 ORGANISM: Artificial Sequence  
22 FEATURE:  
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
24 OTHER INFORMATION: peptide  
25 FEATURE:  
26 OTHER INFORMATION: Synthesised with free amino terminus and as the  
27 OTHER INFORMATION: C-terminal carboxamide  
28 NAME/KEY: MQLSES  
29 LOCATION: (6)  
30 OTHER INFORMATION: Nle  
31 US-09-726-470A-80

Query Match: 36.4% Score 47 DB 11 Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
DB 1  
2 AKKR 5

RESULT 44  
US-09-726-470A-81  
1 Sequence 81, Application US/09726470A  
2 Publication No. US2003036628A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Zheleva, Daniela I  
5 APPLICANT: Fischer, Peter M  
6 APPLICANT: McInnes, Campbell  
7 APPLICANT: Andrews, Martin JI  
8 APPLICANT: Chan, Weng C  
9 APPLICANT: Atkinson, Gail E  
10 TITLE OF INVENTION: p21 Peptides  
11 FILE REFERENCE: C01-014  
12 CURRENT APPLICATION NUMBER: US/09726470A  
13 PRIOR FILING DATE: 2000-11-29  
14 PRIOR APPLICATION NUMBER: GB 9928323.5  
15 NUMBER OF SEQ ID NOS: 275  
16 SOFTWARE: Patent In Ver. 2.1  
17 SEQ ID NO 81  
18 LENGTH: 8  
19 TYPE: PRI  
20 ORGANISM: Artificial Sequence  
21 FEATURE:  
22 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
23 OTHER INFORMATION: peptide  
24 FEATURE:  
25 OTHER INFORMATION: Synthesised with free amino terminus and as the  
26 OTHER INFORMATION: C-terminal carboxamide  
27 NAME/KEY: MQLSES  
28 LOCATION: (6)  
29 OTHER INFORMATION: Nle  
30 US-09-726-470A-81

Query Match: 36.4% Score 47 DB 11 Length 8;  
Best Local Similarity 100.0% Pred. No. 5e+05;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
DB 1  
2 AKKR 5

US 09-726 470A B2  
 ? Sequence B1: Application US/09/726 470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI 014  
 ? CURRENT APPLICATION NUMBER: US/09/726 470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 8:  
 ? LENGTH: 8  
 ? TYPE: P21  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesized with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? FEATURE:  
 ? NAME/KEY: MOD\_RES  
 ? LOCATION: 63  
 ? OTHER INFORMATION: Nva  
 ? US 09 726-470A B1

Query Match: 36.4% Score 41: 100.0% Length 8:  
 Best Local Similarity: 100.0%: Pctid No. 50-05:  
 Matches: 4: Conservative 0: Mismatches 0: Gaps 0:

QY 4 AKRR 7  
 ILL  
 DE 2 AKRR 5

US 09 726 470A B2  
 ? Sequence B2: Application US/09/726 470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI 014  
 ? CURRENT APPLICATION NUMBER: US/09/726 470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 12:  
 ? LENGTH: 8  
 ? TYPE: P21  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesized with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? FEATURE:

NAME/KEY: SITE  
 ? LOCATION: 67  
 ? OTHER INFORMATION: Xaa - Cysteine/alanine  
 ? US 09-726 470A B2  
 Query Match: 36.4% Score 41: 100.0% Length 8:  
 Best Local Similarity: 100.0%: Pctid No. 50-05:  
 Matches: 4: Conservative 0: Mismatches 0: Gaps 0:

QY 4 AKRR 7  
 ILL  
 DE 2 AKRR 5

US 09 726-470A B1  
 ? Sequence B3: Application US/09/726 470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI 014  
 ? CURRENT APPLICATION NUMBER: US/09/726 470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 8:  
 ? LENGTH: 8  
 ? TYPE: P21  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesized with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? US 09 726 470A B1

Query Match: 36.4% Score 41: 100.0% Length 8:  
 Best Local Similarity: 100.0%: Pctid No. 50-05:  
 Matches: 4: Conservative 0: Mismatches 0: Gaps 0:

QY 4 AKRR 7  
 ILL  
 DE 2 AKRR 5

US 09-726 470A-B4  
 ? Sequence B4: Application US/09/726 470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI 014  
 ? CURRENT APPLICATION NUMBER: US/09/726 470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? PRIOR FILING DATE: 1999-11-30  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1



```

1 SEQ ID NO 84
2 LENGTH: 8
3 TYPE: PPT
4 ORGANISM: Artificial Sequence
5 FEATURE:
6 OTHER INFORMATION: Description of Artificial Sequence: p21 peptides
7 OTHER INFORMATION: peptide
8 FEATURE:
9 OTHER INFORMATION: Synthesised with free amino terminus and as the
10 OTHER INFORMATION: C-terminal carboxamide
11 NAME/KEY: SITE
12 LOCATION: (4)
13 OTHER INFORMATION: Xaa 1-Naphthylalanine
14 US 09-726-470A-84
15
16 Query Match 36.4% Score 4; DB 11; Length 8;
17 Best Local Similarity 100.0%; Prod. No. 5e+05;
18 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19
20 QY 4 AKRP 7
21 III
22 2 AKRP 5
23
24 RESULT 4:
25 US 09-726-470A-85
26 Sequence 85: Application US/09726470A
27 Publication No. US2003036628A1
28 GENERAL INFORMATION:
29 APPLICANT: Zheleva, Danjelica I
30 APPLICANT: Fischer, Peter M
31 APPLICANT: Meltnes, Campbell I
32 APPLICANT: Andrews, Martin JI
33 APPLICANT: Chou, Weng C
34 APPLICANT: ATKINSON, Gail E
35 TITLE OF INVENTION: p21 Peptides
36 FILE REFERENCE: OCT 014
37 CURRENT APPLICATION NUMBER: US/09/726,470A
38 PRIOR APPLICATION NUMBER: 2000 11 29 99284246
39 PRIOR FILING DATE: 1999 11 30
40 NUMBER OF SEQ ID NOS: 275
41 SOFTWARE: Patent In Ver. 2.1
42 SEQ ID NO 85
43 LENGTH: 8
44 TYPE: PPT
45 ORGANISM: Artificial Sequence
46 FEATURE:
47 OTHER INFORMATION: Description of Artificial Sequence: p21 peptides
48 OTHER INFORMATION: peptide
49 FEATURE:
50 OTHER INFORMATION: Synthesised with free amino terminus and as the
51 OTHER INFORMATION: C-terminal carboxamide
52 US 09-726-470A-85
53
54 Query Match 36.4% Score 4; DB 11; Length 8;
55 Best Local Similarity 100.0%; Prod. No. 5e+05;
56 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
57
58 QY 4 AKRP 7
59 III
60 2 AKRP 5
61
62 RESULT 4:
63 US 09-726-470A-86
64 Sequence 86: Application US/09726470A
65 Publication No. US2003036628A1
66 GENERAL INFORMATION:
67 APPLICANT: Zheleva, Danjelica I
68 APPLICANT: Fischer, Peter M
69 APPLICANT: Meltnes, Campbell I
70 APPLICANT: Andrews, Martin JI
71 APPLICANT: Chou, Weng C
72 APPLICANT: ATKINSON, Gail E
73 TITLE OF INVENTION: p21 Peptides
74 FILE REFERENCE: OCT 014
75 CURRENT APPLICATION NUMBER: US/09/726,470A
76 PRIOR APPLICATION NUMBER: 2000 11 29 99284246
77 PRIOR FILING DATE: 1999 11 30
78 NUMBER OF SEQ ID NOS: 275
79 SOFTWARE: Patent In Ver. 2.1
80 SEQ ID NO 86
81 LENGTH: 8
82 TYPE: PPT
83 ORGANISM: Artificial Sequence
84 FEATURE:
85 OTHER INFORMATION: Description of Artificial Sequence: p21 peptides
86 OTHER INFORMATION: peptide
87 FEATURE:
88 OTHER INFORMATION: Synthesised with free amino terminus and as the
89 OTHER INFORMATION: C-terminal carboxamide
90 US 09-726-470A-86
91
92 Query Match 36.4% Score 4; DB 11; Length 8;
93 Best Local Similarity 100.0%; Prod. No. 5e+05;
94 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
95
96 QY 4 AKRP 7
97 III
98 2 AKRP 5
99
100 RESULT 4:
101 US 09-726-470A-87
102 Sequence 87: Application US/09726470A
103 Publication No. US2003036628A1
104 GENERAL INFORMATION:
105 APPLICANT: Zheleva, Danjelica I
106 APPLICANT: Fischer, Peter M
107 APPLICANT: Meltnes, Campbell I
108 APPLICANT: Andrews, Martin JI
109 APPLICANT: Chou, Weng C
110 APPLICANT: ATKINSON, Gail E
111 TITLE OF INVENTION: p21 Peptides
112 FILE REFERENCE: OCT 014
113 CURRENT APPLICATION NUMBER: US/09/726,470A
114 PRIOR APPLICATION NUMBER: 2000 11 29 99284246
115 PRIOR FILING DATE: 1999 11 30
116 NUMBER OF SEQ ID NOS: 275
117 SOFTWARE: Patent In Ver. 2.1
118 SEQ ID NO 87
119 LENGTH: 8
120 TYPE: PPT
121 ORGANISM: Artificial Sequence
122 FEATURE:
123 OTHER INFORMATION: Description of Artificial Sequence: p21 peptides
124 OTHER INFORMATION: peptide
125 FEATURE:
126 OTHER INFORMATION: Synthesised with free amino terminus and as the
127 OTHER INFORMATION: C-terminal carboxamide
128 US 09-726-470A-87
129
130 Query Match 36.4% Score 4; DB 11; Length 8;
131 Best Local Similarity 100.0%; Prod. No. 5e+05;
132 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
133
134 QY 4 AKRP 7
135 III
136 2 AKRP 5
137
138 RESULT 4:
139 US 09-726-470A-88
140 Sequence 88: Application US/09726470A
141 Publication No. US2003036628A1
142 GENERAL INFORMATION:
143 APPLICANT: Zheleva, Danjelica I
144 APPLICANT: Fischer, Peter M
145 APPLICANT: Meltnes, Campbell I

```

US-09-726-470A-88  
 ? Sequence 88, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 88  
 ? LENGTH: 8  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? NAME/KEY: Mod RES  
 ? LOCATION: 17  
 ? OTHER INFORMATION: Nie  
 US-09-726-470A-89

Query Match 36.4%, Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%, Pred. No. 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7  
 111  
 DB 2 AKKR 5

RESULT 42  
 US-09-726-470A-89  
 ? Sequence 89, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 89  
 ? LENGTH: 8  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide

? NAME/KEY: Mod RES  
 ? LOCATION: 17  
 ? OTHER INFORMATION: Nie  
 US-09-726-470A-89

Query Match 36.4%, Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%, Pred. No. 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7  
 111  
 DB 2 AKKR 5

RESULT 43  
 US-09-726-470A-90  
 ? Sequence 90, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIOR FILING DATE: 2000-11-29  
 ? PRIOR APPLICATION NUMBER: GB 9928423.6  
 ? NUMBER OF SEQ ID NOS: 275  
 ? SOFTWARE: Patent In Ver. 2.1  
 ? SEQ ID NO 90  
 ? LENGTH: 8  
 ? TYPE: PPT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 ? OTHER INFORMATION: peptide  
 ? FEATURE:  
 ? OTHER INFORMATION: Synthesised with free amino terminus and as the  
 ? OTHER INFORMATION: C-terminal carboxamide  
 ? NAME/KEY: SITE  
 ? LOCATION: 17  
 ? OTHER INFORMATION: Xaa - Cyclohexylalanine  
 US-09-726-470A-90

Query Match 36.4%, Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%, Pred. No. 5e-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKKR 7  
 111  
 DB 2 AKKR 5

RESULT 44  
 US-09-726-470A-91  
 ? Sequence 91, Application US/09726470A  
 ? Publication No. US2003036628A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Zheleva, Daniela I  
 ? APPLICANT: Fischer, Peter M  
 ? APPLICANT: McInnes, Campbell  
 ? APPLICANT: Andrews, Martin JI  
 ? APPLICANT: Chan, Weng C  
 ? APPLICANT: Atkinson, Gail E  
 ? TITLE OF INVENTION: p21 Peptides  
 ? FILE REFERENCE: CCI-014  
 ? CURRENT APPLICATION NUMBER: US/09/726,470A  
 ? PRIOR FILING DATE: 2000-11-29

1 PRIOR APPLICATION NUMBER: GB 9928323.6  
2 PRIOR FILING DATE: 1999-11-30  
3 NUMBER OF SEQ ID NOS: 275  
4 SOFTWARE: PatentIn Ver. 2.1  
5 SEQ ID NO 92  
6 LENGTH: 8  
7 TYPE: PPT  
8 ORGANISM: Artificial Sequence  
9 FEATURE:  
10 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
11 OTHER INFORMATION: peptide  
12 FEATURE:  
13 OTHER INFORMATION: Synthesised with free amino terminus and as the  
14 OTHER INFORMATION: C-terminal carboxamide  
US-09-726-470A-91

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
111  
LD 2 AKRR 5

RESULT 45  
US-09-726-470A-92  
1 Sequence 92, Application US/09726470A  
2 Publication No. US20030036628A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Zieleva, Daniela I  
5 APPLICANT: Fischer, Peter M  
6 APPLICANT: McInnes, Campbell  
7 APPLICANT: Andrews, Martin J  
8 APPLICANT: Chan, Weng C  
9 APPLICANT: Atkinson, Gail E  
10 TITLE OF INVENTION: p21 Peptides  
11 FILE REFERENCE: CCI-014  
12 CURRENT APPLICATION NUMBER: US/09/726-470A  
13 PRIOR FILING DATE: 2003-11-29  
14 PRIOR APPLICATION NUMBER: GB 9928323.6  
15 PRIOR FILING DATE: 1999-11-30  
16 NUMBER OF SEQ ID NOS: 275  
17 SOFTWARE: PatentIn Ver. 2.1  
18 SEQ ID NO 92  
19 LENGTH: 8  
20 TYPE: PPT  
21 ORGANISM: Artificial Sequence  
22 FEATURE:  
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
24 OTHER INFORMATION: peptide  
25 FEATURE:  
26 NAME/KEY: SITE  
27 LOCATION: (7)  
28 OTHER INFORMATION: Xaa = 1-Naphthylalanine  
29 OTHER INFORMATION: Synthesised with free amino terminus and as the  
30 OTHER INFORMATION: C-terminal carboxamide  
US-09-726-470A-92

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
111  
LD 2 AKRR 5

RESULT 46  
US-09-726-470A-14  
1 Sequence 94, Application US/09726470A  
2 Publication No. US20030036628A1

3 GENERAL INFORMATION:  
4 APPLICANT: Zieleva, Daniela I  
5 APPLICANT: Fischer, Peter M  
6 APPLICANT: McInnes, Campbell  
7 APPLICANT: Andrews, Martin J  
8 APPLICANT: Chan, Weng C  
9 APPLICANT: Atkinson, Gail E  
10 TITLE OF INVENTION: p21 Peptides  
11 FILE REFERENCE: CCI-014  
12 CURRENT APPLICATION NUMBER: US/09/726-470A  
13 PRIOR FILING DATE: 2003-11-29  
14 PRIOR APPLICATION NUMBER: GB 9928323.6  
15 PRIOR FILING DATE: 1999-11-30  
16 NUMBER OF SEQ ID NOS: 275  
17 SOFTWARE: PatentIn Ver. 2.1  
18 SEQ ID NO 94  
19 LENGTH: 8  
20 TYPE: PPT  
21 ORGANISM: Artificial Sequence  
22 FEATURE:  
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
24 OTHER INFORMATION: peptide  
25 FEATURE:  
26 OTHER INFORMATION: Synthesised with free amino terminus and as the  
27 OTHER INFORMATION: C-terminal carboxamide  
US-09-726-470A-94

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
111  
LD 2 AKRR 5

RESULT 47  
US-09-726-470A-95  
1 Sequence 95, Application US/09726470A  
2 Publication No. US20030036628A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Zieleva, Daniela I  
5 APPLICANT: Fischer, Peter M  
6 APPLICANT: McInnes, Campbell  
7 APPLICANT: Andrews, Martin J  
8 APPLICANT: Chan, Weng C  
9 APPLICANT: Atkinson, Gail E  
10 TITLE OF INVENTION: p21 Peptides  
11 FILE REFERENCE: CCI-014  
12 CURRENT APPLICATION NUMBER: US/09/726-470A  
13 PRIOR FILING DATE: 2003-11-29  
14 PRIOR APPLICATION NUMBER: GB 9928323.6  
15 PRIOR FILING DATE: 1999-11-30  
16 NUMBER OF SEQ ID NOS: 275  
17 SOFTWARE: PatentIn Ver. 2.1  
18 SEQ ID NO 95  
19 LENGTH: 8  
20 TYPE: PPT  
21 ORGANISM: Artificial Sequence  
22 FEATURE:  
23 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
24 OTHER INFORMATION: peptide  
25 FEATURE:  
26 OTHER INFORMATION: Synthesised with free amino terminus and as the  
27 OTHER INFORMATION: C-terminal carboxamide  
US-09-726-470A-95

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR 7  
111

14 2 AKKR 5

RESULT 4b  
 US-09-726-470A-98  
 Sequence 98, Application US/09/726470A  
 Publication No. US2003036628A1  
 GENERAL INFORMATION:  
 APPLICANT: Zheleva, Daniela I  
 APPLICANT: Fischer, Peter M  
 APPLICANT: McInnes, Campbell J  
 APPLICANT: Andrews, Martin J  
 APPLICANT: Chan, Weng C  
 APPLICANT: Atkinson, Gail E  
 TITLE OF INVENTION: p21 Peptides  
 FILE REFERENCE: CCI 014  
 CURRENT APPLICATION NUMBER: US/09/726-470A  
 CURRENT FILING DATE: 2000-11-29  
 PRIOR APPLICATION NUMBER: GB 9928324.6  
 PRIOR FILING DATE: 1999-11-30  
 NUMBER OF SEQ ID NOS: 275  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 96  
 LENGTH: 8  
 TYPE: PPT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 OTHER INFORMATION: peptide  
 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 OTHER INFORMATION: C-terminal carboxamide  
 US-09-726-470A-98

Query Match 36.4% Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
 1 1  
 2 AKKR 5

RESULT 4c  
 US-09-726-470A-97  
 Sequence 97, Application US/09/726470A  
 Publication No. US2003036628A1  
 GENERAL INFORMATION:  
 APPLICANT: Zheleva, Daniela I  
 APPLICANT: Fischer, Peter M  
 APPLICANT: McInnes, Campbell J  
 APPLICANT: Andrews, Martin J  
 APPLICANT: Chan, Weng C  
 APPLICANT: Atkinson, Gail E  
 TITLE OF INVENTION: p21 Peptides  
 FILE REFERENCE: CCI-014  
 CURRENT APPLICATION NUMBER: US/09/726-470A  
 CURRENT FILING DATE: 2000-11-29  
 PRIOR APPLICATION NUMBER: GB 9928324.6  
 PRIOR FILING DATE: 1999-11-30  
 NUMBER OF SEQ ID NOS: 275  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 97  
 LENGTH: 8  
 TYPE: PPT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: p21 derived

OTHER INFORMATION: peptide

FEATURE:  
 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 OTHER INFORMATION: C-terminal carboxamide  
 FEATURE:  
 NAME/KEY: SITE  
 LOCATION: (8)  
 OTHER INFORMATION: Xaa Homophenylalanine  
 US-09-726-470A-97

Query Match 36.4% Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
 1 1  
 2 AKKR 5

RESULT 50  
 US-09-726-470A-98  
 Sequence 98, Application US/09/726470A  
 Publication No. US2003036628A1  
 GENERAL INFORMATION:  
 APPLICANT: Zheleva, Daniela I  
 APPLICANT: Fischer, Peter M  
 APPLICANT: McInnes, Campbell J  
 APPLICANT: Andrews, Martin J  
 APPLICANT: Chan, Weng C  
 APPLICANT: Atkinson, Gail E  
 TITLE OF INVENTION: p21 Peptides  
 FILE REFERENCE: CCI 014  
 CURRENT APPLICATION NUMBER: US/09/726-470A  
 CURRENT FILING DATE: 2000-11-29  
 PRIOR APPLICATION NUMBER: GB 9928324.6  
 PRIOR FILING DATE: 1999-11-30  
 NUMBER OF SEQ ID NOS: 275  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 98  
 LENGTH: 8  
 TYPE: PPT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: p21 derived  
 OTHER INFORMATION: peptide  
 FEATURE:  
 OTHER INFORMATION: Synthesised with free amino terminus and as the  
 OTHER INFORMATION: C-terminal carboxamide  
 US-09-726-470A-98

Query Match 36.4% Score 4; DB 11; Length 8;  
 Best Local Similarity 100.0%; Prod. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKKR 7  
 1 1  
 2 AKKR 5

Search completed: September 30, 2003, 16:33:03  
 Job time : 21.5 secs







434	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	465	3	27.3	10	1	US-08-071-811A-10	Sequence 16, Appl
435	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	466	3	27.3	10	1	US-08-457-166-9	Sequence 9, Appl
436	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	467	3	27.3	10	1	US-08-240-514-53	Sequence 53, Appl
437	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	468	3	27.3	10	1	US-08-449-902B-4	Sequence 4, Appl
438	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	469	3	27.3	10	1	US-08-449-902B-5	Sequence 5, Appl
439	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	470	3	27.3	10	1	US-08-449-902B-5	Sequence 16, Appl
440	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	471	3	27.3	10	1	US-08-449-902B-16	Sequence 29, Appl
441	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	472	3	27.3	10	1	US-08-449-902B-29	Sequence 22, Appl
442	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	473	3	27.3	10	1	US-08-449-902B-22	Sequence 25, Appl
443	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	474	3	27.3	10	1	US-08-449-902B-25	Sequence 198, Appl
444	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	475	3	27.3	10	1	US-08-449-902B-198	Sequence 8, Appl
445	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	476	3	27.3	10	1	US-08-449-902B-8	Sequence 21, Appl
446	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	477	3	27.3	10	1	US-08-449-902B-21	Sequence 22, Appl
447	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	478	3	27.3	10	1	US-08-449-902B-22	Sequence 21, Appl
448	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	479	3	27.3	10	1	US-08-449-902B-21	Sequence 53, Appl
449	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	480	3	27.3	10	1	US-08-449-902B-53	Sequence 7, Appl
450	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	481	3	27.3	10	1	US-08-449-902B-7	Sequence 2, Appl
451	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	482	3	27.3	10	1	US-08-449-902B-2	Sequence 28, Appl
452	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	483	3	27.3	10	1	US-08-449-902B-28	Sequence 17, Appl
453	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	484	3	27.3	10	1	US-08-449-902B-17	Sequence 2, Appl
454	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	485	3	27.3	10	1	US-08-449-902B-2	Sequence 39, Appl
455	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	486	3	27.3	10	1	US-08-449-902B-39	Sequence 31, Appl
456	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	487	3	27.3	10	1	US-08-449-902B-31	Sequence 283, Appl
457	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	488	3	27.3	10	1	US-08-449-902B-283	Sequence 7, Appl
458	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	489	3	27.3	10	1	US-08-449-902B-7	Sequence 147, Appl
459	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	490	3	27.3	10	1	US-08-449-902B-147	Sequence 169, Appl
460	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	491	3	27.3	10	1	US-08-449-902B-169	Sequence 14, Appl
461	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	492	3	27.3	10	1	US-08-449-902B-14	Sequence 15, Appl
462	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	493	3	27.3	10	1	US-08-449-902B-15	Sequence 21, Appl
463	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	494	3	27.3	10	1	US-08-449-902B-21	Sequence 9, Appl
464	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	495	3	27.3	10	1	US-08-449-902B-9	Sequence 36, Appl
465	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	496	3	27.3	10	1	US-08-449-902B-36	Sequence 9, Appl
466	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	497	3	27.3	10	1	US-08-449-902B-9	Sequence 13, Appl
467	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	498	3	27.3	10	1	US-08-449-902B-13	
468	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	499	3	27.3	10	1	US-08-449-902B-13	
469	3	27.3	9	4	US-09-443-257-1	Sequence 1, Appl	500	3	27.3	10	1	US-08-449-902B-13	

ALIGNMENT:

RESULT 1

US-09-325-601-13

Sequence 13, Application US/09325601

Patent No. 6573045

GENERAL INFORMATION:

APPLICANT: Kato

APPLICANT: Prescott

TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds

FILE REFERENCE: 4950781245

CURRENT APPLICATION NUMBER: US/09325-601

CURRENT FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentLig Ver. 2.1

SEQ ID NO 13

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.

OTHER INFORMATION: U. R. pentapeptide library

US-09-325-601-13

Query Match 45.5%, Score 5, DB 4, Length 13;

Best Local Similarity 100.0%, Pred. No. 20;

Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 5 KRRKG 9

DB 7 KRRKG 11

RESULT 2

US-09-325-601-16



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? SEQ ID NO: 22
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-22

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 5
US-09-425-601-25
? Sequence 25: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO: 25
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-25

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 6
US-09-425-601-28
? Sequence 28: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO: 28
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-28

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 7
US-09-425-601-19
? Sequence 19: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO: 19
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-19

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 8
US-09-425-601-22
? Sequence 22: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
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? SEQ ID NO: 22
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-22

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 5
US-09-425-601-25
? Sequence 25: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO: 25
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-25

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 6
US-09-425-601-28
? Sequence 28: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO: 28
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-28

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 7
US-09-425-601-19
? Sequence 19: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
? SEQ ID NO: 19
? LENGTH: 13
? TYPE: PRI
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Peptide from K.
? OTHER INFORMATION: G. R pentapeptide library
US-09-425-601-19

Query Match 45.5% Score 51 DB 4 Length 13
Best Local Similarity 100.0% Pct. No. 20
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 KKKKG 9
DB 7 KKKKG 11

RESULT 8
US-09-425-601-22
? Sequence 22: Application US/09425601
? Patent No. 6574045
? GENERAL INFORMATION:
? APPLICANT: Kari
? APPLICANT: Prescott
? TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
? FILE REFERENCE: 4950/81235
? CURRENT APPLICATION NUMBER: US/09/425-601
? CURRENT FILING DATE: 1999-06-03
? NUMBER OF SEQ ID NOS: 53
? SOFTWARE: Patent In Ver. 2.1
```

```

Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

RESULT 7
US 09-425 601-41
1 Sequence 41, Application US/09-425601
2 Patent No. 6573045
3 GENERAL INFORMATION:
4 APPLICANT: Karo
5 APPLICANT: Prescott
6 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
7 FILE REFERENCE: US/09-425601
8 CURRENT APPLICATION NUMBER: US/09-425601
9 CURRENT FILING DATE: 1999-06-30
10 NUMBER OF SEQ ID NOS: 53
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO 41
13 LENGTH: 13
14 TYPE: PR1
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
18 OTHER INFORMATION: Q: R pentapeptide library
19 US 09-425 601-41

Query Match      45.5%   Score 53   DB 41   Length 13;
Best Local Similarity 100.0%   Pred. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

RESULT 8
US 09-425 601-41
1 Sequence 46, Application US/09-425601
2 Patent No. 6573045
3 GENERAL INFORMATION:
4 APPLICANT: Karo
5 APPLICANT: Prescott
6 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
7 FILE REFERENCE: US/09-425601
8 CURRENT APPLICATION NUMBER: US/09-425601
9 CURRENT FILING DATE: 1999-06-30
10 NUMBER OF SEQ ID NOS: 53
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO 46
13 LENGTH: 13
14 TYPE: PR1
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
18 OTHER INFORMATION: Q: R pentapeptide library
19 US 09-425 601-41

Query Match      45.5%   Score 53   DB 41   Length 13;
Best Local Similarity 100.0%   Pred. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

RESULT 9
US 09-425 601-41
1 Sequence 49, Application US/09-425601
2 Patent No. 6573045
3 GENERAL INFORMATION:
4 APPLICANT: Karo
5 APPLICANT: Prescott
6 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
7 FILE REFERENCE: US/09-425601
8 CURRENT APPLICATION NUMBER: US/09-425601
9 CURRENT FILING DATE: 1999-06-30
10 NUMBER OF SEQ ID NOS: 53
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO 49
13 LENGTH: 13

```

```

3 GENERAL INFORMATION:
4 APPLICANT: Karo
5 APPLICANT: Prescott
6 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
7 FILE REFERENCE: US/09-425601
8 CURRENT APPLICATION NUMBER: US/09-425601
9 CURRENT FILING DATE: 1999-06-30
10 NUMBER OF SEQ ID NOS: 53
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO 49
13 LENGTH: 13
14 TYPE: PR1
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
18 OTHER INFORMATION: Q: R pentapeptide library
19 US 09-425 601-41

Query Match      45.5%   Score 53   DB 41   Length 13;
Best Local Similarity 100.0%   Pred. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

RESULT 10
US 09-425 601-41
1 Sequence 41, Application US/09-425601
2 Patent No. 6573045
3 GENERAL INFORMATION:
4 APPLICANT: Karo
5 APPLICANT: Prescott
6 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
7 FILE REFERENCE: US/09-425601
8 CURRENT APPLICATION NUMBER: US/09-425601
9 CURRENT FILING DATE: 1999-06-30
10 NUMBER OF SEQ ID NOS: 53
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO 41
13 LENGTH: 13
14 TYPE: PR1
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence:Peptide from K.
18 OTHER INFORMATION: Q: R pentapeptide library
19 US 09-425 601-41

Query Match      45.5%   Score 53   DB 41   Length 13;
Best Local Similarity 100.0%   Pred. No. 20;
Matches      5:  KKKKG 9
              1111
              7 KKKKG 11

RESULT 11
US 09-425 601-44
1 Sequence 44, Application US/09-425601
2 Patent No. 6573045
3 GENERAL INFORMATION:
4 APPLICANT: Karo
5 APPLICANT: Prescott
6 TITLE OF INVENTION: Methods and Kits for Discovery of RNA Binding Compounds
7 FILE REFERENCE: US/09-425601
8 CURRENT APPLICATION NUMBER: US/09-425601
9 CURRENT FILING DATE: 1999-06-30
10 NUMBER OF SEQ ID NOS: 53
11 SOFTWARE: Patent In Ver. 2.1
12 SEQ ID NO 44
13 LENGTH: 13

```

```

1 TYPE: EST
2 ORGANISM: Artificial Sequence
3 FEATURE:
4 OTHER INFORMATION: Description of Artificial Sequence: Coding Frame K
5 OTHER INFORMATION: Q: R-pentapeptide library
6 US 09-425-601-44
7
8 Query Match: 45.5%, Score 51, DP 43, Length 11
9 Best Local Similarity: 100.0%, Pred. No. 20
10 Matches: 9; Conservative 0; Mismatches 0; Gaps 0
11
12 QY 5 KRKG 7
13 11 11
14 7 KRKG 11
15
16 RESULT 12
17 US-09-425-601-47
18 Sequence 47, Application US/09325607
19 Patent No. 6573045
20 GENERAL INFORMATION:
21 APPLICANT: KRG
22 APPLICANT: Pirescott
23 TITLE OF INVENTION: Methods and kits for discovery of RNA binding compounds
24 FILE REFERENCE: 4950/81235
25 CURRENT APPLICATION NUMBER: US/09/425,601
26 CURRENT FILING DATE: 1999-06-03
27 NUMBER OF SEQ ID NOS: 53
28 SOFTWARE: Patent In Ver. 2.1
29 SEQ ID NO 47
30 LENGTH: 11
31 TYPE: EST
32 ORGANISM: Artificial Sequence
33 FEATURE:
34 OTHER INFORMATION: Description of Artificial Sequence: Coding Frame K
35 OTHER INFORMATION: Q: R-pentapeptide library
36 US 09-425-601-47
37
38 Query Match: 45.5%, Score 51, DP 43, Length 11
39 Best Local Similarity: 100.0%, Pred. No. 20
40 Matches: 9; Conservative 0; Mismatches 0; Gaps 0
41
42 QY 5 KRKG 7
43 11 11
44 7 KRKG 11
45
46 RESULT 13
47 US-09-425-601-45
48 Sequence 45, Application US/09325744
49 Patent No. 6422641
50 GENERAL INFORMATION:
51 APPLICANT: Boretta, Alberto
52 TITLE OF INVENTION: HIV PROTEIN EPTOPIES
53 NUMBER OF SEQUENCES: 90
54 CORRESPONDENCE ADDRESS:
55 ADDRESSEE: Baker & Bots, L.L.P.
56 STREET: 40 Rockefeller Plaza
57 CITY: New York
58 STATE: NY
59 COUNTRY: U.S.A.
60 ZIP: 10112-0228
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Diskette
63 COMPUTER: IBM Compatible
64 OPERATING SYSTEM: DOS
65 SOFTWARE: FastSeq Version 1.5
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/08/335,733D
68 FILING DATE: 10-NOV-1994
69 CLASSIFICATION: 435
70 PRIOR APPLICATION DATA:
71 APPLICATION NUMBER:
72 FILING DATE:
73 ATTORNEY/AGENT INFORMATION:
74 NAME: MacLeod, Janet M
75 REGISTRATION NUMBER: 35,263
76 REFERENCE/DOCKET NUMBER: A29328-ECT-USA
77 TELECOMMUNICATION INFORMATION:
78 TELEPHONE: 212-408-2500
79 TELEFAX: 212-765-2519
80 TELEX:
81 INFORMATION FOR SEQ ID NO: 44:
82 SEQUENCE CHARACTERISTICS:
83 LENGTH: 8 amino acids
84 TYPE: amino acid
85 STRANDEDNESS:

```

```

1 APPLICATION NUMBER:
2 FILING DATE:
3 ATTORNEY/AGENT INFORMATION:
4 NAME: MacLeod, Janet M
5 REGISTRATION NUMBER: 35,263
6 REFERENCE/DOCKET NUMBER: A29328-ECT-USA
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 212-408-2500
9 TELEFAX: 212-765-2519
10 TELEX:
11 INFORMATION FOR SEQ ID NO: 43:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 8 amino acids
14 TYPE: amino acid
15 STRANDEDNESS:
16 MOLECULE TYPE: peptide
17 HYPOTHEICAL: NO
18 ANTI-SENSE: NO
19 FRAGMENT TYPE: internal
20 ORIGINAL SOURCE:
21 US-08-335-733D-43
22
23 Query Match: 36.4%, Score 4; DP 3; Length 8;
24 Best Local Similarity: 100.0%; Pred. No. 2.5e+05;
25 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
26
27 QY 4 AKRR 7
28 1 1
29 5 AKRR 8
30
31 DB
32
33 RESULT 14
34 US-08-335-733D-44
35 Sequence 44, Application US/08345733D
36 Patent No. 6042641
37 GENERAL INFORMATION:
38 APPLICANT: Boretta, Alberto
39 TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA
40 NUMBER OF SEQUENCES: 90
41 CORRESPONDENCE ADDRESS:
42 ADDRESSEE: Baker & Bots, L.L.P.
43 STREET: 40 Rockefeller Plaza
44 CITY: New York
45 STATE: NY
46 COUNTRY: U.S.A.
47 ZIP: 10112-0228
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Diskette
50 COMPUTER: IBM Compatible
51 OPERATING SYSTEM: DOS
52 SOFTWARE: FastSeq Version 1.5
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/08/335,733D
55 FILING DATE: 10-NOV-1994
56 CLASSIFICATION: 435
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER:
59 FILING DATE:
60 ATTORNEY/AGENT INFORMATION:
61 NAME: MacLeod, Janet M
62 REGISTRATION NUMBER: 35,263
63 REFERENCE/DOCKET NUMBER: A29328-ECT-USA
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: 212-408-2500
66 TELEFAX: 212-765-2519
67 TELEX:
68 INFORMATION FOR SEQ ID NO: 44:
69 SEQUENCE CHARACTERISTICS:
70 LENGTH: 8 amino acids
71 TYPE: amino acid
72 STRANDEDNESS:

```

1 Topology: linear  
2 MOLECULE TYPE: peptide  
3 HYPOTHETICAL: NO  
4 ANTI SENSE: NO  
5 FRAGMENT TYPE: internal  
6 ORIGINAL SOURCE:  
US 08-335-7330-44

Query Match: 36.4%, Score 41, ID 4, Length 8  
Best Local Similarity 100.0%, Ident. No. 2, 5e+05  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKRR 7  
LD 4 AKRR 7

RESULT 15  
US-08-335-7330-45  
1 Sequence 45, Application US/083357330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betetta, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
7 NUMBER OF SEQUENCES: 90  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Baker & Botts, L.L.P.  
10 STREET: 30 Rockefeller Plaza  
11 CITY: New York  
12 STATE: NY  
13 COUNTRY: U.S.A.  
14 ZIP: 10112-0228  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Diskette  
17 OPERATING SYSTEM: DOS  
18 SOFTWARE: FASTSEQ Version 1.5  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/335,7330  
21 FILING DATE: 10-NOV-1994  
22 CLASSIFICATION: 435  
23 PRIOR APPLICATION DATA:  
24 APPLICATION NUMBER:  
25 FILING DATE:  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: MacLeod, Janet M.  
28 REGISTRATION NUMBER: 35,263  
29 REFERENCE/DOCKET NUMBER: A29928-PCT USA  
30 TELECOMMUNICATION INFORMATION:  
31 TELEPHONE: 212-408-2500  
32 TELEFAX: 212-765-2519  
33 TELEX:  
34 INFORMATION FOR SEQ ID NO: 45:  
35 SEQUENCE CHARACTERISTICS:  
36 LENGTH: 8 amino acids  
37 TYPE: amino acid  
38 STRANDEDNESS:  
39 TOPOLOGY: linear  
40 MOLECULE TYPE: peptide  
41 HYPOTHETICAL: NO  
42 ANTI SENSE: NO  
43 FRAGMENT TYPE: internal  
44 ORIGINAL SOURCE:  
US 08-335-7330-45

Query Match: 36.4%, Score 41, ID 4, Length 8  
Best Local Similarity 100.0%, Ident. No. 2, 5e+05  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKRR 7  
LD 4 AKRR 6

RESULT 16  
US-08-335-7330-46  
1 Sequence 46, Application US/083357330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betetta, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
7 NUMBER OF SEQUENCES: 90  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Baker & Botts, L.L.P.  
10 STREET: 30 Rockefeller Plaza  
11 CITY: New York  
12 STATE: NY  
13 COUNTRY: U.S.A.  
14 ZIP: 10112-0228  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Diskette  
17 OPERATING SYSTEM: DOS  
18 SOFTWARE: FASTSEQ Version 1.5  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/335,7330  
21 FILING DATE: 10-NOV-1994  
22 CLASSIFICATION: 435  
23 PRIOR APPLICATION DATA:  
24 APPLICATION NUMBER:  
25 FILING DATE:  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: MacLeod, Janet M.  
28 REGISTRATION NUMBER: 35,263  
29 REFERENCE/DOCKET NUMBER: A29928-PCT USA  
30 TELECOMMUNICATION INFORMATION:  
31 TELEPHONE: 212-408-2500  
32 TELEFAX: 212-765-2519  
33 TELEX:  
34 INFORMATION FOR SEQ ID NO: 46:  
35 SEQUENCE CHARACTERISTICS:  
36 LENGTH: 8 amino acids  
37 TYPE: amino acid  
38 STRANDEDNESS:  
39 TOPOLOGY: linear  
40 MOLECULE TYPE: peptide  
41 HYPOTHETICAL: NO  
42 ANTI SENSE: NO  
43 FRAGMENT TYPE: internal  
44 ORIGINAL SOURCE:  
US 08-335-7330-46

Query Match: 36.4%, Score 41, ID 4, Length 8  
Best Local Similarity 100.0%, Ident. No. 2, 5e+05  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKRR 7  
LD 4 AKRR 5

RESULT 17  
US-08-335-7330-47  
1 Sequence 47, Application US/083357330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betetta, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
7 NUMBER OF SEQUENCES: 90  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Baker & Botts, L.L.P.  
10 STREET: 30 Rockefeller Plaza  
11 CITY: New York  
12 STATE: NY  
13 COUNTRY: U.S.A.  
14 ZIP: 10112-0228  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Diskette  
17 OPERATING SYSTEM: DOS  
18 SOFTWARE: FASTSEQ Version 1.5  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/335,7330  
21 FILING DATE: 10-NOV-1994  
22 CLASSIFICATION: 435  
23 PRIOR APPLICATION DATA:  
24 APPLICATION NUMBER:  
25 FILING DATE:  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: MacLeod, Janet M.  
28 REGISTRATION NUMBER: 35,263  
29 REFERENCE/DOCKET NUMBER: A29928-PCT USA  
30 TELECOMMUNICATION INFORMATION:  
31 TELEPHONE: 212-408-2500  
32 TELEFAX: 212-765-2519  
33 TELEX:  
34 INFORMATION FOR SEQ ID NO: 47:  
35 SEQUENCE CHARACTERISTICS:  
36 LENGTH: 8 amino acids  
37 TYPE: amino acid  
38 STRANDEDNESS:  
39 TOPOLOGY: linear  
40 MOLECULE TYPE: peptide  
41 HYPOTHETICAL: NO  
42 ANTI SENSE: NO  
43 FRAGMENT TYPE: internal  
44 ORIGINAL SOURCE:  
US 08-335-7330-47

Query Match: 36.4%, Score 41, ID 4, Length 8  
Best Local Similarity 100.0%, Ident. No. 2, 5e+05  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKRR 7  
LD 4 AKRR 6

RESULT 18  
US-08-335-7330-48  
1 Sequence 48, Application US/083357330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betetta, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
7 NUMBER OF SEQUENCES: 90  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Baker & Botts, L.L.P.  
10 STREET: 30 Rockefeller Plaza  
11 CITY: New York  
12 STATE: NY  
13 COUNTRY: U.S.A.  
14 ZIP: 10112-0228  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Diskette  
17 OPERATING SYSTEM: DOS  
18 SOFTWARE: FASTSEQ Version 1.5  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/335,7330  
21 FILING DATE: 10-NOV-1994  
22 CLASSIFICATION: 435  
23 PRIOR APPLICATION DATA:  
24 APPLICATION NUMBER:  
25 FILING DATE:  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: MacLeod, Janet M.  
28 REGISTRATION NUMBER: 35,263  
29 REFERENCE/DOCKET NUMBER: A29928-PCT USA  
30 TELECOMMUNICATION INFORMATION:  
31 TELEPHONE: 212-408-2500  
32 TELEFAX: 212-765-2519  
33 TELEX:  
34 INFORMATION FOR SEQ ID NO: 48:  
35 SEQUENCE CHARACTERISTICS:  
36 LENGTH: 8 amino acids  
37 TYPE: amino acid  
38 STRANDEDNESS:  
39 TOPOLOGY: linear  
40 MOLECULE TYPE: peptide  
41 HYPOTHETICAL: NO  
42 ANTI SENSE: NO  
43 FRAGMENT TYPE: internal  
44 ORIGINAL SOURCE:  
US 08-335-7330-48

Query Match: 36.4%, Score 41, ID 4, Length 8  
Best Local Similarity 100.0%, Ident. No. 2, 5e+05  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKRR 7  
LD 4 AKRR 6

RESULT 19  
US-08-335-7330-49  
1 Sequence 49, Application US/083357330  
2 Patent No. 6042831  
3 GENERAL INFORMATION:  
4 APPLICANT: Betetta, Alberto  
5 TITLE OF INVENTION: HIV PROTEIN EPITOPES  
6 TITLE OF INVENTION: IMMUNOLOGICALLY HOMOLOGOUS TO HLA  
7 NUMBER OF SEQUENCES: 90  
8 CORRESPONDENCE ADDRESS:  
9 ADDRESSEE: Baker & Botts, L.L.P.  
10 STREET: 30 Rockefeller Plaza  
11 CITY: New York  
12 STATE: NY  
13 COUNTRY: U.S.A.  
14 ZIP: 10112-0228  
15 COMPUTER READABLE FORM:  
16 MEDIUM TYPE: Diskette  
17 OPERATING SYSTEM: DOS  
18 SOFTWARE: FASTSEQ Version 1.5  
19 CURRENT APPLICATION DATA:  
20 APPLICATION NUMBER: US/08/335,7330  
21 FILING DATE: 10-NOV-1994  
22 CLASSIFICATION: 435  
23 PRIOR APPLICATION DATA:  
24 APPLICATION NUMBER:  
25 FILING DATE:  
26 ATTORNEY/AGENT INFORMATION:  
27 NAME: MacLeod, Janet M.  
28 REGISTRATION NUMBER: 35,263  
29 REFERENCE/DOCKET NUMBER: A29928-PCT USA  
30 TELECOMMUNICATION INFORMATION:  
31 TELEPHONE: 212-408-2500  
32 TELEFAX: 212-765-2519  
33 TELEX:  
34 INFORMATION FOR SEQ ID NO: 49:  
35 SEQUENCE CHARACTERISTICS:  
36 LENGTH: 8 amino acids  
37 TYPE: amino acid  
38 STRANDEDNESS:  
39 TOPOLOGY: linear  
40 MOLECULE TYPE: peptide  
41 HYPOTHETICAL: NO  
42 ANTI SENSE: NO  
43 FRAGMENT TYPE: internal  
44 ORIGINAL SOURCE:  
US 08-335-7330-49

Query Match: 36.4%, Score 41, ID 4, Length 8  
Best Local Similarity 100.0%, Ident. No. 2, 5e+05  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 AKRR 7  
LD 4 AKRR 6

```
1 STATE: NY
2 COUNTRY: U.S.A.
3 ZID: 10112-0228
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Diskette
6 COMPILER: IBM Compatible
7 OPERATING SYSTEM: DOS
8 SOFTWARE: FASTSEQ Version 1.5
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/09/485,745
11 FILING DATE: 10-NOV-1994
12 CLASSIFICATION: 435
13 PRIOR APPLICATION DATA:
14 FILING DATE:
15 ATTORNEY/AGENT INFORMATION:
16 NAME: MacLeod, Janet M
17 REGISTRATION NUMBER: 35,263
18 REFERENCE/DOCKET NUMBER: A29722-PCT-USA
19 TELEPHONE: 212-408-2500
20 TELEFAX: 212-765-2519
21 TELEX:
22 INFORMATION FOR SEQ ID NO: 47:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 8 amino acids
25 TYPE: amino acid
26 STRANDEDNESS:
27 TOPOLOGY: linear
28 MOLECULE TYPE: peptide
29 HYDROPHATIC NO:
30 ANTI-SENSE NO:
31 FRAGMENT TYPE: Internal
32 ORIGINAL SOURCE:
33 US 08-485,735-47
34
35 Query Match 36.4% Score 4: DB 4: Length 8:
36 Best Local Similarity 100.0% Pred. No. 2.5e+05;
37 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
38
39 QY 4 AKK 7
40 1 1
41 1 AKK 4
42
43 PASHI 18
44 US-09-485-286-4
45 Sequence 4: Application US/09485726
46 Patent No. 6559524
47 GENERAL INFORMATION:
48 APPLICANT: Stahl, Stefan
49 APPLICANT: Jonasson, Per
50 APPLICANT: Nyren, Per-Ake
51 APPLICANT: Ulen, Mathias
52 TITLE OF INVENTION: RECOMBINANT EXPRESSION OF INSULIN
53 TITLE OF INVENTION: C-PEPTIDE
54 FILE REFERENCE: 11541-00200
55 CURRENT APPLICATION NUMBER: US/09/485,286
56 CURRENT FILING DATE: 2000-02-07
57 PRIOR APPLICATION NUMBER: PCT/SE98/2183
58 PRIOR FILING DATE: 1998-08-07
59 PRIOR APPLICATION NUMBER: CH 9716390.2
60 PRIOR FILING DATE: 1997-08-07
61 NUMBER OF SEQ ID NOS: 14
62 SOFTWARE: FASTSEQ for Windows Version 4.0
63 SEQ ID NO 4
64 LENGTH: 8
65 TYPE: PRT
66 ORGANISM: Artificial Sequence
67 FEATURE:
68 OTHER INFORMATION: Representative linker region
69 US 09-485-286-4
70
71 Query Match 36.4% Score 4: DB 1: Length 9:
72 Best Local Similarity 100.0% Pred. No. 2.5e+05;
73 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
74
75 QY 5 KKK b
76
77 STATE: NY
78 COUNTRY: U.S.A.
79 ZID: 10112-0228
80 COMPUTER READABLE FORM:
81 MEDIUM TYPE: Diskette
82 COMPILER: IBM Compatible
83 OPERATING SYSTEM: DOS
84 SOFTWARE: FASTSEQ Version 1.5
85 CURRENT APPLICATION DATA:
86 APPLICATION NUMBER: US/09/432,518
87 FILING DATE: 10-NOV-1994
88 CLASSIFICATION: 435
89 PRIOR APPLICATION DATA:
90 FILING DATE:
91 ATTORNEY/AGENT INFORMATION:
92 NAME: MacLeod, Janet M
93 REGISTRATION NUMBER: 35,263
94 REFERENCE/DOCKET NUMBER: A29722-PCT-USA
95 TELEPHONE: 212-408-2500
96 TELEFAX: 212-765-2519
97 TELEX:
98 INFORMATION FOR SEQ ID NO: 47:
99 SEQUENCE CHARACTERISTICS:
100 LENGTH: 8 amino acids
101 TYPE: amino acid
102 STRANDEDNESS:
103 TOPOLOGY: linear
104 MOLECULE TYPE: peptide
105 HYDROPHATIC NO:
106 ANTI-SENSE NO:
107 FRAGMENT TYPE: Internal
108 ORIGINAL SOURCE:
109 US 08-432,518-2
110
111 Query Match 36.4% Score 4: DB 4: Length 8:
112 Best Local Similarity 100.0% Pred. No. 2.5e+05;
113 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
114
115 QY 1 ASQA 4
116 1 1 1 1
117 1 ASQA 4
118
119 RESULT 14
120 US-08-432-518-2
121 Sequence 2: Application US/08332518
122 Patent No. 5803200
123 GENERAL INFORMATION:
124 APPLICANT: TWIST, Michael
125 APPLICANT: SUMNER SMITH, Martin
126 TITLE OF INVENTION: TREATMENT OF CYTOMEGALOVIRUS INFECTION
127 NUMBER OF SEQUENCES: 26
128 CORRESPONDENCE ADDRESS:
129 ADDRESSEE: Foxy & Hardner
130 STREET: 3000 K Street, N.W., Suite 800
131 CITY: Washington
132 STATE: D.C.
133 COUNTRY: USA
134 ZIP: 20007-5109
135 COMPUTER READABLE FORM:
136 MEDIUM TYPE: Floppy disk
137 COMPUTER: IBM PC compatible
138 OPERATING SYSTEM: PC-DOS/MS-DOS
139 SOFTWARE: Patent Release #1.0, Version #1.30
140 CURRENT APPLICATION DATA:
141 APPLICATION NUMBER: US/08/332,518
142 FILING DATE: 31-OCT-1994
143 CLASSIFICATION: 514
144 PRIOR APPLICATION DATA:
145 APPLICATION NUMBER: US 08/139,757
146 FILING DATE: 22-OCT-1993
147 PRIOR APPLICATION DATA:
148 APPLICATION NUMBER: US 07/872,398
149 FILING DATE: 23-APR-1992
150 PRIOR APPLICATION DATA:
151 APPLICATION NUMBER: US 07/779,735
152 FILING DATE: 24-OCT-1991
153 PRIOR APPLICATION DATA:
154 APPLICATION NUMBER: US 07/602,953
155 FILING DATE: 24-OCT-1990
156 PRIOR APPLICATION DATA:
157 APPLICATION NUMBER: US 07/995,742
158 FILING DATE: 22-DEC-1992
159 PRIOR APPLICATION DATA:
160 APPLICATION NUMBER: US 07/872,318
161 FILING DATE: 23-APR-1992
162 ATTORNEY/AGENT INFORMATION:
163 NAME: BENT, Stephen A.
164 REGISTRATION NUMBER: 29,768
165 REFERENCE/DOCKET NUMBER: 16777/266/ALLE
166 TELECOMMUNICATION INFORMATION:
167 TELEPHONE: (202)672-5300
168 TELEFAX: (202)672-5399
169 TELEX: 904136
170 INFORMATION FOR SEQ ID NO: 2:
171 SEQUENCE CHARACTERISTICS:
172 LENGTH: 9 amino acids
173 TYPE: amino acid
174 STRANDEDNESS:
175 TOPOLOGY: linear
176 US-08-332-518-2
177
178 Query Match 36.4% Score 4: DB 1: Length 9:
179 Best Local Similarity 100.0% Pred. No. 2.5e+05;
180 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
181
182 QY 5 KKK b
```

```

US-08-439-747A-23
: Sequence 23, Application US/084 19747A
: Patent No. 5757233
: GENERAL INFORMATION:
: APPLICANT: Zhang, Kunlin
: APPLICANT: Karamathan, Lela
: TITLE OF INVENTION: Soluble, Circulable Substrates of the Hepatitis
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schering Corp.
: STREET: 2000 Gallopina Hill Road
: CITY: Kenilworth,
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07033-0530
: COMPUTER RELEASABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: Apple Macintosh
: SOFTWARE: Microsoft Word 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/439,747A
: FILING DATE: May 12, 1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Linn, Paul G.
: REGISTRATION NUMBER: 32,743
: REFERENCE/DOCKET NUMBER: J060509
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-298-5361
: TELEFAX: 908-298-5368
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: MOLECULE TYPE: polypeptide
: FEATURE:
: NAME/KEY: hydrophobic tail
US-08-439-747A-25
: Query Match 36.4% Score 4, DB 1, Length 9:
: Best Local Similarity 100.0%, Pred. No. 2,5e+05;
: Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps
:
QY 5 KRK 8
:
DB 4 KRK 7
:
RESULT 42
US-08-439-709-4
: Sequence 3, Application US/08474709
: Patent No. 5611033
: GENERAL INFORMATION:
: APPLICANT: Twist, Michael
: APPLICANT: Barnett, Richard
: APPLICANT: Reid, Lorrie
: APPLICANT: Sumner-Smith, Mattie
: TITLE OF INVENTION: TREATMENT OF HERPES VIRUS INFECTION
: NUMBER OF SEQUENCES: 33
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 1800 Diagonal Road, Suite 500
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22313-0299
: COMPUTER RELEASABLE FORM:
: MEDIUM TYPE: Floppy disk

```

```

1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patent In Release #1.0, Virus #1.0
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/09/378,709
6  FILING DATE:
7  CLASSIFICATION: 530
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 01/874,498
10 FILING DATE: 21-APR-1992
11 APPLICATION NUMBER: US 07/773,740
12 FILING DATE: 21-OCT-1991
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/602,434
15 FILING DATE: 24-OCT-1990
16 ATTORNEY/AGENT INFORMATION:
17 NAME: BENT, Stephen A.
18 REGISTRATION NUMBER: 29,768
19 REFERENCE/DOCKET NUMBER: 16777/17 ALLE
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (703)836-9400
22 TELEX: 899143
23 INFORMATION FOR SEQ ID NO: 1:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 9 amino acids
26 TYPE: amino acid
27 TOPOLOGY: linear
28 US 09 378-709-11
29
30 Query Match: 96.4%; Score 4; DB 2; Length 9;
31 Best Local Similarity: 100.0%; Pctd. No. 2.5e+05;
32 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
33
34 QY 5 KKKK R
35 1 1 1
36 3 KKKK S
37
38 RESULT 24
39 US-09-440-409B-23
40 Sequence 23, Application US/08440479P
41 Patent No. 5843752
42 GENERAL INFORMATION:
43 APPLICANT: Basmahapatir, Rimal
44 APPLICANT: Murray, Michael
45 APPLICANT: Ramakrishnan, Lata
46 APPLICANT: Rakiewicz, Nancy
47 TITLE OF INVENTION: Soluble Active Hepatitis C Virus Protease
48 NUMBER OF SEQUENCES: 14
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Schering Corp.
51 STREET: 2060 Gallop Hill Road
52 CITY: Kenilworth
53 STATE: New Jersey
54 COUNTRY: USA
55 ZIP: 07033-0530
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Floppy disk
58 COMPUTER: Apple Macintosh
59 OPERATING SYSTEM: Macintosh 7.5.3
60 SOFTWARE: Microsoft Word 5.1.2
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/08/440,409B
63 FILING DATE: May 12, 1995
64 CLASSIFICATION: 435
65 ATTORNEY/AGENT INFORMATION:
66 NAME: Good, Paul G.
67 REGISTRATION NUMBER: 42,743
68 REFERENCE/DOCKET NUMBER: JH0494
69 TELECOMMUNICATION INFORMATION:
70 TELEPHONE: 908-298-5061
71 TELEX: 908-298-5388
72 INFORMATION FOR SEQ ID NO: 23:
73 SEQUENCE CHARACTERISTICS:
74 LENGTH: 9 amino acids
75 TYPE: amino acid
76 STRANDNESS: single
77 TOPOLOGY: linear
78 MOLECULE TYPE: polypeptide
79 FEATURE:
80 NAME/KEY: hydrophobic tail
81 US-08-440-409B-23
82
83 Query Match: 96.4%; Score 4; DB 2; Length 9;
84 Best Local Similarity: 100.0%; Pctd. No. 2.5e+05;
85 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patent In Release #1.0, Virus #1.0
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/09/378,709
6  FILING DATE:
7  CLASSIFICATION: 530
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 01/874,498
10 FILING DATE: 21-APR-1992
11 APPLICATION NUMBER: US 07/773,740
12 FILING DATE: 21-OCT-1991
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 07/602,434
15 FILING DATE: 24-OCT-1990
16 ATTORNEY/AGENT INFORMATION:
17 NAME: BENT, Stephen A.
18 REGISTRATION NUMBER: 29,768
19 REFERENCE/DOCKET NUMBER: 16777/17 ALLE
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (703)836-9400
22 TELEX: 899143
23 INFORMATION FOR SEQ ID NO: 1:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 9 amino acids
26 TYPE: amino acid
27 TOPOLOGY: linear
28 US 09 378-709-11
29
30 Query Match: 96.4%; Score 4; DB 2; Length 9;
31 Best Local Similarity: 100.0%; Pctd. No. 2.5e+05;
32 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
33
34 QY 5 KKKK R
35 1 1 1
36 3 KKKK S
37
38 RESULT 23
39 US-09-378-709-11
40 Sequence 11, Application US/08440479P
41 Patent No. 5843752
42 GENERAL INFORMATION:
43 APPLICANT: Basmahapatir, Rimal
44 APPLICANT: Murray, Michael
45 APPLICANT: Ramakrishnan, Lata
46 APPLICANT: Rakiewicz, Nancy
47 TITLE OF INVENTION: Soluble Active Hepatitis C Virus Protease
48 NUMBER OF SEQUENCES: 14
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Schering Corp.
51 STREET: 2060 Gallop Hill Road
52 CITY: Kenilworth
53 STATE: New Jersey
54 COUNTRY: USA
55 ZIP: 07033-0530
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: Floppy disk
58 COMPUTER: Apple Macintosh
59 OPERATING SYSTEM: Macintosh 7.5.3
60 SOFTWARE: Microsoft Word 5.1.2
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/08/440,409B
63 FILING DATE: May 12, 1995
64 CLASSIFICATION: 435
65 ATTORNEY/AGENT INFORMATION:
66 NAME: Good, Paul G.
67 REGISTRATION NUMBER: 42,743
68 REFERENCE/DOCKET NUMBER: JH0494
69 TELECOMMUNICATION INFORMATION:
70 TELEPHONE: 908-298-5061
71 TELEX: 908-298-5388
72 INFORMATION FOR SEQ ID NO: 23:
73 SEQUENCE CHARACTERISTICS:
74 LENGTH: 9 amino acids
75 TYPE: amino acid
76 STRANDNESS: single
77 TOPOLOGY: linear
78 MOLECULE TYPE: polypeptide
79 FEATURE:
80 NAME/KEY: hydrophobic tail
81 US-08-440-409B-23
82
83 Query Match: 96.4%; Score 4; DB 2; Length 9;
84 Best Local Similarity: 100.0%; Pctd. No. 2.5e+05;
85 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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CY 1 KKKK 4
ID 1 1
4 KKKK 7

RESULT 25
US-08-455-765-4
1 Sequence 4, Application US/08-455-765-4
2 Patent No. 6052943
3 GENERAL INFORMATION:
4 APPLICANT: Borella, Alberto
5 TITLE OF INVENTION: HIV PROTEIN FOLDING
6 TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE HIV PROTEIN
7 NUMBER OF SEQUENCES: 90
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Baker & Botts, LLP
10 STREET: 30 Rockefeller Plaza
11 CITY: New York
12 STATE: NY
13 COUNTRY: U.S.A.
14 ZIP: 10112-0228
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM PC Compatible
18 OPERATING SYSTEM: DOS
19 SOFTWARE: FastSeq Version 1.0
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08-455-765-4
22 FILING DATE: 10-NOV-1994
23 CLASSIFICATION: 445
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:
26 FILING DATE:
27 ATTORNEY/AGENT INFORMATION:
28 NAME: McGowan, Janet M
29 REGISTRATION NUMBER: 45,274
30 REFERENCE/DECKET NUMBER: A276517, USA
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 212-498-2503
33 TELEFAX: 212-765-2519
34 TELEX:
35 INFORMATION FOR SEQ ID NO: 43
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 9 amino acids
38 TYPE: amino acid
39 STRANDEDNESS:
40 TOPOLOGY: linear
41
42 QUOTE Match 46.48% Score 4: 49.0% DB 3: 46.7%
43 Best Local Similarity 100.0% Pred. No. 2 Seq+05
44 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
45
46 4 AKKR 7
47 11
48 4 AKKR 7

RESULT 26
US-08-726-807B-17
1 Sequence 17, Application US/08-726-807B-17
2 Patent No. 6090518
3 GENERAL INFORMATION:
4 APPLICANT: Parmacek, Michael S.
5 APPLICANT: Sorwy, Julian
6 TITLE OF INVENTION: PROTEIN EXPRESSION
7 TITLE OF INVENTION:

```

```

8 NUMBER OF SEQUENCES: 55
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Arnold, White & Decker
11 STREET: P.O. Box 4433
12 CITY: Houston
13 STATE: Texas
14 COUNTRY: USA
15 ZIP: 77216
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC Compatible
19 OPERATING SYSTEM: PC DOS/MS DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.10
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08-726-807B
23 FILING DATE: 07-01-1996
24 CLASSIFICATION: 514
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:
27 FILING DATE: 05-01-1995
28 ATTORNEY/AGENT INFORMATION:
29 NAME: McMillan, Rebecca R.
30 REGISTRATION NUMBER: P-43,363
31 REFERENCE/DECKET NUMBER: ARSB:510
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (512) 418-4000
34 TELEFAX: (512) 474-7577
35 INFORMATION FOR SEQ ID NO: 17:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 9 amino acids
38 TYPE: amino acid
39 STRANDEDNESS:
40 TOPOLOGY: linear
41
42 US-08-726-807B-17
43
44 QUOTE Match 36.48% Score 4: DB 3: Length 9:
45 Best Local Similarity 100.0% Pred. No. 2 Seq+05:
46 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
47
48 5 KKKK 6
49 111
50 6 KKKK 9

RESULT 27
US-08-478-859-1
1 Sequence 1, Application US/08-478-859-1
2 Patent No. 628554
3 GENERAL INFORMATION:
4 APPLICANT: Gossyp, Andrew R.
5 APPLICANT: Sloop, Patricia
6 APPLICANT: van Hek, Hendrik
7 APPLICANT: Rotzenko, Stephen
8 APPLICANT: Wozniak, John R.
9 APPLICANT: Johnson, Richard A.
10 APPLICANT: Wood, Patricia C.
11 APPLICANT: Burton, Steven J.
12 APPLICANT: Glick, Alan V.
13 TITLE OF INVENTION: High Purity Albumin
14 NUMBER OF SEQUENCES: 4
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: The BCC Group, Inc.
17 STREET: 100 Mountain Avenue
18 CITY: Murray Hill, New Providence
19 STATE: New Jersey
20 COUNTRY: United States of America
21 ZIP: 07974
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Floppy disk
24 COMPUTER: IBM PC compatible
25 OPERATING SYSTEM: PC DOS/MS-DOS
26 SOFTWARE: Patent In Release #1.0, Version #1.25
27 CURRENT APPLICATION DATA:

```



```

1  APPLICATION NUMBER: US/08/478,659
2  FILING DATE: 26-JAN-1995
3  CLASSIFICATION: 435
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Swope, R Halin
6  REGISTRATION NUMBER: 24,864
7  REFERENCE/DOCKET NUMBER: 92H8501
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: (908) 771 6292
10  TELEFAX: (908) 771 6159
11  INFORMATION FOR SEQ ID NO: 1:
12  SEQUENCE CHARACTERISTICS:
13  LENGTH: 10 amino acids
14  TYPE: amino acid
15  STRANDEDNESS: single
16  TOPOLOGY: linear
17  MOLECULE TYPE: peptide
18  HYPOTHETICAL: NO
19  ANTI-SENSE: NO
20  FRAGMENT TYPE: internal
21  ORGANISM: Peptide fragment of human serum albumin
22  US-08 478-659-1
23
24  Query Match 36.4%; Score 4; DR 1; Length 10;
25  Best Local Similarity 100.0%; Pred. No. 1.8e+02;
26  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27
28  QY 1 ASQA 4
29  LL 4 ASQA 7
30
31  RESULT 28
32  US-08 726-66A 6
33  Sequence 6, Application US/08/726-66A
34  Patent No. 5958684
35  GENERAL INFORMATION:
36  APPLICANT: van Leeuwen, Frederik Willem
37  APPLICANT: Burbach, Johannes Peter Heert
38  APPLICANT: Grosveld, Franklin G.
39  TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
40  NUMBER OF SEQUENCES: 189
41  CORRESPONDENCE ADDRESS:
42  ADDRESSEE: Warner & Witcoff, Inc.
43  STREET: 1 Financial Center
44  CITY: Boston
45  STATE: MA
46  COUNTRY: US
47  ZIP: 02111
48  COMPUTER READABLE FORM:
49  MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, 800000
50  OPERATING SYSTEM: PC DOS/MS-DOS
51  SOFTWARE: WordPerfect 6.1
52  CURRENT APPLICATION DATA:
53  APPLICATION NUMBER: US/08/726,60A
54  FILING DATE: 02 Oct-1996
55  PRIOR APPLICATION DATA:
56  APPLICATION NUMBER: GB 95/200867 4
57  FILING DATE: 02-Oct-1995
58  PRIOR APPLICATION DATA:
59  APPLICATION NUMBER: US 60/039,854
60  FILING DATE: 03-Jan-1996
61  ATTORNEY/AGENT INFORMATION:
62  NAME: Williams, Ph.D., Kathleen M
63  REGISTRATION NUMBER: 34,380
64  REFERENCE/DOCKET NUMBER: 95,045 A (2.5/007-41)
65  TELECOMMUNICATION INFORMATION:
66  TELEPHONE: (617) 345 9100
67  TELEFAX: (617) 345-9111
68  INFORMATION FOR SEQ ID NO: 6:
69  SEQUENCE CHARACTERISTICS:

```

```

1  LENGTH: 10 amino acids
2  TYPE: amino acid
3  STRANDEDNESS: single
4  TOPOLOGY: unknown
5  MOLECULE TYPE: peptide
6  US-08-726-306A-6
7
8  Query Match 36.4%; Score 4; DR 2; Length 10;
9  Best Local Similarity 100.0%; Pred. No. 1.8e+02;
10  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
11
12  QY 7 RGGP 10
13  LL 6 RGGP 9
14
15  RESULT 29
16  US-08-970-648-1
17  Sequence 1, Application US/08/970648
18  Patent No. 6034221
19  GENERAL INFORMATION:
20  APPLICANT: Goodey, Andrew R
21  APPLICANT: Sleep, Darrell
22  APPLICANT: van Dijk, Hendrik
23  APPLICANT: Berezutsko, Stephen
24  APPLICANT: Kowalew, John R
25  APPLICANT: Johnson, Richard A
26  APPLICANT: Wood, Patricia C
27  APPLICANT: Buttol, Steven J
28  APPLICANT: Quirk, Alan V
29  TITLE OF INVENTION: High Purity Albumin
30  NUMBER OF SEQUENCES: 4
31  CORRESPONDENCE ADDRESS:
32  ADDRESSEE: The BOC Group, Inc
33  STREET: 100 Mountain Avenue
34  CITY: Murray Hill, New Providence
35  STATE: New Jersey
36  COUNTRY: United States of America
37  ZIP: 07974
38  COMPUTER READABLE FORM:
39  MEDIUM TYPE: Floppy Disk
40  OPERATING SYSTEM: IBM PC compatible
41  SOFTWARE: Patent Release #1.0, Version #1.25
42  CURRENT APPLICATION DATA:
43  APPLICATION NUMBER: US/08/970,648
44  FILING DATE:
45  CLASSIFICATION: 530
46  PRIOR APPLICATION DATA:
47  APPLICATION NUMBER: US 08/378,859
48  FILING DATE: 26-JAN-1995
49  ATTORNEY/AGENT INFORMATION:
50  NAME: Swope, R Halin
51  REGISTRATION NUMBER: 24,864
52  REFERENCE/DOCKET NUMBER: 92H8501
53  TELECOMMUNICATION INFORMATION:
54  TELEPHONE: (908) 771 6292
55  TELEFAX: (908) 771 6159
56  INFORMATION FOR SEQ ID NO: 1:
57  SEQUENCE CHARACTERISTICS:
58  LENGTH: 10 amino acids
59  TYPE: amino acid
60  STRANDEDNESS: single
61  TOPOLOGY: linear
62  MOLECULE TYPE: peptide
63  HYPOTHETICAL: NO
64  ANTI-SENSE: NO
65  FRAGMENT TYPE: internal
66  ORIGINAL SOURCE:
67  ORGANISM: Peptide fragment of human serum albumin
68  US-08-970-648-1
69
70  Query Match 36.4%; Score 4; DR 3; Length 10;

```

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Best Local Similarity 100.0%; Seq. No. 3 Best 2;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ASQA 4
DB 4 ASQA 7

RESULT 40
US 09-159-399A-746
: Sequence 746; Application US/09159A-746
: Patent No. 6495654
: GENERAL INFORMATION:
: APPLICANT: Kugo, Ralph T.
: APPLICANT: Grey, Howard M.
: APPLICANT: Sette, Alessandro
: APPLICANT: Davis, Eschbar
: TITLE OF INVENTION: HLA Binding peptides and their
: NUMBER OF SEQUENCES: 1254
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3643
: COMPUTER READABLE FORM:
: MEDIA TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09159A-746
: FILING DATE: 29-NOV-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/926,460
: FILING DATE: 07-AUG-1992
: APPLICATION NUMBER: US 08/227,746
: FILING DATE: 05-MAR-1995
: APPLICATION NUMBER: US 08/154,300
: FILING DATE: 06-APR-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Weber, Ellen Leaver
: REGISTRATION NUMBER: 32,762
: REFERENCE/DOCKET NUMBER: 5100-23-01000-02
: TELEPHONE: (415) 575-0209
: TELEFAX: (415) 576-0406
: TELEX:
: 3125X
: INFORMATION FOR SEQ ID NO: 746:
: SEQUENCE CHARACTERISTICS
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-159-399A-746

Query Match 96.4%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Seq. No. 1 Best 2;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY # KQPR 11
DB 7 KQPR 10

RESULT 41
US-09-434-476A-4
: Sequence 4; Application US/09434A-746
: Patent No. 6495138
: GENERAL INFORMATION:
: APPLICANT: van Nieuwstadt, Antoine
: APPLICANT: Jangeveld, Jan
: APPLICANT: Meulenbergh, Janneke
: TITLE OF INVENTION: PRRSV Antigenic Sites Identifying Peptide Sequences of PRRS
: FILE REFERENCE: 2184-421718
: CURRENT APPLICATION NUMBER: US/09434A-476A
: PRIOR FILING DATE: 1999-11-05
: PRIOR APPLICATION NUMBER: EP 97231443.2
: PRIOR FILING DATE: 1997-05-16
: PRIOR APPLICATION NUMBER: PCT/NL98/00251
: PRIOR FILING DATE: 1998-05-05
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: Patent In version 3.0
: SEQ ID NO: 4
: LENGTH: 10
: TYPE: PKI
: ORGANISM: Porcine reproductive and respiratory syndrome virus
US-09-434-476A-4

Query Match 96.4%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Seq. No. 1 Best 2;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 QAKS 6
DB 5 QAKS 8

RESULT 42
US 09-129-192C-56
: Sequence 56; Application US/09129192C
: Patent No. 6495664
: GENERAL INFORMATION:
: APPLICANT: Aurora Biosciences Corporation
: APPLICANT: Cubitt, Andrew B.
: TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modification
: FILE REFERENCE: AUR-2270 (08366/031001)
: CURRENT APPLICATION NUMBER: US/09/129,192C
: CURRENT FILING DATE: 1998-07-24
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: Patent In version 3.0
: SEQ ID NO: 56
: LENGTH: 10
: TYPE: PKI
: ORGANISM: Artificial sequence
: FEATURES:
: OTHER INFORMATION: Phosphorylation motif
US 09-129-192C-56

Query Match 96.4%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Seq. No. 1 Best 2;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 RRG 9
DB 4 RRG 7

RESULT 43
US-09-129-192C-57
: Sequence 57; Application US/09129192C
: Patent No. 6495664
: GENERAL INFORMATION:
: APPLICANT: Aurora Biosciences Corporation
: APPLICANT: Cubitt, Andrew B.
: TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modification
: FILE REFERENCE: AUR-2270 (08366/031001)
: CURRENT APPLICATION NUMBER: US/09/129,192C
: CURRENT FILING DATE: 1998-07-24
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: Patent In version 3.0

```

SEQ ID NO: 57  
LENGTH: 10  
TYPE: PPT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Phosphorylation Ser4,1

US 09/129,192C 57

Query Match 36.4% Score 41 DB 1 Length 10  
Best Local Similarity 100.0% Pctd No. 26-02  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 AKKG 7  
DB 4 AKKG 7

RESULT 35

US-08-378-859 4  
Sequence 4, Application US/08378859  
Patent No. 5728553  
GENERAL INFORMATION:  
APPLICANT: Goodby, Andrew R  
APPLICANT: Sheep, Darrell  
APPLICANT: van Urk, Hendrik  
APPLICANT: Berezenko, Stephen  
APPLICANT: Woodrow, John R  
APPLICANT: Johnson, Richard A  
APPLICANT: Wood, Patricia C  
APPLICANT: Burton, Steven J  
APPLICANT: Quirk, Alan V  
TITLE OF INVENTION: High Purity Alumin  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: The ROC Group, Inc  
STREET: 100 Mountain Avenue  
CITY: Murray Hill, New Providence  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07974  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,859  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Swopo, R Hain  
REGISTRATION NUMBER: 24,864  
REFERENCE/DECKET NUMBER: 92H580  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 771 6292  
TELEFAX: (908) 771 6159  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Peptide fragment of human serum albumin

Query Match 36.4% Score 41 DB 1 Length 11  
Best Local Similarity 100.0% Pctd No. 26-02  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ASQA 4  
DB 4 ASQA 7

RESULT 35

US-08-669-721 17  
Sequence 17, Application US/08669721  
Patent No. 5814236  
GENERAL INFORMATION:  
APPLICANT: Lamb et al., Christopher J.  
TITLE OF INVENTION: NOVEL TRANSCRIPTION ENHANCER ELEMENT AND  
TITLE OF INVENTION: TRANSCRIPTION FACTOR AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/669,721  
FILING DATE: 27-JUN 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ellison, Eldora L.  
REGISTRATION NUMBER: 39,967  
REFERENCE/DECKET NUMBER: 07251/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678 5099  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match 36.4% Score 41 DB 2 Length 11  
Best Local Similarity 100.0% Pctd No. 26-02  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 AKKR 7  
DB 2 AKKR 5

RESULT 36

US-08-540-388 1  
Sequence 1, Application: US/08540388  
Patent No. 5858964  
GENERAL INFORMATION:  
APPLICANT: ARARONI, Rana  
APPLICANT: ARNON, Ruth  
APPLICANT: CHAO, Nelson J.  
APPLICANT: SCHLEGEL, Paul G.  
APPLICANT: SELA, Michael  
APPLICANT: TEITELBAUM, David  
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING  
TITLE OF INVENTION: SYNTHETIC PEPTIDE COPOLYMER FOR PREVENTION OF GVHD  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BOWDY AND NEIMARK  
STREET: 419 Seventh Street N.W., Ste. 300

1 CITY: Washington  
 2 STATE: D.C.  
 3 COUNTRY: United States of America  
 4 ZIP: 20004  
 5 COMPUTER READABLE FORM:  
 6 MEDIUM TYPE: Floppy disk  
 7 COMPIER: IBM PC compatible  
 8 OPERATING SYSTEM: PC-DOS/MS-DOS  
 9 SOFTWARE: Patent In Release #1.0, Version #1.25  
 10 CURRENT APPLICATION DATA:  
 11 APPLICATION NUMBER: US/09/548,443  
 12 FILING DATE:  
 13 CLASSIFICATION: 514  
 14 PRIOR APPLICATION DATA:  
 15 APPLICATION NUMBER: US 08/421,412  
 16 FILING DATE: 14-APR-1995  
 17 ATTORNEY/AGENT INFORMATION:  
 18 NAME: BROWNY, Roger L.  
 19 REGISTRATION NUMBER: 25,618  
 20 REFERENCE/DCKET NUMBER: AHARONI 1A  
 21 TELEPHONE: (202) 528-5197  
 22 TELEFAX: (202) 737-3528  
 23 TELEX: 248643  
 24 INFORMATION FOR SEQ ID NO: 1:  
 25 SEQUENCE CHARACTERISTICS:  
 26 LENGTH: 12 amino acids  
 27 TYPE: amino acid  
 28 STRANDEDNESS: single  
 29 TOPOLOGY: linear  
 30 FEATURE:  
 31 OTHER INFORMATION: The diagram at position 1 is not yet filed  
 32 US 08 548 443

33 Query Match: 46.4% Score 4: 100.0% Length 11:  
 34 Best Local Similarity 100.0% Prod. No. 200221  
 35 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

36 1 ASQA 4  
 37 1 ASQA 4

38 RESULT 37  
 39 US 08 448 443  
 40 Sequence 3: Application US/08/448,443  
 41 Patent No. 5968512  
 42 GENERAL INFORMATION:  
 43 APPLICANT: Tachibana, Ralf  
 44 APPLICANT: Masuro, Robert  
 45 TITLE OF INVENTION: Antibody Recognizing Endothelial Cell  
 46 TITLE OF INVENTION: Liquid for Leukocyte CR1  
 47 NUMBER OF SEQUENCES: 36  
 48 CORRESPONDENCE ADDRESS:  
 49 ADDRESSEE: Klausner & Jackson  
 50 STREET: 411 Hackensack Avenue  
 51 CITY: Hackensack  
 52 STATE: New Jersey  
 53 COUNTRY: U.S.A.  
 54 ZIP: 07601  
 55 COMPUTER READABLE FORM:  
 56 MEDIUM TYPE: Floppy disk  
 57 COMPUTER: IBM PC compatible  
 58 OPERATING SYSTEM: PC-DOS/MS-DOS  
 59 SOFTWARE: Patent In Release #1.0, Version #1.25  
 60 CURRENT APPLICATION DATA:  
 61 APPLICATION NUMBER: US/08/448,443  
 62 FILING DATE: 06-JUN-1995  
 63 CLASSIFICATION: 524  
 64 PRIOR APPLICATION DATA:  
 65 APPLICATION NUMBER: 08/421,412  
 66 FILING DATE: 30-NOV-1994  
 67 CLASSIFICATION: 425  
 68 ATTORNEY/AGENT INFORMATION:  
 69 APPLICATION NUMBER: 08/247,572  
 70 FILING DATE: 23-MAY-1994  
 71 CLASSIFICATION: 424  
 72 PRIOR APPLICATION DATA:  
 73 APPLICATION NUMBER: 07/059276/0725  
 74 FILING DATE: 04-MAY-1992  
 75 CLASSIFICATION: 424  
 76 PRIOR APPLICATION DATA:  
 77 APPLICATION NUMBER: 07/495,613  
 78 FILING DATE: 03-MAY-1991  
 79 CLASSIFICATION: 424  
 80 ATTORNEY/AGENT INFORMATION:  
 81 NAME: Jackson, David  
 82 REGISTRATION NUMBER: 25,742  
 83 REFERENCE/DCKET NUMBER: 600 1 097CIP101V2  
 84 TELEPHONE: 201-447-1484  
 85 TELEFAX: 201-447-1484  
 86 INFORMATION FOR SEQ ID NO: 1:  
 87 SEQUENCE CHARACTERISTICS:  
 88 LENGTH: 24,742

1 REFERENCE/DCKET NUMBER: 600-1-097CIP1  
 2 TELECOMMUNICATION INFORMATION:  
 3 TELEPHONE: 201-487-5800  
 4 TELEFAX: 201-343-1484  
 5 INFORMATION FOR SEQ ID NO: 1:  
 6 SEQUENCE CHARACTERISTICS:  
 7 LENGTH: 11 amino acids  
 8 TYPE: amino acid  
 9 STRANDEDNESS: single  
 10 TOPOLOGY: linear  
 11 FEATURE TYPE: peptide  
 12 US 08 448 443

13 Query Match: 46.4% Score 4: 100.0% Length 11:  
 14 Best Local Similarity 100.0% Prod. No. 200221  
 15 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

16 1 ASQA 4  
 17 1 ASQA 4

18 RESULT 38  
 19 US 08 465 463  
 20 Sequence 3: Application US/08/465,463  
 21 Patent No. 5968512  
 22 GENERAL INFORMATION:  
 23 APPLICANT: Tachibana, Ralf  
 24 APPLICANT: Masuro, Robert  
 25 TITLE OF INVENTION: Antibody Recognizing Endothelial Cell  
 26 TITLE OF INVENTION: Liquid for Leukocyte CR1  
 27 NUMBER OF SEQUENCES: 38  
 28 CORRESPONDENCE ADDRESS:  
 29 ADDRESSEE: Klausner & Jackson  
 30 STREET: 411 Hackensack Avenue  
 31 CITY: Hackensack  
 32 STATE: New Jersey  
 33 COUNTRY: U.S.A.  
 34 ZIP: 07601  
 35 COMPUTER READABLE FORM:  
 36 MEDIUM TYPE: Floppy disk  
 37 COMPUTER: IBM PC compatible  
 38 OPERATING SYSTEM: PC-DOS/MS-DOS  
 39 SOFTWARE: Patent In Release #1.0, Version #1.25  
 40 CURRENT APPLICATION DATA:  
 41 APPLICATION NUMBER: US/08/465,463  
 42 FILING DATE: 06-JUN-1995  
 43 CLASSIFICATION: 524  
 44 PRIOR APPLICATION DATA:  
 45 APPLICATION NUMBER: 08/421,412  
 46 FILING DATE: 30-NOV-1994  
 47 CLASSIFICATION: 425  
 48 ATTORNEY/AGENT INFORMATION:  
 49 APPLICATION NUMBER: 08/247,572  
 50 FILING DATE: 23-MAY-1994  
 51 CLASSIFICATION: 424  
 52 PRIOR APPLICATION DATA:  
 53 APPLICATION NUMBER: 07/059276/0725  
 54 FILING DATE: 04-MAY-1992  
 55 CLASSIFICATION: 424  
 56 PRIOR APPLICATION DATA:  
 57 APPLICATION NUMBER: 07/495,613  
 58 FILING DATE: 03-MAY-1991  
 59 CLASSIFICATION: 424  
 60 ATTORNEY/AGENT INFORMATION:  
 61 NAME: Jackson, David  
 62 REGISTRATION NUMBER: 25,742  
 63 REFERENCE/DCKET NUMBER: 600 1 097CIP101V2  
 64 TELEPHONE: 201-447-1484  
 65 TELEFAX: 201-447-1484  
 66 INFORMATION FOR SEQ ID NO: 1:  
 67 SEQUENCE CHARACTERISTICS:  
 68 LENGTH: 24,742





OTHER INFORMATION: /note "Alked carboxy-terminal  
OTHER INFORMATION: glycine residue"  
PCT US92 10068 7

Query Match 36.4% Score 4: DB 5 Length 11  
Best Local Similarity 100.0% Pred. No. 20027 0: Indels 0: Gaps 0:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ASQA 6  
DB 111  
4 ASQA 7

## RESULT 44

PCT US95 11127-16  
Sequence 16: Application PCT/US9511127  
GENERAL INFORMATION:  
APPLICANT: ROBERT WEHNER  
TITLE OF INVENTION: DOPAMINE RECEPTOR PEPTIDES AND  
ANTIBODIES  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIELEN, PETERSON & LAMKE  
STREET: 1990 N. CALIFORNIA BOULEVARD, SUITE 720  
CITY: WALNUT CREEK  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94596

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE 5.25 INCH, 1.2 MB FLOPPY  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/11127  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NONE  
FILING DATE: NONE

ATTORNEY/AGENT INFORMATION:  
NAME: THEODORE J. BIELEN, JR.  
REGISTRATION NUMBER: 27,420  
REFERENCE/DOCKET NUMBER: 1206#

TELEPHONE: (510) 937-1515  
TELEFAX: (510) 937-1529

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11  
TYPE: AMINO ACID  
STRANDEDNESS: LINEAR  
TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE  
FEATURES:  
NAME/KEY: D3 RECEPTOR (22-42)  
IDENTIFICATION METHOD: AMINO ACID ANALYSIS

OTHER INFORMATION: DOPAMINE D3 RECEPTOR PEPTIDE  
PCT US95 11127-16

Query Match 36.4% Score 4: DB 5 Length 11  
Best Local Similarity 100.0% Pred. No. 20027 0: Indels 0: Gaps 0:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ASQA 4  
DB 2 ASQA 5

## RESULT 45

US CR 012-846-20  
Sequence 20: Application US/08012846  
Patent No. 5662596

GENERAL INFORMATION:  
APPLICANT: Barber, Jack R.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Respass, James G.  
TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
TITLE OF INVENTION: CANCER IMMUNOTHERAPY  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 600 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104 7072  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: PileUp, Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/012,846  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: McMASTER, David D.  
REGISTRATION NUMBER: 31,963  
REFERENCE/DOCKET NUMBER: 930049.40R  
TELEPHONE: (206) 622-4903  
TELEFAX: (206) 682-6633  
TELEX: 4723636  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYDROTHERMAL: NO  
FRAGMENT TYPE: N-terminal  
US-08-032-846-20

Query Match 46.4% Score 4: DB 1: Length 12:  
Best Local Similarity 100.0% Pred. No. 2,1e-02:  
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ASQA 4  
DB 4 ASQA 7

## RESULT 46

US-08-330-599-5  
Sequence 5: Application US/08330599  
Patent No. 5731409

GENERAL INFORMATION:

APPLICANT: Furcht, Leo I.

APPLICANT: McCarthy, James B.

APPLICANT: Fields, Gregg B.

TITLE OF INVENTION: Polypeptides with Type 1 Collagen

TITLE OF INVENTION: Activity

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

STREET: 3100 No. 5731409west Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

1 MEDIUM TYPE: Floppy disk  
 2 COMPUTER: IBM PC compatible  
 3 OPERATING SYSTEM: PC-DOS/MS-DOS  
 4 SOFTWARE: Patent in Release #113, Version #1.2  
 5 CURRENT APPLICATION DATA:  
 6 APPLICATION NUMBER: US/09/300,500  
 7 FILING DATE: 28-OCT-1994  
 8 CLASSIFICATION: 530  
 9 ATTORNEY/AGENT INFORMATION:  
 10 NAME: CARTOT, Charles G.  
 11 REGISTRATION NUMBER: 45,054  
 12 REFERENCE/DOCKET NUMBER: 600,265,881  
 13 TELECOMMUNICATION INFORMATION:  
 14 TELEPHONE: 612-332-5300  
 15 TELEFAX: 612-332-9081  
 16 INFORMATION FOR SEQ ID NO: 51  
 17 SEQUENCE CHARACTERISTICS:  
 18 LENGTH: 12 amino acids  
 19 TYPE: amino acid  
 20 TOPOLOGY: linear  
 21 MOLECULE TYPE: peptide  
 22 US 09-300,500-5

Query Match 36.4%, Score 4, DB 1, Length 12;  
 Best Local Similarity 100.0%, Pred. No. 2, 1e+02;  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0;

QY 8 KKP 11  
 DB 6 KKP 9

1 RESULT 47  
 2 US-08-478-709-41  
 3 Sequence 31, Application US/08/3787-9  
 4 Patent No. 5958684  
 5 GENERAL INFORMATION:  
 6 APPLICANT: TWIST, Michael  
 7 APPLICANT: HARNETT, Richard  
 8 APPLICANT: REID, Lorne  
 9 APPLICANT: SUMNER-SMITH, Martin  
 10 TITLE OF INVENTION: TREATMENT OF HEADS VIBES EXPLOSION  
 11 NUMBER OF SEQUENCES: 33  
 12 CORRESPONDENCE ADDRESS:  
 13 ADDRESSEE: Foley & Lardner  
 14 STREET: 500 Diagonal Road, Suite 500  
 15 CITY: Alexandria  
 16 STATE: VA  
 17 COUNTRY: USA  
 18 ZIP: 22303-2299  
 19 COMPUTER READABLE FORM:  
 20 MEDIUM TYPE: Floppy disk  
 21 OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 SOFTWARE: Patent in Release #113, Version #1.2  
 23 CURRENT APPLICATION DATA:  
 24 APPLICATION NUMBER: US/08/478,709  
 25 FILING DATE:  
 26 CLASSIFICATION: 530  
 27 PRIOR APPLICATION DATA:  
 28 APPLICATION NUMBER: US 07/872,348  
 29 FILING DATE: 23-APR-1992  
 30 APPLICATION NUMBER: US 07/739,746  
 31 FILING DATE: 23-OCT-1991  
 32 PRIOR APPLICATION DATA:  
 33 APPLICATION NUMBER: US 07/602,954  
 34 FILING DATE: 24-OCT-1990  
 35 ATTORNEY/AGENT INFORMATION:  
 36 NAME: BENT, Stephen A.  
 37 REGISTRATION NUMBER: 29,748  
 38 REFERENCE/DOCKET NUMBER: 16737/176 AL...  
 39 TELECOMMUNICATION INFORMATION:  
 40 TELEPHONE: (703)836-9300

1 TELEFAX: (703)683-4109  
 2 TELEX: 899149  
 3 INFORMATION FOR SEQ ID NO: 31:  
 4 SEQUENCE CHARACTERISTICS:  
 5 LENGTH: 12 amino acids  
 6 TYPE: amino acid  
 7 TOPOLOGY: linear  
 8 US 08-478-709-41

Query Match 36.4%, Score 4, DB 2, Length 12;  
 Best Local Similarity 100.0%, Pred. No. 2, 1e+02;  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0;

QY 5 KKP 8  
 DB 5 KKP 8

1 RESULT 48  
 2 US-08-726-306A-140  
 3 Sequence 140, Application US/08/726306A  
 4 Patent No. 5958684  
 5 GENERAL INFORMATION:  
 6 APPLICANT: Van Leeuwen, Frederik Willem  
 7 APPLICANT: Buitach, Johannes Peter Henri  
 8 APPLICANT: Grasveld, Franklie G.  
 9 TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS  
 10 NUMBER OF SEQUENCES: 189  
 11 CORRESPONDENCE ADDRESS:  
 12 ADDRESSEE: Banner & Witcomb, Ltd.  
 13 STREET: 1 Financial Center  
 14 CITY: Boston  
 15 STATE: MA  
 16 COUNTRY: US  
 17 ZIP: 02111

18 COMPUTER READABLE FORM:  
 19 MEDIUM TYPE: Diskette, 4.50 inch, 1.44 Mb storage  
 20 COMPUTER: IBM PC compatible  
 21 OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 SOFTWARE: Wordperfect 6.1  
 23 CURRENT APPLICATION DATA:  
 24 APPLICATION NUMBER: US/08/726,306A  
 25 FILING DATE: 02-OCT-1996  
 26 PRIOR APPLICATION DATA:  
 27 APPLICATION NUMBER: GB 95/20080.4  
 28 FILING DATE: 02-OCT-1995  
 29 PRIOR APPLICATION DATA:  
 30 APPLICATION NUMBER: US 60/009,832  
 31 FILING DATE: 01-Jan-1996  
 32 ATTORNEY/AGENT INFORMATION:  
 33 NAME: Williams, Ph.D., Kathleen M.  
 34 REGISTRATION NUMBER: 34,380  
 35 REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)  
 36 TELECOMMUNICATION INFORMATION:  
 37 TELEPHONE: (617) 345 9100  
 38 TELEFAX: (617) 345 9111  
 39 INFORMATION FOR SEQ ID NO: 140:  
 40 SEQUENCE CHARACTERISTICS:  
 41 LENGTH: 12 amino acids  
 42 TYPE: amino acid  
 43 STRANDEDNESS: single  
 44 TOPOLOGY: unknown  
 45 MOLECULE TYPE: peptide  
 46 US 08-726-306A-140

Query Match 36.4%, Score 4, DB 2, Length 12;  
 Best Local Similarity 100.0%, Pred. No. 2, 1e+02;  
 Matches 4: Conservative 0; Mismatches 0; Gaps 0;

QY 7 KKP 10  
 DB 8 KKP 11



RESULT 49  
 US-09-188-579-51  
 1 Sequence 51: Application US/091495748  
 2 Patent No. 6,107,410  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Shomani, Stewart  
 5 TITLE OF INVENTION: Pharmacological interaction of RNA cap formation  
 6 FILE REFERENCE: 06185  
 7 CURRENT APPLICATION NUMBER: US/09/188-579  
 8 CURRENT FILING DATE: 1998-11-09  
 9 NUMBER OF SEQ ID NOS: 114  
 10 SEQ ID NO 51  
 11 LENGTH: 12  
 12 TYPE: PKG  
 13 ORGANISM: Crithidia fasciculata  
 14 FEATURE:  
 15 OTHER INFORMATION: Motif: 114 of RNA quality/translation  
 US-09-188-579-51

Query Match: 36.4% Score 40.10 C Length 12  
 Best Local Similarity 100.0% Prod No. 2 14-921  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

27 3 GAKR 6  
 14 3 GAKR 12

RESULT 50  
 US-09-115-444-51  
 1 Sequence 51: Application US/09145444A  
 2 Patent No. 6,232,012  
 3 GENERAL INFORMATION:  
 4 APPLICANT: Shomani, Stewart  
 5 TITLE OF INVENTION: Pharmacological interaction of RNA cap formation  
 6 FILE REFERENCE: 06185CIP  
 7 CURRENT APPLICATION NUMBER: US/09/115-444  
 8 CURRENT FILING DATE: 1999-05-20  
 9 PRIOR APPLICATION NUMBER: US 09/188,579  
 10 PRIOR FILING DATE: 1998-11-09  
 11 NUMBER OF SEQ ID NOS: 116  
 12 SEQ ID NO 51  
 13 LENGTH: 12  
 14 TYPE: PKG  
 15 ORGANISM: Crithidia fasciculata  
 16 FEATURE:  
 17 OTHER INFORMATION: Motif: 114 of RNA quality/translation  
 US-09-115-444-51

Query Match: 36.4% Score 40.10 C Length 12  
 Best Local Similarity 100.0% Prod No. 2 14-921  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

27 3 GAKR 6  
 14 3 GAKR 12

Search completed: September 30, 2003, Page 6  
 Job Time: 14.9187 secs

old protein. Protein search, using a model

Title: US-09-787-443-15  
Perfect score: 1  
Sequence: ASQAKRRKQPK 11

Source table: G160  
G160 60.0 , data: 60.0

Source: 830525 sqs, 2806298 sqs

Wissenschaften 11

total number of bits satisfying chosen parameters: 459

Maximum DB size	Length
Maximum DB size	Length: 8
Maximum DB size	Length: 15

**Journal of Interpersonal Violence**

Database : SPTREMBL 23 : \*

2. *St. bacterioides*.

**SUBJECT:**

REGISTRATION - 9  
# of members 05

100-443887-100

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ll: sp_rodent: *
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13: sp_vert,brd:
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51 : survival : \*

17: sparis : 41

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247	2	18.2	10	Q8LLP6	Q8LLP6 gryza sativ	310	2	18.2	11	8	Q8MES1
248	2	18.2	10	Q8LLP6	Q8LLP6 zea mays (m	311	2	18.2	11	8	Q8MEP3
249	2	18.2	10	Q8LLP7	Q8LLP7 philangdomn	312	2	18.2	11	8	Q8MEQ7
250	2	18.2	10	Q8LLP7	Q8LLP7 acallipus sa	313	2	18.2	11	8	Q8MEI9
251	2	18.2	10	Q8LLP7	Q8LLP7 nicotiana t	314	2	18.2	11	8	Q8MER0
252	2	18.2	10	Q8LLP7	Q8LLP7 pinus dale	315	2	18.2	11	8	Q8MES4
253	2	18.2	10	Q8LLP7	Q8LLP7 raltus sp.	316	2	18.2	11	8	Q8MEP5
254	2	18.2	10	Q8LLP7	Q8LLP7 mus sp. pro	317	2	18.2	11	8	Q8MER1
255	2	18.2	10	Q8LLP7	Q8LLP7 rattus tori	318	2	18.2	11	8	Q8SKP8
256	2	18.2	10	Q8LLP7	Q8LLP7 mus muscu	319	2	18.2	11	8	Q8MER7
257	2	18.2	10	Q8LLP7	Q8LLP7 mus sp. pro	320	2	18.2	11	8	Q8HGX5
258	2	18.2	10	Q8LLP7	Q8LLP7 somitricae	321	2	18.2	11	10	Q8G626
259	2	18.2	10	Q8LLP7	Q8LLP7 hepatis q	322	2	18.2	11	10	Q8G590
260	2	18.2	10	Q8LLP7	Q8LLP7 hepatis simp	323	2	18.2	11	10	Q8G784
261	2	18.2	10	Q8LLP7	Q8LLP7 hepatis q	324	2	18.2	11	10	Q8G270
262	2	18.2	10	Q8LLP7	Q8LLP7 human papil	325	2	18.2	11	10	Q841R5
263	2	18.2	10	Q8LLP7	Q8LLP7 pseudotab	326	2	18.2	11	10	Q84131
264	2	18.2	10	Q8LLP7	Q8LLP7 galus gall	327	2	18.2	11	10	Q84092
265	2	18.2	10	Q8LLP7	Q8LLP7 sparus aida	328	2	18.2	11	11	Q8QXM5
266	2	18.2	10	Q8LLP7	Q8LLP7 galus gall	329	2	18.2	11	11	Q89N81
267	2	18.2	10	Q8LLP7	Q8LLP7 galus gall	330	2	18.2	11	11	Q8O807
268	2	18.2	10	Q8LLP7	Q8LLP7 xenopus lae	331	2	18.2	11	11	Q8QYF6
269	2	18.2	10	Q8LLP7	Q8LLP7 moloney mur	332	2	18.2	11	11	Q82207
270	2	18.2	10	Q8LLP7	Q8LLP7 moloney mur	333	2	18.2	11	11	Q8R217
271	2	18.2	10	Q8LLP7	Q8LLP7 moloney mur	334	2	18.2	11	11	Q8QXN6
272	2	18.2	10	Q8LLP7	Q8LLP7 human immun	335	2	18.2	11	12	Q8CS92
273	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	336	2	18.2	11	12	Q8P269
274	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	337	2	18.2	11	12	Q897C1
275	2	18.2	10	Q8LLP7	Q8LLP7 pseudomoc	338	2	18.2	11	12	Q86565
276	2	18.2	10	Q8LLP7	Q8LLP7 bacitracin ap	339	2	18.2	11	13	Q8PS64
277	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	340	2	18.2	11	13	Q8PS22
278	2	18.2	10	Q8LLP7	Q8LLP7 enterococ	341	2	18.2	11	15	Q83410
279	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	342	2	18.2	11	15	Q8DYW4
280	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	343	2	18.2	12	2	Q50959
281	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	344	2	18.2	12	2	Q8KH47
282	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	345	2	18.2	12	2	Q83A08
283	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	346	2	18.2	12	2	Q53579
284	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	347	2	18.2	12	2	Q46747
285	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	348	2	18.2	12	2	Q84M9
286	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	349	2	18.2	12	2	Q47251
287	2	18.2	10	Q8LLP7	Q8LLP7 anabaena sp	350	2	18.2	12	2	Q87134
288	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	351	2	18.2	12	2	Q8R383
289	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	352	2	18.2	12	2	Q8KHU9
290	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	353	2	18.2	12	2	Q8ZAM7
291	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	354	2	18.2	12	2	Q82128
292	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	355	2	18.2	12	2	Q8G8Y8
293	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	356	2	18.2	12	3	Q8J1C6
294	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	357	2	18.2	12	4	Q8UMK0
295	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	358	2	18.2	12	4	Q8H126
296	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	359	2	18.2	12	4	Q8P116
297	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	360	2	18.2	12	4	Q8H001
298	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	361	2	18.2	12	4	Q8UM09
299	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	362	2	18.2	12	4	Q8UC29
300	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	363	2	18.2	12	4	Q8HBU4
301	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	364	2	18.2	12	4	Q8H3W2
302	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	365	2	18.2	12	4	Q81365
303	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	366	2	18.2	12	4	Q8UET4
304	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	367	2	18.2	12	4	Q8NTR7
305	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	368	2	18.2	12	4	Q8N6B2
306	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	369	2	18.2	12	4	Q81V15
307	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	370	2	18.2	12	5	Q8ST99
308	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	371	2	18.2	12	5	Q81740
309	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	372	2	18.2	12	5	Q8T6E8
310	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	373	2	18.2	12	5	Q8T0Y6
311	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	374	2	18.2	12	5	Q26429
312	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	375	2	18.2	12	5	Q8TVU2
313	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	376	2	18.2	12	6	Q8MJQ0
314	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	377	2	18.2	12	6	Q8MJP8
315	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	378	2	18.2	12	6	Q8N2B9
316	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	379	2	18.2	12	6	Q8XS31
317	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	380	2	18.2	12	6	Q8MJP7
318	2	18.2	10	Q8LLP7	Q8LLP7 escherichia	381	2	18.2	12	6	Q8MJP9

482	2	18.2	12	6	QRMJ76	Q81361 ceneclia py	455	2	18.2	12	10	Q9S9J8	Q9S9J8 beta vulgar
483	2	18.2	12	6	Q81R18	Q81R18 bos laurus	456	2	18.2	12	10	Q41744	Q41744 zea mays (m
484	2	18.2	12	6	Q8M153	Q81361 salmuri sci	457	2	18.2	12	10	Q41856	Q41856 zea mays (m
485	2	18.2	12	6	Q8M153	Q81361 atelates fuse	458	2	18.2	12	10	Q8LPT6	Q8LPT6 pinus taeda
486	2	18.2	12	6	Q8M153	Q81361 cecbas apeli	459	2	18.2	12	10	Q9SQF8	Q9SQF8 pinus taeda
487	2	18.2	12	6	Q9N270	Q9N270 pao trolod	460	2	18.2	12	10	P82246	P82246 spinacia ol
488	2	18.2	12	6	Q9S897	Q9S897 equis cubal	461	2	18.2	12	10	P82247	P82247 spinacia ol
489	2	18.2	12	6	Q8M154	Q8M154 actus avata	462	2	18.2	12	10	P82325	P82325 pisum sativ
490	2	18.2	12	6	Q8M154	Q8M154 ceneclia taci	463	2	18.2	12	10	P84011	P84011 arabidopsis
491	2	18.2	12	6	Q8M154	Q8M154 bos laurus	464	2	18.2	12	11	Q8K301	Q8K301 mus musculu
492	2	18.2	12	6	P84127	P84127 bos laurus	465	2	18.2	12	11	Q58608	Q58608 mus musculu
493	2	18.2	12	7	Q41336	Q41336 bos laurus	466	2	18.2	12	11	Q64242	Q64242 rattus sp.
494	2	18.2	12	8	Q8M154	Q8M154 ratiscus bi	467	2	18.2	12	11	Q64313	Q64313 rattus norv
495	2	18.2	12	8	Q8M154	Q8M154 ratiscus es	468	2	18.2	12	11	Q54970	Q54970 mus musculu
496	2	18.2	12	8	Q8M154	Q8M154 ratiscus wa	469	2	18.2	12	11	Q9Q2Y4	Q9Q2Y4 mus musculu
497	2	18.2	12	8	Q8M154	Q8M154 bos laurus	470	2	18.2	12	11	Q925V7	Q925V7 mus musculu
498	2	18.2	12	8	Q8M154	Q8M154 ratiscus so	471	2	18.2	12	11	Q8R2F6	Q8R2F6 rattus norv
499	2	18.2	12	8	Q8M154	Q8M154 gossypium sh	472	2	18.2	12	11	Q91YF5	Q91YF5 mus musculu
500	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	473	2	18.2	12	11	Q8G332	Q8G332 rattus sp.
501	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	474	2	18.2	12	11	Q8CFD7	Q8CFD7 rattus sp.
502	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	475	2	18.2	12	12	Q8S666	Q8S666 rcovirus (t
503	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	476	2	18.2	12	12	Q69232	Q69232 bovine herp
504	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	477	2	18.2	12	12	Q90713	Q90713 xenopus lae
505	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	478	2	18.2	12	12	P82820	P82820 rana catesb
506	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	479	2	18.2	12	12	Q8AUP8	Q8AUP8 salmo trutt
507	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	480	2	18.2	12	12	Q8AUP7	Q8AUP7 salmo salar
508	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	481	2	18.2	12	12	Q9Q0D1	Q9Q0D1 human immun
509	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	482	2	18.2	12	12	Q91CE5	Q91CE5 human immun
510	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	483	2	18.2	12	13	Q50831	Q50831 methanococ
511	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	484	2	18.2	12	13	Q9AMK2	Q9AMK2 xanthomonas
512	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	485	2	18.2	12	13	Q55094	Q55094 synchocyst
513	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	486	2	18.2	12	13	Q9R8K9	Q9R8K9 streptococ
514	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	487	2	18.2	12	13	Q9X3G1	Q9X3G1 prochloroco
515	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	488	2	18.2	12	13	Q916V1	Q916V1 pseudomonas
516	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	489	2	18.2	12	13	Q04220	Q04220 escherichia
517	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	490	2	18.2	12	13	Q9X3J6	Q9X3J6 prochloroco
518	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	491	2	18.2	12	13	Q9RE12	Q9RE12 acidiphiliu
519	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	492	2	18.2	12	13	Q9R5L4	Q9R5L4 streptococ
520	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	493	2	18.2	12	13	Q82835	Q82835 synchococ
521	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	494	2	18.2	12	13	Q53693	Q53693 streptomyce
522	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	495	2	18.2	12	13	Q47607	Q47607 escherichia
523	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	496	2	18.2	12	13	Q8RS09	Q8RS09 uncultured
524	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	497	2	18.2	12	13	Q9X3E1	Q9X3E1 prochloroco
525	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	498	2	18.2	12	13	P97140	P97140 borrelia bu
526	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	499	2	18.2	12	13	Q8KY46	Q8KY46 enterococcu
527	2	18.2	12	8	Q8M154	Q8M154 ratiscus sh	500	2	18.2	12	13	Q9RF24	Q9RF24 mycoplasma

## ALIGNMENTS

RESULT 1	Q9FXC5	PRELIMINARY:	PHI:	15 AA.
AC	Q9FXC5			
DE	01-MAY-2000 (11EMBLrel. 16, Created)			
DE	01-MAY-2000 (11EMBLrel. 13, Last sequence update)			
DE	01-MAY-2000 (11EMBLrel. 13, Last annotation update)			
DE	Small nuclear inclusion polyprotein cleavage product.			
OS	Tobacco etch virus (TEV)			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;			
OC	Polyviruses			
OX	NTBL:TaxID=12227;			
OX	(1)			
RP	SEQUENCE:			
RX	MEDLINE: Q9FXC5:1-155; Pubmed:1851555;			
RA	Dougherty W.G., Parks T.D.;			
RT	"Post-translational processing of the tobacco etch virus 49-kDa small			
RT	nuclear inclusion polyprotein: identification of an internal cleavage			
RT	site and determination of VPg and proteinase domains.";			
PL	Viridory 16:4449-456(1991).			
SQ	SEQUENCE 15 AA: 227-4646100P28C CRC64;			



100 4 QPR 4

RESULT 8

AC Q50434 PRELIMINARY: PRT: 12 AA.  
 DI 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DI 21-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical 1.4 kDa Protein (Fragment).  
 OS Bacillus stearothermophilus.  
 GC Bacteria; Firmicutes; Bacillales; Geobacillales.  
 GX NCBI\_TaxID:1422.  
 RN [1].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN:CM 2483.  
 RX MEDLINE:25194855; PubMed:13732707.  
 RA Vlasova A., Krasny L., Furek V., Jonak J.,  
 RT "The pyzAB Gene Coding for the Large Subunit of Carbamoylphosphate  
 KT Synthetase from Bacillus stearothermophilus: Molecular cloning and  
 KL Functional Characterization".  
 RL Eukla Roda. (1994) 44:163-174(1999).  
 DR EMBL: A001465; CAA05021.1.  
 KW Hypothetical protein.  
 EC NONTER 12 12  
 SQ SEQUENCE 12 AA: 1479 MW: 730870B0E8A6843B CRC64:

Query Match: 27.3% Score 3; PB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASQ 3

11

2 ASQ 4

RESULT 9

AC Q52112 PRELIMINARY: PRT: 12 AA.  
 DI 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Acinetobacter calcoaceticus.  
 GS Bacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Acetivibrio.  
 GX NCBI\_TaxID:471.  
 RN [1].  
 RP SEQUENCE FROM N.A.  
 RC SPECIES A celvocatricus: PLASMID PKH2;  
 RX MEDLINE:9414947; PubMed:8402945;  
 RA Kishimoto G., Kozovskaya G.L., Gorlenko Z.M., Mindlin S.Z.,  
 RT "Molecular characterization of an aberrant mercury resistance  
 PL transposon element from an environmental Acinetobacter strain".  
 RL Plasmid 93:329-308(1994).  
 RN [2].  
 RP SEQUENCE FROM N.A.  
 RC SPECIES Pseudomonas, Alcaligenes sp., E. coli, and E. coli;  
 RX MEDLINE:9740508; PubMed:9159519;  
 RA Nikitov V., Kozovskaya G.L., Mindlin L., Gorlenko Z., Kalyaeva E.,  
 RT "Interferential spread of promiscuous mercury resistance transposons  
 PL in environmental bacteria".  
 RL Mol. Microbiol. 24:321-329(1997).

QY 1 ASQ 3

11

3 ASQ 5

RESULT 10

AC Q52112 PRELIMINARY: PRT: 12 AA.  
 DI 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Acinetobacter calcoaceticus.  
 GS Bacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Acetivibrio.  
 GX NCBI\_TaxID:471.  
 RN [1].  
 RP SEQUENCE FROM N.A.  
 RC SPECIES A celvocatricus: PLASMID PKH2;  
 RX MEDLINE:9414947; PubMed:8402945;  
 RA Kishimoto G., Kozovskaya G.L., Gorlenko Z.M., Mindlin S.Z.,  
 RT "Molecular characterization of an aberrant mercury resistance  
 PL transposon element from an environmental Acinetobacter strain".  
 RL Plasmid 93:329-308(1994).  
 RN [2].  
 RP SEQUENCE FROM N.A.  
 RC SPECIES Pseudomonas, Alcaligenes sp., E. coli, and E. coli;  
 RX MEDLINE:9740508; PubMed:9159519;  
 RA Nikitov V., Kozovskaya G.L., Mindlin L., Gorlenko Z., Kalyaeva E.,  
 RT "Interferential spread of promiscuous mercury resistance transposons  
 PL in environmental bacteria".  
 RL Mol. Microbiol. 24:321-329(1997).

QY 1 ASQ 3

11

3 ASQ 5





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30          1 ASQ 5
RESULT 13
Q8302
ID Q8302 PRELIMINARY: PRT: 13 AA
DI 01 MAR 2003 (TrEMBLrel. 23, Created)
DI 01 MAR 2003 (TrEMBLrel. 23, Last sequence update)
DI 01 MAR 2003 (TrEMBLrel. 23, Last annotation update)
DE luxR (Fragment)
GN luxR
OS Vibrio parvulus
OC Bacteriota; Proteobacteria; Gammaproteobacteria; Vibrionales
OC Vibrionaceae; Vibrionaceae
OX NCBI_TaxID:669
RN 1
RP SEQUENCE FROM N.A.
RA STRAIN B142
RX MELLING 94417855; PubMed 820047
SA Miyamoto C.M., Chatterjee J., Swartzman E., Swartzman E., Kishimoto E.
ST "The role of lux autoinducers in regulation of gene expression in Vibrio
ST parvulus: control of luxR expression."
SC Mol. Microbiol. 19:767-775(1997).
DR EMBL: S84266; AAC56265.1
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1473 MW: 548849.9 P.I.: 5.04
Query Match 27.4% Score 3; DB 3; Length 13;
Best Local Similarity 100.0%; Prod. No. 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AKR 6
DB 5 AKR 7
RESULT 14
Q97N08
ID Q97N08 PRELIMINARY: PRT: 10 AA
DI 01 MAY 2002 (TrEMBLrel. 23, Created)
DI 01 MAY 2002 (TrEMBLrel. 23, Last sequence update)
DI 01 JUN 2002 (TrEMBLrel. 21, Last annotation update)
DE H1A-A2 associated peptide (fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
OX NCBI_TaxID:9606
RN 1
RP SEQUENCE
SA MEDLINE:9222361; PubMed:197112
RA Wei M.L., Grosswell P.J.
ST "H1A-A2 molecules in an antigenic proteinase and are a cell coat and signal
ST sequence-derived peptides."
SC Nature 456:444-446(1992).
FT NON_TER 1 1
SQ SEQUENCE 13 AA: 1355 MW: 151662.06 P.I.: 5.64
Query Match 27.4% Score 6; DB 3; Length 13;
Best Local Similarity 100.0%; Prod. No. 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GPR 11
DB 6 GPR 8
RESULT 15
P82432
ID P82432 PRELIMINARY: PRT: 13 AA
DI 01 JUN 2000 (TrEMBLrel. 14, Created)
DI 01 JUN 2000 (TrEMBLrel. 14, Last sequence update)
DI 01 JUN 2000 (TrEMBLrel. 14, Last annotation update)
DE 42 kDa cell wall protein (Fragment)
OS Nicotiana glauca (Common tobacco)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteroideae; Lamiales; Solanales; Solanaceae; Nicotiana
OX NCBI_TaxID:4097
RN 1
RP SEQUENCE
RA STRAIN CV, PEFF HAVANA
RA Bloc K.A., Bohner V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Woloszek P., Bo. wall G.P.
ST "Proteomic study of secondary cell wall proteins from transformed
ST tobacco cultures."
PL Planta 193:6(2000).
OC 1- SUBCELLULAR LOCATION: CELL WALL.
OC 1- TISSUE SPECIFICITY: XYLEM
KW Cell wall.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1337 MW: 150229.70869706 P.I.: 5.04
Query Match 27.4% Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Prod. No. 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SQA 4
DB 5 SQA 7
RESULT 16
Q8J1G2
ID Q8J1G2 PRELIMINARY: PRT: 14 AA
DI 01 MAR 2003 (TrEMBLrel. 23, Created)
DI 01 MAR 2003 (TrEMBLrel. 23, Last sequence update)
DI 01 MAR 2003 (TrEMBLrel. 23, Last annotation update)
DE YPL156 (Fragment)
GN YPL156
OS Asbya gossypii (Tetrahymena gossypii)
OC Eukaryota; Fungi; Ascomycota; Saccaromycotina; Saccaromycetes;
OC Saccaromycetales; Saccaromycetaceae; Asbya
OX NCBI_TaxID:34169
RN 1
RP SEQUENCE FROM N.A.
RA Alberti-Segall C., Dierick F., Philippson P.
ST "Identification of kinesin related proteins in the filamentous fungus
ST Asbya gossypii."
SC Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF18570; AAC9739.1
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1646 MW: 183128.8081015 P.I.: 5.04
Query Match 27.4% Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Prod. No. 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PKG 9
DB 8 PKG 10
RESULT 17
G15998
ID G15998 PRELIMINARY: PRT: 14 AA
AC G15998
DI 01 NOV 1996 (TrEMBLrel. 01, Created)
DI 01 NOV 1996 (TrEMBLrel. 01, Last sequence update)
DI 01 DEC 2001 (TrEMBLrel. 19, Last annotation update)
DE Neurothrombin type 1 gene protein (fragment)

```

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OS Brca sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 93216281; PubMed 8465367;
RA Anisworth P.J., Rodenhiser D.L., Gusto R.L.;
RT "Identification and characterization of sporadic and inherited
KI mutations in exon 31 of the breast tumour suppressor gene (NFI) gene."
AC Hum. Genet. 91:151-156(1993);
DR EMBL: S07966; A013890.1;
FT NON-TER 1
SQ SEQUENCE 14 AA: 1660 MW: 667950EBC67572 1660;
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKK 5
DB 1
PB 2 AKK 4

RESULT 19
ID P82452 PRELIMINARY; PRI: 14 AA.
AC P82452;
DT 01-JUN-2000 (TRENBLER, 14, Created)
DT 01-MAR-2001 (TRENBLER, 14, Last sequence update)
DE Unknown protein from 2D page of thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fatales; Fabaceae; Papilionoideae; Viciaeae; Pisum;
OX NCBI_TaxID=3838;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX STRAIN CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE 20181728; PubMed-10715320;
RA Peltier J.-H., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of lumenal and peripheral thylakoid proteins."
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
KW Chloroplast; Thylakoid membrane.
FT NON-TER 14
SQ SEQUENCE 14 AA: 1502 MW: 856610E2A00001 1502;
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QAK 5
DB 1
PB 2 QAK 4

RESULT 19
ID P82452 PRELIMINARY; PRI: 14 AA.
AC P82452;
DT 01-JUN-2000 (TRENBLER, 14, Created)
DT 01-MAR-2001 (TRENBLER, 14, Last sequence update)
DE 60S ribosomal protein L26 (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Gamopetalaceae; Spinacia;
OX NCBI_TaxID=3562;

```

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RN [1]
RP SEQUENCE.
RC SIRAIN-CV. ALMARO; TISSUE=LEAF;
RA Yamaguchi K., Subramanian A.R.;
RT "N-terminal sequence of spinach cytosolic 60S ribosomal protein L26."
RL Submitted (APR 2000) to the SWISS-PROT data bank.
CC -!- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
DR INTERPRO: IPR005625; RIBOSOMAL_L24_26.
DR PROSITE: PS01128; RIBOSOMAL_L24_26.
KW Ribosomal protein.
FT NON-TER 14
SQ SEQUENCE 14 AA: 1723 MW: 1876068AC21AD9CA2 CRC64;
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 RAK 6
DB 1
PB 11 RAK 14

RESULT 20
ID P82340 PRELIMINARY; PRI: 14 AA.
AC P82340;
DT 01-JUN-2000 (TRENBLER, 14, Created)
DT 01-JUN-2000 (TRENBLER, 14, Last sequence update)
DT 01-OCT-2000 (TRENBLER, 15, Last annotation update)
DE Unknown protein from 2D page of thylakoid lumen (SPOT204) (Fragment).
OS Pisum sativum (Garden pea)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fatales; Fabaceae; Papilionoideae; Viciaeae; Pisum;
OX NCBI_TaxID=3838;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX STRAIN CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE 20181728; PubMed-10715320;
RA Peltier J.-H., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of lumenal and peripheral thylakoid proteins."
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
KW Chloroplast; Thylakoid membrane.
FT NON-TER 14
SQ SEQUENCE 14 AA: 1505 MW: 2EABFAF980F3D7D7 CRC64;
Query Match 27.3%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKG 5
DB 1
PB 11 RKG 14

RESULT 21
ID Q9EPX6 PRELIMINARY; PRI: 14 AA.
AC Q9EPX6;
DT 01-MAR-2001 (TRENBLER, 16, Created)
DT 01-MAR-2001 (TRENBLER, 16, Last sequence update)
DT 01-MAR-2001 (TRENBLER, 16, Last annotation update)
DE ITSN (Fragment).
GN ITSN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID=10090;
RN [1]

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AT arrayed cDNAs and cosmid libraries";
RL Hum. Mol. Genet. 0:0-0(1995);
DB EMBL: L142079; AAA73800.1;
FI NON_TER 8
SQ SEQUENCE 8 AA: 975 MW: 6556A6C5BEA5A2D3 CRC64:
  18.2%, Score 2; DB 4; Length 8;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
  2 SQ 3
  1
  5 SQ 6

RESULT 41
ID Q15893 PRELIMINARY: PRT: 8 AA.
AC Q15893.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
UT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
GX NCBI_TaxID:9606;
FN [1]
PP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RA Lee C.-C., Yazdani A., Weinert M., Bailey J., Couch J., Xiong M.,
RA Coolbaugh M.L., Chinault C.A., Haldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995);
DB EMBL: L142079; AAA73800.1;
FI NON_TER 8
SQ SEQUENCE 8 AA: 874 MW: DAA1B6D7376456C5 CRC64:
  18.2%, Score 2; DB 4; Length 8;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
  2 SQ 3
  1
  5 SQ 6

RESULT 42
ID Q15468 PRELIMINARY: PRT: 8 AA.
AC Q15468.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
UT 01-MAY-1999 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA for cosmid cC13-1134 PCR primer 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
GX NCBI_TaxID:9606;
FN [1]
PP SEQUENCE FROM N.A.
RC MEDLINE-96445920; PubMed-8838806;
RA James L.A., Inilivie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
RA Amond R.;
RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
RT Es's including 3 members of the Cystatin gene family and
RT identification of CpG islands."
RL Genomics 32:425-440(1996);
DB EMBL: X88976; CAA61407.1;
FI NON_TER 8
SQ SEQUENCE 8 AA: 925 MW: FD5411A7376871E6 CRC64:
  18.2%, Score 2; DB 4; Length 8;

Query Match
  1
  5 SQ 6

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AT arrayed cDNAs and cosmid libraries";
RL Hum. Mol. Genet. 0:0-0(1995);
DB EMBL: L142079; AAA73800.1;
FI NON_TER 8
SQ SEQUENCE 8 AA: 975 MW: 6556A6C5BEA5A2D3 CRC64:
  18.2%, Score 2; DB 4; Length 8;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
  2 SQ 3
  1
  5 SQ 6

RESULT 41
ID Q15893 PRELIMINARY: PRT: 8 AA.
AC Q15893.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
UT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
GX NCBI_TaxID:9606;
FN [1]
PP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RA Lee C.-C., Yazdani A., Weinert M., Bailey J., Couch J., Xiong M.,
RA Coolbaugh M.L., Chinault C.A., Haldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995);
DB EMBL: L142079; AAA73800.1;
FI NON_TER 8
SQ SEQUENCE 8 AA: 874 MW: DAA1B6D7376456C5 CRC64:
  18.2%, Score 2; DB 4; Length 8;
  Best Local Similarity 100.0%; Pred. No. 8.3e+05;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
  2 SQ 3
  1
  5 SQ 6

RESULT 42
ID Q15468 PRELIMINARY: PRT: 8 AA.
AC Q15468.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
UT 01-MAY-1999 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNA for cosmid cC13-1134 PCR primer 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID:9606;
GX NCBI_TaxID:9606;
FN [1]
PP SEQUENCE FROM N.A.
RC MEDLINE-96445920; PubMed-8838806;
RA James L.A., Inilivie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
RA Amond R.;
RT "Walking, cloning and mapping with YACs in 3q27. Localisation of 5
RT Es's including 3 members of the Cystatin gene family and
RT identification of CpG islands."
RL Genomics 32:425-440(1996);
DB EMBL: X88976; CAA61407.1;
FI NON_TER 8
SQ SEQUENCE 8 AA: 925 MW: FD5411A7376871E6 CRC64:
  18.2%, Score 2; DB 4; Length 8;

Query Match
  1
  5 SQ 6

```





```

IN ARAC.
AC Physarum polycephalum (Slime mold)
CC Eukaryota: Mycetozoa: Myxogastria: Myxosporium: Physarales
CC Physarum.
CX NCBI_TaxID:5741;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE:96182131; PubMed:8622766;
SA Record M.C. Garner; C. Garret to be published;
RT *Mapping of a replication origin within the plasmid of strain 120,
RT polyphedral strain.
RI Nature 4:966-970(1996)
RL Mol. Cell. Biol. 16:966-970(1996)
RR EMBL: M7455; AAC03766.1;
FI N-N TER 8
SQ SEQUENCE 8 AA: 878 MW: 14762.666; kDa: 16.24;
      Query Match: 16.2%; Score 2; DB 6; Length 8;
      Best Local Similarity: 100.0%; Pred. No. B: 3e-05;
      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 1 QA 4
      QL 11
      QZ 7 QA 5

RESULT 4:
P22686
ID P22686 PRELIMINARY: PRI: 8 AA.
AC Q939H1;
DI 01-MAR-2001 (TrEMBLrel. 16, created)
DI 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
DE Art. 15. (Statement).
US Laccorhynchus obscurus (bushy dolphin).
CC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
CC Mammalia: Cetartiodactyla: Cetacea: Odontoceti: Delphinidae;
CC Laccorhynchus.
CX NCBI_TaxID:27611;
RN 11;
RP SEQUENCE FROM N.A.
RX Harte M.P.; Chapman F.; Colambo, S.P.;
RX "Slow Evolution of Genetic Morphology in Dolphins: Implications for
RX Speciation, Systematics and Conservation".
RX Submitted (Apr 1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF143943; AAF9866; 1;
FI N-N TER 8
SQ SEQUENCE 8 AA: 962 MW: 58018.41774086240; kDa:
      Query Match: 16.2%; Score 2; DB 6; Length 8;
      Best Local Similarity: 100.0%; Pred. No. B: 3e-05;
      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 10 PR 11
      QL 11
      QZ 5 PR 6

Search completed: September 01, 2003, 10:17:31
Core time: 15.6697 secs

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IN ARAC.
AC Physarum polycephalum (Slime mold)
CC Eukaryota: Mycetozoa: Myxogastria: Myxosporium: Physarales
CC Physarum.
CX NCBI_TaxID:5741;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE:96182131; PubMed:8622766;
SA Record M.C. Garner; C. Garret to be published;
RT *Mapping of a replication origin within the plasmid of strain 120,
RT polyphedral strain.
RI Nature 4:966-970(1996)
RL Mol. Cell. Biol. 16:966-970(1996)
RR EMBL: M7455; AAC03766.1;
FI N-N TER 8
SQ SEQUENCE 8 AA: 878 MW: 14762.666; kDa: 16.24;
      Query Match: 16.2%; Score 2; DB 6; Length 8;
      Best Local Similarity: 100.0%; Pred. No. B: 3e-05;
      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 1 QA 4
      QL 11
      QZ 7 QA 5

RESULT 4:
P22686
ID P22686 PRELIMINARY: PRI: 8 AA.
AC Q939H1;
DI 01-MAR-2001 (TrEMBLrel. 16, created)
DI 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
DE Art. 15. (Statement).
US Laccorhynchus obscurus (bushy dolphin).
CC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
CC Mammalia: Cetartiodactyla: Cetacea: Odontoceti: Delphinidae;
CC Laccorhynchus.
CX NCBI_TaxID:27611;
RN 11;
RP SEQUENCE FROM N.A.
RX Harte M.P.; Chapman F.; Colambo, S.P.;
RX "Slow Evolution of Genetic Morphology in Dolphins: Implications for
RX Speciation, Systematics and Conservation".
RX Submitted (Apr 1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF143943; AAF9866; 1;
FI N-N TER 8
SQ SEQUENCE 8 AA: 962 MW: 58018.41774086240; kDa:
      Query Match: 16.2%; Score 2; DB 6; Length 8;
      Best Local Similarity: 100.0%; Pred. No. B: 3e-05;
      Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      QY 10 PR 11
      QL 11
      QZ 5 PR 6

Search completed: September 01, 2003, 10:17:31
Core time: 15.6697 secs

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Complete version 5.1.6  
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of protein - protein search, using sw model

Run date: September 30, 2003, 11:06:56, Server time: 0.24 seconds  
(without localizations)  
#2/67 MUs and 60,141 pairs/sw

File: us-09-787-443-15

Perfect score: 13

Sequence: 1 ASQAKKKCPK 11

Search: 127864 seqs, 47026765 residues

Word size: 6

Total number of hits satisfying chosen parameters: 707

Minimum hit seq length: 8

Maximum hit seq length: 15

Post processing: Listing first 500 summaries

Database: SwissProt\_41\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Accession No.	Score	Match	Length	DB	Hit	Description
1	4	46.4	8	RS7_MUCL	1	14744 Myoblastin
2	3	27.3	9	FA57_ASNS1	1	14741 ASNS1
3	3	27.3	9	FA57_ASNS1	1	14742 ASNS1
4	3	27.3	9	TRF4_P12	1	10245 TRF4
5	3	27.3	14	PRK6_PERAM	1	18293 PRK6
6	3	27.3	15	KL1A_SPT1C	1	18294 KL1A
7	2	18.2	8	AL15_CASMS	1	18295 AL15
8	2	18.2	8	AL15_CASMS	1	18296 AL15
9	2	18.2	8	AL15_CASMS	1	18297 AL15
10	2	18.2	8	AL15_CASMS	1	18298 AL15
11	2	18.2	8	AL15_CASMS	1	18299 AL15
12	2	18.2	8	AL15_CASMS	1	18300 AL15
13	2	18.2	8	AL15_CASMS	1	18301 AL15
14	2	18.2	8	AL15_CASMS	1	18302 AL15
15	2	18.2	8	AL15_CASMS	1	18303 AL15
16	2	18.2	8	AL15_CASMS	1	18304 AL15
17	2	18.2	8	AL15_CASMS	1	18305 AL15
18	2	18.2	8	AL15_CASMS	1	18306 AL15
19	2	18.2	8	AL15_CASMS	1	18307 AL15
20	2	18.2	8	AL15_CASMS	1	18308 AL15
21	2	18.2	8	AL15_CASMS	1	18309 AL15
22	2	18.2	8	AL15_CASMS	1	18310 AL15
23	2	18.2	8	AL15_CASMS	1	18311 AL15
24	2	18.2	8	AL15_CASMS	1	18312 AL15
25	2	18.2	8	AL15_CASMS	1	18313 AL15
26	2	18.2	8	AL15_CASMS	1	18314 AL15
27	2	18.2	8	AL15_CASMS	1	18315 AL15
28	2	18.2	8	AL15_CASMS	1	18316 AL15
29	2	18.2	8	AL15_CASMS	1	18317 AL15
30	2	18.2	8	AL15_CASMS	1	18318 AL15
31	2	18.2	8	AL15_CASMS	1	18319 AL15
32	2	18.2	8	AL15_CASMS	1	18320 AL15
33	2	18.2	8	AL15_CASMS	1	18321 AL15

34	2	18.2	9	PR6_CALVO	1	PR6_CALVO
35	2	18.2	9	HCTU_KLEAB	1	HCTU_KLEAB
36	2	18.2	9	HCTU_KLEAB	1	HCTU_KLEAB
37	2	18.2	9	LMT1_LCCMI	1	LMT1_LCCMI
38	2	18.2	9	NEUC_CAVPO	1	NEUC_CAVPO
39	2	18.2	9	NEUC_HUMAN	1	NEUC_HUMAN
40	2	18.2	9	OXY1_CYPCA	1	OXY1_CYPCA
41	2	18.2	9	PRK1_PERAM	1	PRK1_PERAM
42	2	18.2	9	RT13_HCVIN	1	RT13_HCVIN
43	2	18.2	9	TK11_LCCMI	1	TK11_LCCMI
44	2	18.2	9	ULAK_MGUSE	1	ULAK_MGUSE
45	2	18.2	9	YAFR_AZONI	1	YAFR_AZONI
46	2	18.2	9	ABV_PROSE	1	ABV_PROSE
47	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
48	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
49	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
50	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
51	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
52	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
53	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
54	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
55	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
56	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
57	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
58	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
59	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
60	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
61	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
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63	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
64	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
65	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
66	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
67	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
68	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
69	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
70	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
71	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
72	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
73	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
74	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
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77	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
78	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
79	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
80	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
81	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
82	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
83	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
84	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
85	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
86	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
87	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
88	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
89	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
90	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
91	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
92	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
93	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
94	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
95	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
96	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
97	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
98	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
99	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
100	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
101	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
102	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
103	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
104	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
105	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA
106	2	18.2	9	BPP2_HCTJA	1	BPP2_HCTJA







```

>>> HAMAN: KF 95480: 27.4% Score 3; DB 1; Length 9;
DB Info: PDB: 1P600245; KIBOSMAL_S7; LAPTIA;
KW Kibosomal protein; RNA-binding; RNA binding; RNA binding;
FT CNI_MEF 0 0 KY SIMILARITY;
FT NUN_LPR 4 8
SQ SEQUENCE 8 AA; 850 MW; 6527467665433333 CRC64;

Query Match: 27.4% Score 3; DB 1; Length 9;
Best Local Similarity: 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GKR 11
LD 1 GKR 1

RESULT 1
TYPE: LIG
ID THYL_F05 STANDARD: PRT 9 AA.
AC 201259;
DI 21-JUL-1995 (Rel. 32, Created);
DI 21-JUL-1995 (Rel. 33, Last sequence update);
DI 28-FEB-2001 (Rel. 41, Last annotation update);
DE Thymic factor;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eumetaria; Cetartiodactyla; Suina; Suidae; Sus;
OX NCBI_TaxID: 9823;
RN [1];
RZ SEQUENCE;
RX MEDLINE: 7802671; PubMed: 914862;
RA Plead C. M., Gaudin M., Blouquit Y., Bach J.-F.;
RT "Structural Study of circulating thymic factor: a peptide isolated
RT from pig serum. II. Amino acid sequence.";
RL J. Biol. Chem. 252:8045-8047(1977);
CC 1 MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR: A01527; YFPG;
KW Pyroglutamic carboxylic acid;
FT MOD_RES 1;
SQ SEQUENCE 9 AA; 876 MW; 1500887866533333 CRC64;

Query Match: 27.4% Score 3; DB 1; Length 9;
Best Local Similarity: 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAK 5
LD 1 GAK 5

RESULT 5
TYPE: PERAM
ID PERAM STANDARD: PRT 14 AA.
AC 082594;
DI 16-JUL-2001 (Rel. 40, Created);
DI 16-JUL-2001 (Rel. 40, Last sequence update);
DI 16-JUL-2001 (Rel. 40, Last annotation update);
DE Pyroglutamic 6 (P6a-PK6) (EXPI-amide);
OS Periplaneta americana (American cockroach);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthoptera; Dermaptera; Blattellidae; Blattodea;
OC Blattellidae; Periplaneta;
OX NCBI_TaxID: 5978;
RN [1];
RZ SEQUENCE;
RX MEDLINE: 10723010; PubMed: 10723010;
RA Predict R., Eckert M.;
RT "Tissue-specific distribution of EXPI-amides in the nervous system of
RT the American cockroach.";
OS J. Comp. Neurol. 419:352-363(2000);
CC 1 FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
CC 1 TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN
CC ABNORMAL PERISYMPATHETIC ORGANS.
CC 1 MASS SPECTROMETRY: MW-1590.6; METHO-MALDI;
CC 1 SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW Neuropeptide; Amidation.

```

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>>> HAMAN: KF 95480: 27.4% Score 3; DB 1; Length 9;
DB Info: PDB: 1P600245; KIBOSMAL_S7; LAPTIA;
KW Kibosomal protein; RNA-binding; RNA binding; RNA binding;
FT CNI_MEF 0 0 KY SIMILARITY;
FT NUN_LPR 4 8
SQ SEQUENCE 8 AA; 850 MW; 6527467665433333 CRC64;

Query Match: 27.4% Score 3; DB 1; Length 9;
Best Local Similarity: 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKR 10
LD 2 GKR 5

RESULT 2
TYPE: ASNSU
ID FAP7_ASNSU STANDARD: PRT 9 AA.
AC 243717;
DI 01-NOV-1995 (Rel. 32, Created);
DI 01-NOV-1995 (Rel. 32, Last sequence update);
DI 01-FEB-1996 (Rel. 33, Last annotation update);
DE FPRamide-like neuropeptide A27;
OS Ascaris suum (Pig roundworm); (Ascaris lumbricoides);
OC Eukaryota; Metazoa; Nematoda; Chordata; Ascarididae; Ascarididae;
OX NCBI_TaxID: 6253;
RN [1];
RZ SEQUENCE;
RX MEDLINE: 95490362; PubMed: 7651954;
RA Cowden C., Strutton A.O.W.;
RT "Eight novel FPRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:497-500(1995);
CC 1 SIMILARITY: BELONGS TO THE FAP7 (FPRAMIDE) FAMILY;
KW Neuropeptide; Amidation.

Query Match: 27.4% Score 3; DB 1; Length 9;
Best Local Similarity: 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GKR 4
LD 2 GKR 4

RESULT 4
TYPE: ASNSU
ID FAP9_ASNSU STANDARD: PRT 9 AA.
AC 243727;
DI 01-NOV-1995 (Rel. 32, Created);
DI 01-NOV-1995 (Rel. 32, Last sequence update);
DI 01-FEB-1996 (Rel. 33, Last annotation update);
DE FPRamide-like neuropeptide A9;
OS Ascaris suum (Pig roundworm); (Ascaris lumbricoides);
OC Eukaryota; Metazoa; Nematoda; Chordata; Ascarididae; Ascarididae;
OX NCBI_TaxID: 6253;
RN [1];
RZ SEQUENCE;
RX MEDLINE: 95490362; PubMed: 7651954;
RA Cowden C., Strutton A.O.W.;
RT "Eight novel FPRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995);
CC 1 SIMILARITY: BELONGS TO THE FAP7 (FPRAMIDE) FAMILY;
KW Neuropeptide; Amidation.

```



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OX NCBI_TaxID:6759;
RN
SEQUENCE:
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed:9461295;
RA Duve H., Johnson A.H., Maestro J.L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT *Isolation and identification of multiple neuropeptides of the
RT allatostatinsuperfamily in the shore crab Carcinus maenas.*;
RL Eur. J. Biochem. 250:727-734(1997);
DE Carcinus maenas (Common shore crab) (Green crab).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT M06.RES 8
SQ SEQUENCE 8 AA: 813 MW: 702848.485 68% 47%
Query Match 18.2% Score 2: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GP 10
LB 11
2 GP 3

RESULT 10
ALIB_CALVO STANDARD: PRI: 8 AA.
AC P41441;
DT 01 NOV 1995 (Rel. 32, Created);
DT 01 NOV 1995 (Rel. 32, Last sequence update);
DT 15-SEP-2000 (Rel. 42, Last annotation update);
DE Calliphora vicina (Blue blowfly).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
KW Eukaryota; Metazoa; Arthropoda; Insecta; Diptera; Phlebotomina; Calliphoridae; Calliphora.
CX NCBI_TaxID:27454;
RN
SEQUENCE:
RX MEDLINE=94211950; PubMed 6400167;
RA Duve H., Johnson A.H., Scott A.G., Jaros P.P., Thorpe A.G.,
RA Thorpe A.;
RT *Calliphorins: neuropeptides from the blowfly Calliphora vicina
RT with sequence homology to cockroach allatostatins.*;
RL Proc. Natl. Acad. Sci. U.S.A. 90:2455-2459(1993);
RN
SEQUENCE:
RX MEDLINE=94142269; PubMed 8661726;
RA Duve H., Johnson A.H., Scott A.G., Jaros P.P., Thorpe A.G.,
RA Thorpe A.;
RT *Hypophorin: calliphorin-like peptide with biological properties of
RT a novel neuropeptide from the blowfly Calliphora vicina.*;
RL B.J. Chem. 269:2105-2109(1994);
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN, MAY BE
CC INVOLVED IN THE CONTROL OF VISUAL RESPONSES, AND ALSO
CC BEHAVE AS POTENT INHIBITORS OF PERIPHERAL MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE IN MUSCLES OF THE GUT AND HEART.
CC -1- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DE PIR: E47393; E47394;
KW Neuropeptide; Amidation; Hydroxylation.
FT M06.RES 3 3 HYDROXYLATION
SQ SEQUENCE 8 AA: 883 MW: 719679.683 77% 46%

Query Match 18.2% Score 2: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GP 10
LB 11
2 GP 3

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DB 1 GP 2
RESULT 11
ALIB_CARMA STANDARD: PRI: 8 AA.
AC P81609; P81604; P81830;
DT 30-MAY-2000 (Rel. 39, Created);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 15-SEP-2000 (Rel. 42, Last annotation update);
DE Carcinus maenas (Common shore crab) (Green crab).
CC -1- FUNCTION: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
KW Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CX NCBI_TaxID:6754;
RN
SEQUENCE:
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed:9461295;
RA Duve H., Johnson A.H., Maestro J.L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT *Isolation and identification of multiple neuropeptides of the
RT allatostatinsuperfamily in the shore crab Carcinus maenas.*;
RL Eur. J. Biochem. 250:727-734(1997);
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
KW Neuropeptide; Amidation; Multigene family.
FT M06.RES 8
SQ SEQUENCE 8 AA: 795 MW: 922879.008 75% 47%

Query Match 18.2% Score 2: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
LB 1 AS 2

RESULT 12
ALIB_CARMA STANDARD: PRI: 8 AA.
AC P81611;
DT 30-MAY-2000 (Rel. 39, Created);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 30-MAY-2000 (Rel. 39, Last annotation update);
DE Carcinus maenas (Common shore crab) (Green crab).
KW Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
KW Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
CX NCBI_TaxID:6754;
RN
SEQUENCE:
RX TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed:9461295;
RA Duve H., Johnson A.H., Maestro J.L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT *Isolation and identification of multiple neuropeptides of the
RT allatostatinsuperfamily in the shore crab Carcinus maenas.*;
RL Eur. J. Biochem. 250:727-734(1997);
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
KW Neuropeptide; Amidation; Multigene family.
FT M06.RES 8
SQ SEQUENCE 8 AA: 795 MW: 922879.008 75% 47%

Query Match 18.2% Score 2: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

```





**PN** SEQUENCE FROM N.A.  
**RP** STRAIN=968;  
**RX** MEDLINE=91041730; PubMed 223255;  
**RA** Ross J.L., Eady B.A., Gave J.H., Canlitte W.J., Baumberg S.,  
Wootton J.C.;  
**RT** "Inducible erythromycin resistance in staphylococci is encoded by a  
member of the ATP-binding transport super-gene family";  
**RL** Mol. Microbiol. 4:1207-1214(1990).  
**CC** FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE  
PROTEIN.

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entities requires a license agreement (See http://www.isb-sib.ch/announce/  
or send an email to license@isb-sib.ch).

**DE** PIR: X520F5; CAA46303.1;  
**DR** PIR: S11157; LFSAME;  
**KW** leader peptide; Plasmid.  
**SQ** SEQUENCE 5 AA: 517 MW: FA74406B5HOC1A6 CRC64;

Query Match 18.2%, Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 AS 2  
**DB** 3 AS 4

**RESULT 19**  
**NS3\_MYC1U** STANDARD: PKT; 8 AA.  
**AC** P81152;  
**DI** 15-JUL-1999 (Rel. 38, Created)  
**DI** 15-JUL-1999 (Rel. 38, Last sequence update)  
**DI** 16-OCT-2001 (Rel. 40, Last annotation update)  
**DE** 30 kDa non-secretory protein 3 (fragment).  
**GS** Mycobacterium tuberculosis  
**OC** Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
**GC** Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
**GX** NCBI\_TaxID=1774;  
**RN** (  
**RC** SEQUENCE.  
**FP** STRAIN-H47Kv.  
**EC** F1ased H.K.; Annotated P.S.;  
**RI** Submitted (DEC-1997) to the SWISS PROI data bank.  
**CC** CAUTION: We are unable to find this protein in the translation of  
the genome of strain H47Kv.  
**FT** NON\_TER 1;  
**FT** NON\_TER 8;  
**SQ** SEQUENCE 8 AA: 919 MW: ED4DC40B19DCD2D2 CRC64;

Query Match 18.2%, Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 4 AK 5  
**DB** 7 AK 8

**RESULT 20**  
**PKK2\_PERAM** STANDARD: PRI; 8 AA.  
**ID** PKK2\_PERAM  
**AC** P82692;  
**DI** 16-OCT-2001 (Rel. 40, Created)  
**DI** 16-OCT-2001 (Rel. 40, Last sequence update)  
**DI** 16-OCT-2001 (Rel. 40, Last annotation update)  
**GX** NCBI\_TaxID=1282;

**PN** SEQUENCE FROM N.A.  
**RP** STRAIN=968;  
**RX** MEDLINE=91041730; PubMed 223255;  
**RA** Ross J.L., Eady B.A., Gave J.H., Canlitte W.J., Baumberg S.,  
Wootton J.C.;  
**RT** "Inducible erythromycin resistance in staphylococci is encoded by a  
member of the ATP-binding transport super-gene family";  
**RL** Mol. Microbiol. 4:1207-1214(1990).  
**CC** FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE  
PROTEIN.

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modified and this statement is not removed, usage by and for commercial  
entities requires a license agreement (See http://www.isb-sib.ch/announce/  
or send an email to license@isb-sib.ch).

**DE** PIR: X520F5; CAA46303.1;  
**DR** PIR: S11157; LFSAME;  
**KW** leader peptide; Plasmid.  
**SQ** SEQUENCE 5 AA: 517 MW: FA74406B5HOC1A6 CRC64;

Query Match 18.2%, Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 AS 2  
**DB** 3 AS 4

**RESULT 19**  
**NS3\_MYC1U** STANDARD: PKT; 8 AA.  
**AC** P81152;  
**DI** 15-JUL-1999 (Rel. 38, Created)  
**DI** 15-JUL-1999 (Rel. 38, Last sequence update)  
**DI** 16-OCT-2001 (Rel. 40, Last annotation update)  
**DE** 30 kDa non-secretory protein 3 (fragment).  
**GS** Mycobacterium tuberculosis  
**OC** Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;  
**GC** Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
**GX** NCBI\_TaxID=1774;  
**RN** (  
**RC** SEQUENCE.  
**FP** STRAIN-H47Kv.  
**EC** F1ased H.K.; Annotated P.S.;  
**RI** Submitted (DEC-1997) to the SWISS PROI data bank.  
**CC** CAUTION: We are unable to find this protein in the translation of  
the genome of strain H47Kv.  
**FT** NON\_TER 1;  
**FT** NON\_TER 8;  
**SQ** SEQUENCE 8 AA: 919 MW: ED4DC40B19DCD2D2 CRC64;

Query Match 18.2%, Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 4 AK 5  
**DB** 7 AK 8

**RESULT 20**  
**PKK2\_PERAM** STANDARD: PRI; 8 AA.  
**ID** PKK2\_PERAM  
**AC** P82692;  
**DI** 16-OCT-2001 (Rel. 40, Created)  
**DI** 16-OCT-2001 (Rel. 40, Last sequence update)  
**DI** 16-OCT-2001 (Rel. 40, Last annotation update)  
**GX** NCBI\_TaxID=1282;



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CX NCBI_Lox1L-4577;
RX [11]
RE SEQUENCE
RC TISSUE: Colloquial;
RA Touzet P., Ricard F., Melis J., Combes G., L'Homme J. C.,
RI Perinot J. C., Zivy M., de Vries F.
RI *The maize two dimensional gel protein database contains an integrated
RI genome analysis program.*
RG TAGS: Appl. Genet. 93997-1995(1995)
RC 1- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 52.2 KDa.
LR Maize ZMOAB; Rec642; Colloquial;
ET NON-TER 1
ET NON-TER 5
SQ SEQUENCE 8 AA: 990 MW: 99000Da; length: 8 AA.

Query Match 18.2% Score 2: DB 1; length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1R 11
QZ 4 4R 4

RESULT 24
QUERY_KAT
ID: CHOU_KAT STANDARD: PSI 8 AA.
AC P66575.
ET 15 DEC-1998 (Rel. 37, Created)
ET 15 DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (SP: P1) (Francia);
OS Rattus norvegicus (Rat);
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
CX NCBI_Lox1L-10116;
ET NON-TER 1
ET NON-TER 5
RE SEQUENCE
RC STRAIN Wistar TISSUE: Heart;
RA L. X. L., Flossner K. P., Schaefer C., Reutter-Zandrasek V., Salkov J.,
RI Jundt, P. S.
RI Submitted (SEP 1998) to the SWISS-PROT data bank.
CC 1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 KDa.
ET NON-TER 8
ET NON-TER 8
SQ SEQUENCE 8 AA: 1029 MW: 98277Da; length: 765-4;

Query Match 18.2% Score 2: DB 1; length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1R 7
QZ 4 4R 4

RESULT 25
QUERY_KAT
ID: CHOU_KAT STANDARD: PSI 8 AA.
AC P4087.
ET 01 APR-1993 (Rel. 25, Created)
ET 01 APR-1993 (Rel. 25, Last sequence update)
DT 16 JUL-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (SP: P2) (Francia);
OS Rattus norvegicus (Rat);
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
CX NCBI_Lox1L-9606;
ET NON-TER 1
ET NON-TER 11
RE SEQUENCE
RC TISSUE: Heart;
RA L'Homme J. C., Zivy M., de Vries F.,
RI Perinot J. C., Zivy M., de Vries F.
RI *The maize two dimensional gel protein database contains an integrated
RI genome analysis program.*
RG TAGS: Appl. Genet. 93997-1995(1995)
CC 1- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 52.2 KDa.
LR Maize ZMOAB; Rec642; Colloquial;
ET NON-TER 1
ET NON-TER 5
SQ SEQUENCE 8 AA: 990 MW: 99000Da; length: 8 AA.

Query Match 18.2% Score 2: DB 1; length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1R 11
QZ 4 4R 4

RESULT 26
QUERY_KAT
ID: CHOU_KAT STANDARD: PSI 8 AA.
AC P66575.
ET 15 DEC-1998 (Rel. 37, Created)
ET 15 DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glycoprotein G (Francia);
OS Herpes simplex virus (type 2 / strain H4270R);
CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC Alphaherpesvirinae; Simpliciviruses;
CX NCBI_Lox1L-103921;
ET NON-TER 1
ET NON-TER 11
RE SEQUENCE
RC STRAIN Wistar TISSUE: Heart;
RA L'Homme J. C., Zivy M., de Vries F.,
RI Perinot J. C., Zivy M., de Vries F.
RI *The maize two dimensional gel protein database contains an integrated
RI genome analysis program.*
RG TAGS: Appl. Genet. 93997-1995(1995)
CC 1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GE,
CC 3: GH, GB, GC, GD, GE,
CC 4: MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
CX Glycoprotein;
ET NON-TER 8
ET NON-TER 8
SQ SEQUENCE 8 AA: 683 MW: 784786772Da; length: 588-6;

Query Match 18.2% Score 2: DB 1; length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1R 11
QZ 4 4R 7

RESULT 27
QUERY_KAT
ID: CHOU_KAT STANDARD: PSI 9 AA.
AC P25486.
ET 01 NOV-1988 (Rel. 09, Created)
ET 01 NOV-1988 (Rel. 09, Last sequence update)
DT 24 FEB-2003 (Rel. 41, Last annotation update)
DE Lysosomal protein G;
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CX NCBI_Lox1L-6491;
ET NON-TER 1
ET NON-TER 11
RE SEQUENCE
RC MEDLINE: 88055512; PubMed 3680228;
RA Gray W. P., Zatyarski V., Zatyarski G. C., Ramilo C. A., Zeikus K. D.,

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RA Hughes G. J., Pringle S., Paquet N., Ravier F., Pasquali G.,
RA Sanchez J. C., Games R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D. F.;
RI *Plasma protein map: an update by microsequencing.*;
RI Electrophoresis 13:707-714(1992).
CC 1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
CC PROTEIN IS: 4.9, ITS MW IS: 65 KDa.
LR Swiss ZUPAGE; P6087; HUMAN;
ET NON-TER 1
ET NON-TER 1
ET NON-TER 8
ET NON-TER 8
SQ SEQUENCE 8 AA: 943 MW: 94377Da; length: 8 AA.

Query Match 18.2% Score 2: DB 1; length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1R 11
QZ 7 7R 8

RESULT 28
QUERY_KAT
ID: CHOU_KAT STANDARD: PSI 8 AA.
AC P61780.
ET 15 DEC-1998 (Rel. 37, Created)
ET 15 DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Glycoprotein G (Francia);
OS Herpes simplex virus (type 2 / strain H4270R);
CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC Alphaherpesvirinae; Simpliciviruses;
CX NCBI_Lox1L-103921;
ET NON-TER 1
ET NON-TER 11
RE SEQUENCE
RC STRAIN Wistar TISSUE: Heart;
RA L'Homme J. C., Zivy M., de Vries F.,
RI Perinot J. C., Zivy M., de Vries F.
RI *The maize two dimensional gel protein database contains an integrated
RI genome analysis program.*
RG TAGS: Appl. Genet. 93997-1995(1995)
CC 1- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GD, GE,
CC 3: GH, GB, GC, GD, GE,
CC 4: MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
CX Glycoprotein;
ET NON-TER 8
ET NON-TER 8
SQ SEQUENCE 8 AA: 683 MW: 784786772Da; length: 588-6;

Query Match 18.2% Score 2: DB 1; length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 1R 11
QZ 4 4R 7

RESULT 29
QUERY_KAT
ID: CHOU_KAT STANDARD: PSI 9 AA.
AC P25486.
ET 01 NOV-1988 (Rel. 09, Created)
ET 01 NOV-1988 (Rel. 09, Last sequence update)
DT 24 FEB-2003 (Rel. 41, Last annotation update)
DE Lysosomal protein G;
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CX NCBI_Lox1L-6491;
ET NON-TER 1
ET NON-TER 11
RE SEQUENCE
RC MEDLINE: 88055512; PubMed 3680228;
RA Gray W. P., Zatyarski V., Zatyarski G. C., Ramilo C. A., Zeikus K. D.,

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BA Schenckeburger G.A., Maier P.F., Lohler H.J., Wilson K., Mancier S.  
 "The delta EEG (sleep)-inducing peptide (DSIP): XI. Amino acid  
 analysis, sequence, synthesis and activity of the nonapeptide."  
 J. Neurosci. Arch. 376:119-129(1973).  
 EN 31  
 RP REVIEWS  
 RA MEDLINE 87175129; PubMed 8560726.  
 RX Graf S.V., Kastin A.J.:  
 "Delta-sleep-inducing peptide (DSIP): an update."  
 Peptides 7:1165-1187(1986).  
 RL Peptides 7:1165-1187(1986).  
 CC -1- FUNCTION: WHEN INFUSED INTO THE MESS LIEN RHALIC VENTRICLE OF  
 RECEPTIVE RABBITS INDUCES SINGLE AND DOUBLE EEG ACTIVITY AND  
 REDUCED MOTOR ACTIVITIES.  
 CC -1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM CALYCEAL OF  
 OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KILLED BY ELECTRIC  
 STIMULATION OF THE THALAMUS.  
 CC -1- LATABASE: NAME-PROTEIN Spotlight  
 CC NIDF Issue 8 of March 2001.  
 CC WWW:"http://www.expasy.org/spotlight/articles/spotlight.html".  
 DR PIR: A01422; Q00B. 849 MW; 050365RDAAB7675 (2004).  
 SQ SEQUENCE 9 AA: 849 MW; 050365RDAAB7675 (2004).

Query Match 18.2% Score 2: DB 1: Length 9;  
 Best Local Similarity 100.0% Pred. No. 1.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

DE 6 AS 7

RESULT 31

FAK2\_CALVO  
 ID FAK2\_CALVO STANDARD; PRT; 9 AA.  
 AC P41857;  
 DI 01-NOV-1995 (Rel. 32, Created)  
 DI 01-NOV-1995 (Rel. 32, Last sequence update)  
 DI 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliophora vomitoria (Blue blowfly).  
 OS Calliophora vomitoria.  
 OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OS Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestridae;  
 OS Calliophoridae; Calliphora.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 DR PIR: A01422; Q00B. 849 MW; 050365RDAAB7675 (2004).  
 SQ SEQUENCE 9 AA: 849 MW; 050365RDAAB7675 (2004).

Query Match 18.2% Score 2: DB 1: Length 9;  
 Best Local Similarity 100.0% Pred. No. 1.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3

DE 3 SQ 4

RESULT 32

FAK3\_CALVO  
 ID FAK3\_CALVO STANDARD; PRT; 9 AA.  
 AC P41858;  
 DI 01-NOV-1995 (Rel. 32, Created)  
 DI 01-NOV-1995 (Rel. 32, Last sequence update)  
 DI 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliophora vomitoria (Blue blowfly).  
 OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OS Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestridae;  
 OS Calliophoridae; Calliphora.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 DR PIR: A01422; Q00B. 849 MW; 050365RDAAB7675 (2004).  
 SQ SEQUENCE 9 AA: 849 MW; 050365RDAAB7675 (2004).

Query Match 18.2% Score 2: DB 1: Length 9;  
 Best Local Similarity 100.0% Pred. No. 1.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3

DE 3 SQ 4

RESULT 33

FAK4\_CALVO  
 ID FAK4\_CALVO STANDARD; PRT; 9 AA.  
 AC P84319;  
 DI 28-FEB-2003 (Rel. 41, Created)  
 DI 28-FEB-2003 (Rel. 41, Last sequence update)  
 DI 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLIP4 (SQPSMRIRP-amide).  
 OS Penaeus monodon (Pencoid shrimp).  
 OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OS Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OS Penaeidae; Penaeus.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 DR PIR: A01422; Q00B. 849 MW; 050365RDAAB7675 (2004).  
 SQ SEQUENCE 9 AA: 849 MW; 050365RDAAB7675 (2004).

Query Match 18.2% Score 2: DB 1: Length 9;  
 Best Local Similarity 100.0% Pred. No. 1.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQ 3

DE 3 SQ 4







10 EXPRESSION: Pyridoxal.  
 11 NCBI\_TaxID: 7962, 7752;  
 12 11  
 13 SEQUENCE: 9 AA: 1011 MW: 165176059087001 CRC64;  
 14  
 15 QUERY MATCH: 16.2%, Score 21, ID: 1, Length 9;  
 16 Best Local Similarity: 100.0%, Pred. No.: 1, 4e-05;  
 17 Matches: 2, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;  
 18  
 19 RESULT 42  
 20 RX: NCBI\_TaxID: 99, 12;  
 21 A: 162924;  
 22 28 FEB 2004 (rel. 4); Created;  
 23 28 FEB 2004 (rel. 4); Last sequence update;  
 24 28 FEB 2004 (rel. 4); Last annotation update;  
 25 DE Mitochondrial 26S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).  
 26 EN MRP-S33.  
 27 OS Bos taurus (bovine).  
 28 EKaryota; Metazoa; Chordata; Mammalia; Euteleostomi;  
 29 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 30 Bovidae; Bos taurus; Bos.  
 31 NCBI\_TaxID: 99, 12;  
 32 RN 121  
 33 RP SEQUENCE.  
 34 RS TISSUE: Liver.  
 35 RX MEDLINE: 21270492 PubMed: 11279124;  
 36 KGO: E. C. Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;  
 37 "The small subunit of the mammalian mitochondrial ribosome:  
 38 Identification of the full complement of ribosomal proteins present";  
 39 RI J. Biol. Chem. 276:19378-19374(2001).  
 40 CV 1-1 SUBUNIT: Component of the 28S rRNA and about 30 distinct proteins.  
 41 1-28S which comprises a 12S rRNA and about 30 distinct proteins.  
 42 1-3 SUBCELLULAR LOCATION: Mitochondrial.  
 43 KW Ribosomal protein; Mitochondrion.  
 44 FT N N TER 1  
 45 FT N N TER 9  
 46 SEQUENCE: 9 AA: 1052 MW: 104137477608589 CRC64;  
 47  
 48 QUERY MATCH: 16.2%, Score 21, ID: 1, Length 9;  
 49 Best Local Similarity: 100.0%, Pred. No.: 1, 3e-05;  
 50 Matches: 2, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;  
 51  
 52 RESULT 43  
 53 RX: NCBI\_TaxID: 99, 12;  
 54 A: 162924;  
 55 01 APR 1996 (rel. 4); Created;  
 56 01 APR 1996 (rel. 4); Last sequence update;  
 57 01 SEP 2003 (rel. 4); Last annotation update;  
 58 DE Locustatactykinin 1 (LTK-1)  
 59 OS Locusta migratoria (Migratory locust).  
 60 EKaryota; Metazoa; Arthropoda; Insecta; Preyptota;  
 61 Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;  
 62 Acrididae; Acrididae; Orthopodidae; Locusta.  
 63 NCBI\_TaxID: 7964.  
 64 RN 111  
 65 RP SEQUENCE.  
 66 RS TISSUE: Protein.  
 67 RX MEDLINE: 90164489; PubMed: 211766;  
 68 Schwartz J., Bismuth M., Hayes L.K., Nachman R.J., de laof A.;  
 69 "Locustatactykinin 1 and 11: two novel insect neuropeptides with  
 70 homology to peptides of the vertebrate tachykinin family";

10 EXPRESSION: Pyridoxal.  
 11 NCBI\_TaxID: 7962, 7752;  
 12 11  
 13 SEQUENCE: 9 AA: 1011 MW: 165176059087001 CRC64;  
 14  
 15 QUERY MATCH: 16.2%, Score 21, ID: 1, Length 9;  
 16 Best Local Similarity: 100.0%, Pred. No.: 1, 4e-05;  
 17 Matches: 2, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;  
 18  
 19 RESULT 42  
 20 RX: NCBI\_TaxID: 99, 12;  
 21 A: 162924;  
 22 28 FEB 2004 (rel. 4); Created;  
 23 28 FEB 2004 (rel. 4); Last sequence update;  
 24 28 FEB 2004 (rel. 4); Last annotation update;  
 25 DE Mitochondrial 26S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).  
 26 EN MRP-S33.  
 27 OS Bos taurus (bovine).  
 28 EKaryota; Metazoa; Chordata; Mammalia; Euteleostomi;  
 29 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 30 Bovidae; Bos taurus; Bos.  
 31 NCBI\_TaxID: 99, 12;  
 32 RN 121  
 33 RP SEQUENCE.  
 34 RS TISSUE: Liver.  
 35 RX MEDLINE: 21270492 PubMed: 11279124;  
 36 KGO: E. C. Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;  
 37 "The small subunit of the mammalian mitochondrial ribosome:  
 38 Identification of the full complement of ribosomal proteins present";  
 39 RI J. Biol. Chem. 276:19378-19374(2001).  
 40 CV 1-1 SUBUNIT: Component of the 28S rRNA and about 30 distinct proteins.  
 41 1-28S which comprises a 12S rRNA and about 30 distinct proteins.  
 42 1-3 SUBCELLULAR LOCATION: Mitochondrial.  
 43 KW Ribosomal protein; Mitochondrion.  
 44 FT N N TER 1  
 45 FT N N TER 9  
 46 SEQUENCE: 9 AA: 1052 MW: 104137477608589 CRC64;  
 47  
 48 QUERY MATCH: 16.2%, Score 21, ID: 1, Length 9;  
 49 Best Local Similarity: 100.0%, Pred. No.: 1, 3e-05;  
 50 Matches: 2, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;  
 51  
 52 RESULT 43  
 53 RX: NCBI\_TaxID: 99, 12;  
 54 A: 162924;  
 55 01 APR 1996 (rel. 4); Created;  
 56 01 APR 1996 (rel. 4); Last sequence update;  
 57 01 SEP 2003 (rel. 4); Last annotation update;  
 58 DE Locustatactykinin 1 (LTK-1)  
 59 OS Locusta migratoria (Migratory locust).  
 60 EKaryota; Metazoa; Arthropoda; Insecta; Preyptota;  
 61 Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;  
 62 Acrididae; Acrididae; Orthopodidae; Locusta.  
 63 NCBI\_TaxID: 7964.  
 64 RN 111  
 65 RP SEQUENCE.  
 66 RS TISSUE: Protein.  
 67 RX MEDLINE: 90164489; PubMed: 211766;  
 68 Schwartz J., Bismuth M., Hayes L.K., Nachman R.J., de laof A.;  
 69 "Locustatactykinin 1 and 11: two novel insect neuropeptides with  
 70 homology to peptides of the vertebrate tachykinin family";





07 4 AK 5  
14 11  
14 4 AK 4

Source: compacted: September 30, 2003, 10:26:00  
Sub time: 7.25 sec







395	2	18.2	13	2	A46443	prolactin-binding domain
396	2	18.2	13	2	382369	unidentified 85K P
397	2	18.2	13	2	A61289	spore protease-like 3
398	2	18.2	13	2	S36867	ribosomal protein
399	2	18.2	13	2	S32565	Ribosomal protein L10
400	2	18.2	13	2	FA0041	protein QA00041
401	2	18.2	13	2	S28425	20K protein tube
402	2	18.2	13	2	S29716	25 kDa protein
403	2	18.2	13	2	S40316	phosphorylated 10K
404	2	18.2	13	2	S44972	protein L7
405	2	18.2	13	2	S33840	chaperone, 17 kDa
406	2	18.2	13	2	S56253	ribonuclease phospho
407	2	18.2	13	2	PA0087	protein GP250051
408	2	18.2	13	2	FE1343	epitope-binding
409	2	18.2	13	2	AC1514	glutathione trans
410	2	18.2	13	2	A27909	carboxylesterase I
411	2	18.2	13	2	B61620	proteasome activator
412	2	18.2	13	2	P83443	proteinase
413	2	18.2	13	2	B27955	polysialic acid synthet
414	2	18.2	13	2	S13273	polysialic acid synthet
415	2	18.2	13	2	S0718	novel protein
416	2	18.2	13	2	A27789	antibacterial stre
417	2	18.2	13	2	A54326	glutathione S-transfer
418	2	18.2	13	2	S24356	hypothetical prote
419	2	18.2	13	2	P76365	heavy chain 3
420	2	18.2	13	2	S23548	heavy chain 3
421	2	18.2	13	2	S23440	heavy chain 3
422	2	18.2	13	2	S27350	heavy chain 3
423	2	18.2	13	2	S27357	heavy chain 3
424	2	18.2	13	2	S47352	heavy chain 3
425	2	18.2	13	2	S47359	heavy chain 3
426	2	18.2	13	2	S47362	heavy chain 3
427	2	18.2	13	2	S47365	heavy chain 3
428	2	18.2	13	2	S47366	heavy chain 3
429	2	18.2	13	2	S47371	heavy chain 3
430	2	18.2	13	2	S47372	heavy chain 3
431	2	18.2	13	2	S47374	heavy chain 3
432	2	18.2	13	2	S47377	heavy chain 3
433	2	18.2	13	2	S47377	heavy chain 3
434	2	18.2	13	2	S47377	heavy chain 3
435	2	18.2	13	2	S47380	heavy chain 3
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437	2	18.2	13	2	S47381	heavy chain 3
438	2	18.2	13	2	S47382	heavy chain 3
439	2	18.2	13	2	S47383	heavy chain 3
440	2	18.2	13	2	S47385	heavy chain 3
441	2	18.2	13	2	S47388	heavy chain 3
442	2	18.2	13	2	S47389	heavy chain 3
443	2	18.2	13	2	S47390	heavy chain 3
444	2	18.2	13	2	S47390	heavy chain 3
445	2	18.2	13	2	S47394	heavy chain 3
446	2	18.2	13	2	S47394	heavy chain 3
447	2	18.2	13	2	P83136	heavy chain 3
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450	2	18.2	13	2	S45235	heavy chain 3
451	2	18.2	13	2	A32846	heavy chain 3
452	2	18.2	13	2	S78755	heavy chain 3
453	2	18.2	13	2	S04374	heavy chain 3
454	2	18.2	13	2	S51275	heavy chain 3
455	2	18.2	13	2	S51275	heavy chain 3
456	2	18.2	13	2	P87646	heavy chain 3
457	2	18.2	13	2	P81594	heavy chain 3
458	2	18.2	13	2	G37266	heavy chain 3
459	2	18.2	13	2	S37267	heavy chain 3
460	2	18.2	13	2	H38932	heavy chain 3
461	2	18.2	13	2	A30933	heavy chain 3
462	2	18.2	13	2	B23406	heavy chain 3
463	2	18.2	13	2	P83756	heavy chain 3
464	2	18.2	13	2	FN1346	heavy chain 3
465	2	18.2	13	2	P87428	heavy chain 3
466	2	18.2	13	2	A47630	heavy chain 3
467	2	18.2	13	2	C47630	heavy chain 3
468	2	18.2	13	2	C47630	heavy chain 3
469	2	18.2	13	2	C47630	heavy chain 3
470	2	18.2	13	2	C47630	heavy chain 3
471	2	18.2	13	2	C47630	heavy chain 3
472	2	18.2	13	2	C47630	heavy chain 3
473	2	18.2	13	2	C47630	heavy chain 3
474	2	18.2	13	2	C47630	heavy chain 3
475	2	18.2	13	2	C47630	heavy chain 3
476	2	18.2	13	2	C47630	heavy chain 3
477	2	18.2	13	2	C47630	heavy chain 3
478	2	18.2	13	2	C47630	heavy chain 3
479	2	18.2	13	2	C47630	heavy chain 3
480	2	18.2	13	2	C47630	heavy chain 3
481	2	18.2	13	2	C47630	heavy chain 3
482	2	18.2	13	2	C47630	heavy chain 3
483	2	18.2	13	2	C47630	heavy chain 3
484	2	18.2	13	2	C47630	heavy chain 3
485	2	18.2	13	2	C47630	heavy chain 3
486	2	18.2	13	2	C47630	heavy chain 3
487	2	18.2	13	2	C47630	heavy chain 3
488	2	18.2	13	2	C47630	heavy chain 3
489	2	18.2	13	2	C47630	heavy chain 3
490	2	18.2	13	2	C47630	heavy chain 3
491	2	18.2	13	2	C47630	heavy chain 3
492	2	18.2	13	2	C47630	heavy chain 3
493	2	18.2	13	2	C47630	heavy chain 3
494	2	18.2	13	2	C47630	heavy chain 3
495	2	18.2	13	2	C47630	heavy chain 3
496	2	18.2	13	2	C47630	heavy chain 3
497	2	18.2	13	2	C47630	heavy chain 3
498	2	18.2	13	2	C47630	heavy chain 3
499	2	18.2	13	2	C47630	heavy chain 3
500	2	18.2	13	2	C47630	heavy chain 3

## ALIGNMENTS

## RESULT 1

S35538  
 Ribosomal protein S7 - Mycobacterium intracellulare (fragment)  
 C:Species: Mycobacterium intracellulare  
 C:Date: 09-Dec-1993 #sequence\_revision 14-Nov-1997 #text\_change 13-Aug-1999  
 C:Accession: S35538  
 R:Naik, J., Rouse, D., Morris, S.  
 Nucleic Acids Res. 21, 1039, 1993  
 A:Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium int  
 A:Reference number: S35537; M019:93/9130; PMID:8451173  
 A:Accession: S35538  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 159, 5 NAs  
 A:Cross-references: EMBL:08171; NID:0149994; PIDN:ANA25376.1; PID:9551901  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 199  
 C:Superfamily: Escherichia coli ribosomal protein S7  
 C:Keywords: protein biosynthesis; ribosome

Query Match: 36.4%; Score 4; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKGP 10

36 RKGP 6

## RESULT 2

164842

Ca2+-Transporting ATPase (EC 3.6.3.8) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 19-Apr 2002

C:Accession: 164842

R:Wu, K.



Accession: 264, 333-341, 1993  
 A:Title: Molecular cloning and quantitation of mRNA and protein encoding P21+ kinase  
 A:Reference number: 151892  
 A:Accession: 264842

A>Status: preliminary; translated from cDNA/EMBL/GenBank

A:Molecule type: mRNA

A:Residues: 1-8 <RES>

A:Cross references: BR: M9223; NID: 420-44; PDB: AAA3-092 11 130420343

C:Comment:

A:Gene: SPCALB

C:Keywords: hydrolase

Query Match: 27.4% Score 3; DB 2; Length 9;

Best Local Similarity: 100.0% Pred. No. 2 Re-03;

Matches: 3; Conservative 0; Mismatches 0; Indels 0;

QY 6 RPK 8

DB 11

6 RPK 3

RESULT 4

YFEG

Protein factor - P10

A:Alternate name: FIS (lactate dehydrogenase)

A:Species: Sus scrofa domestica (domestic pig)

C:Date: 13 Jul 1981 #sequence\_revision 13 Jul 1981 #text\_change 37 May 1999

C:Accession: A01523; A60983

R:Picot, J.M.; Gardette, M.; Riquart, Y.; Bach, J.F.

J. Biol. Chem. 252, 8045-8047, 1977

A:Title: Structural study of circulating lymphocyte a peptide isolated from pig serum

A:Reference number: A01523; M0127802437; PMID: 91496

A:Accession: A01523

A:Molecule type: protein

A:Residues: 1-9 <PLE>

R:Bauch, J.F.; Gardette, M.; Picot, J.M.; Bach, J.F.

Nature 266, 55-57, 1977

A:Title: Biochemical characterization of a serum thymic factor

A:Reference number: A60983; M0127124623; PMID: 91496

A:Accession: A60983

A:Molecule type: protein

A:Residues: 2-24, 27-69 <BAT>

C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral

in a variety of immunoassays

C:Comment: See PIR-A60957 (Sheep) for discussion of another possible N-terminal modification

A:Superfamily: Thymic factor

C:Keywords: Pyroglutamic acid

E1/Modified site: pyroglutamic acid; 1-24, 27-69 <BAT> experimental

Query Match: 27.4% Score 3; DB 2; Length 9;

Best Local Similarity: 100.0% Pred. No. 2 Re-03;

Matches: 3; Conservative 0; Mismatches 0; Indels 0;

QY 4 QAK 5

DB 11

4 QAK 4

RESULT 4

S78762

ribosomal protein MKP-SL2, mitochondrial

C:Species: Bos primigenius taurus (cattle)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: S78762

R:Graack, H.R.

submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760

A:Accession: S78762

A:Molecule type: protein

A:Residues: 1-9 <GRA>

C:Keywords: mitochondrion

E1/9/Protein: ribosomal protein MKP-SL2 (transmembrane) #Status: experimental <MAI>

Query Match: 27.4% Score 3; DB 2; Length 9;

Best Local Similarity: 100.0% Pred. No. 2 Re-05;

Matches: 3; Conservative 0; Mismatches 0; Indels 0;

QY 6 RPK 8

DB 11

2 RPK 4

RESULT 5

S66456

terreoxin - Rhizobium meliloti (strain)

C:Species: Rhizobium meliloti

C:Date: 15 Feb 1997 #sequence\_revision 13-Mar 1997 #text\_change 17-Mar 1999

C:Accession: S66456

R:Riedel, K.O.; Donnan, Y.; Masquedo, B.; Pechler, A.; Klipp, W.

Bur. J. Biochem. 243, 742-746, 1995

A:Title: A Rhizobium meliloti terreoxin (FdxN) purified from Escherichia coli; donat

A:Reference number: S66456; M0129537307; PMID: 7649175

A:Accession: S66456

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <RIE>

C:Comment:

A:Gene: tdxN

Query Match: 27.4% Score 3; DB 2; Length 10;

Best Local Similarity: 100.0% Pred. No. 2 Re-03;

Matches: 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 ASQ 3

DB 6 ASQ 6

RESULT 6

A40693

Transgelin sheep (transmembrane)

C:Species: Ovis orientalis aries, avis ammon aries (domestic sheep)

C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 31-Oct-1997

C:Accession: A40693

R:Shapland, C.; Hsueh, J.J.; Totty, N.F.; Lawson, D.

J. Cell. Biol. 121, 1065-1075, 1993

A:Title: Purification and properties of transgelin: a transmembrane and shape chang

A:Reference number: A40693; M0129323790; PMID: 8501116

A:Accession: A40693

A:Molecule type: protein

A:Residues: 1-11 <SHA>

A:Experimental source: actin

C:Comment: This protein gels actin and is down regulated by transformation or loss of

C:Superfamily: smooth muscle protein S622; calponin repeat homology; smooth muscle f

C:Keywords: actin binding; cytoskeleton

Query Match: 27.4% Score 3; DB 2; Length 11;

Best Local Similarity: 100.0% Pred. No. 4e-03;

Matches: 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 RKP 10

DB 11

8 RKP 3

RESULT 7

S00616

paraspinal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galle

N:Alternate name: delta-endotoxin; parasporal crystal protein positive chain

C:Species: Bacillus thuringiensis

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 13-Sep-1996

C:Accession: S00616

R:Chetukhina, G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.

FEBS Lett. 242, 249-251, 1988

A:Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-enc

A:Reference number: S00616



A:Species: Bos primigenius (cattle)  
 C:Date: 20-Jul-1990 #sequence\_revision 20-Jul-1990 #text\_change 19-Jul-1990  
 C:Accession: A34858  
 R:Ramirez, G.A.; Fletcher, C.; P.L.; Pessenti, L.B.  
 J. Biol. Chem. 265:297, 1990  
 A:Title: Characterization of the venom from Proboscidea moscosus (Proboscidea)  
 A:Reference number: A34858; M01D:90260871; PMID:1440854  
 A:Accession: A34858  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 (KRR)  
 Query Match 27.4%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 KRR 6  
 IB 11  
 2 KRR 4  
 RESULT 14  
 S71383  
 A:Title: Isolation and characterization of the Vipera lebetina  
 C:Species: Vipera lebetina  
 C:Date: 11-Mar-1998 #sequence\_revision 12-Apr-1998 #text\_change 19-Mar-1999  
 C:Accession: S71383  
 R:Barbieri, R.; Marrakchi, N.; Mansueti, P.; Kratoch, M.; Pannetier, C.; Schat, H.; El  
 PERS, L.; 1992, 6-10, 1996  
 A:Title: Novel anti-phospholipase A2 polypeptides from Vipera lebetina venom: isolation  
 A:Reference number: S71383; M01D:96354866; PMID:769904  
 A:Accession: S71383  
 A:Molecule type: protein  
 A:Residues: 1-12 (KRR)  
 A:Experimental source: venom  
 C:Keywords: antivenom; venom  
 Query Match 27.4%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 KRR 10  
 IB 7 KRR 9  
 RESULT 15  
 E42762  
 A:Title: Phospholipase A2 system of the proboscidea moscosus (Proboscidea)  
 C:Species: Proboscidea moscosus  
 C:Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 11-Jun-2003  
 C:Accession: E42762  
 R:van der Kleij, R.; van Schalkwijk, S.; de Vries, W.P.  
 J. Biol. Chem. 265:7176-7181, 1991  
 A:Title: Molecular cloning, characterization, and purification of the phospholipase A2  
 A:Reference number: A35778; M01D:91201359; PMID:1440854  
 A:Accession: E42762  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-15 (KRR)  
 A:Cross-references: GB:J05748  
 C:Species family: regulatory protein; quaternary  
 C:Keywords: LNA binding; transfection; translation  
 Query Match 27.4%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KRR 7  
 IB 10 KRR 12

RESULT 16  
 PH1316  
 A:Title: Heavy chain of raton (clone C188-107) - human (fragment)  
 C:Species: Bos primigenius (cattle)  
 C:Date: 30-Sep-1994 #sequence\_revision 30-Sep-1994 #text\_change 07-May-1999  
 C:Accession: PH1316  
 R:Wasserman, R.; Chell, N.; Ho, Y.; Reichard, B.A.; Shane, S.; Rozera, G.  
 J. Exp. Med. 176:1577-1587, 1992  
 A:Title: Purification of total type DIII joining in young children with B precursor B  
 A:Reference number: PH1316; M01D:93394761; PMID:1460419  
 A:Accession: PH1316  
 A:Molecule type: DNA  
 A:Residues: 1-13 (KRR)  
 C:Keywords: heterodimer; immunoglobulin  
 Query Match 27.4%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 QRR 11  
 IB 5 QRR 11

RESULT 17  
 PH1479  
 A:Title: T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
 C:Accession: PH1479  
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.  
 J. Exp. Med. 177:811-826, 1993  
 A:Title: T cell receptor selection by and recognition of two class I major histocomp  
 A:Reference number: PH1479; M01D:94171821; PMID:8436911  
 A:Accession: PH1479  
 A:Molecule type: mRNA  
 A:Residues: 1-17 (KRR)  
 A:Experimental source: cytochrome 2-lymphocyte  
 C:Superfamily: immunoglobulin hematology  
 C:Keywords: receptor; T-cell  
 Query Match 27.4%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QRR 4  
 IB 4 QRR 6

RESULT 18  
 E42762  
 A:Title: Phospholipase A2 complex (B014.4.25.1) subunit 13 - bovine (fragment)  
 C:Species: Bos primigenius (cattle)  
 C:Date: 04-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 17-Feb-2003  
 C:Accession: E42762  
 R:Dieck, D.K.; Mochly, R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.  
 Biochemistry 31:7347-7355, 1992  
 A:Title: Identification and localization of a cysteinyl residue critical for the try  
 A:Reference number: A42762; M01D:92378961; PMID:1510924  
 A:Accession: E42762  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-13 (KRR)  
 A:Note: Sequence extracted from N.B. backbone (NCBI:P112180)  
 C:Keywords: hydrolase

Query Match 27.4%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KRR 7  
 IB 10 KRR 12

2 SQA 4  
111  
11 SQA 14

## RESULT 19

PH0135  
C:Species: Arabidopsis thaliana (ThaArab1)  
C:Date: 07-Apr-1995 #sequence\_revision 26-947 #seq\_text\_change 30-Jan-1995  
C:Accession: P60109  
C:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the co  
A:Reference number: PH0135; M1119108543; PMID:1702137  
A:Accession: P60109  
A:Molecule type: protein  
A:Residues: 1-14 <AA>  
A:Experimental source: root

Query Match 27.4% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 GPR 10  
111  
11 SQA 4

## RESULT 20

PH0049  
C:Species: Arabidopsis thaliana (ThaArab1)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1995 #seq\_text\_change 23-Mar-1995  
C:Accession: P60045  
C:Title: The sequence around the phosphorylation site of the porcine heart type phos  
A:Reference number: P60045; M1118913523; PMID:3224509  
A:Accession: P60045  
A:Molecule type: protein  
A:Residues: 1-14 <AA>  
A:Experimental source: root

Query Match 27.4% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 GPR 10  
111  
11 SQA 4

## RESULT 21

S1688  
C:Species: Arabidopsis thaliana (ThaArab1)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #seq\_text\_change 31-Oct-1997  
C:Accession: S1688  
C:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Myc  
A:Reference number: S1688; M1118400553; PMID:8405418  
A:Accession: S1688  
A:Molecule type: protein  
A:Residues: 1-14 <AA>

Query Match 27.4% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 9 GPR 11  
111  
9 GPR 11

## RESULT 22

PH0135  
C:Species: Homo sapiens (man)  
C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #seq\_text\_change 30-May-1997  
C:Accession: P60109  
C:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the co  
A:Reference number: PH0135; M1119108543; PMID:1702137  
A:Accession: P60109  
A:Molecule type: mRNA  
A:Residues: 1-14 <AA>  
A:Experimental source: root

Query Match 27.4% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 9 GPR 11  
111  
9 GPR 11

## RESULT 23

PH0049  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #seq\_text\_change 11-May-2000  
C:Accession: P60045  
C:Title: The sequence around the phosphorylation site of the porcine heart type phos  
A:Reference number: P60045; M1118913523; PMID:3224509  
A:Accession: P60045  
A:Molecule type: protein  
A:Residues: 1-14 <AA>  
A:Experimental source: root  
A:Keywords: allosteric regulation; cardiac muscle; glycogen metabolism; glycosyltran  
P15/Binding site: phosphate (Ser); (cova.ent) #status experimental

Query Match 27.4% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 GPR 8  
111  
8 GPR 7

## RESULT 24

S1688  
C:Species: Mycobacterium bovis (fragment)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #seq\_text\_change 31-Oct-1997  
C:Accession: S1688  
C:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Myc  
A:Reference number: S1688; M1118400553; PMID:8405418  
A:Accession: S1688  
A:Molecule type: protein  
A:Residues: 1-14 <AA>  
A:Experimental source: root  
A:Keywords: protein biosynthesis; ribosome

Query Match 27.4% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 9 GPR 11  
111  
9 GPR 11



C:Superfamily: probable msrA leader peptide

Query Match 18.2% Score 2; 18.2% Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

DB 1

3 AS 4

RESULT 1:

S43972

Unlabeled associated antigen K012 mouse

C:Species: Mus musculus (house mouse)

C:Date: 20 Oct 1994 #sequence\_revision 17 Nov 1995 #text\_change 14 Aug 2000

C:Accession: S43972

R:Ratna, Rami, G.; Becker, G.; Fritzk, M.; Feldman, M.; Eisenstein, R.; Eisenbach, L.

Refuge 66; 6/7/11, 1994

A:Title: CTL induction by a tumour associated antigen: a peptide derived from a murine

A:Reference number: S43971; M010:94,178,1; EMBL:08,61342

A:Accession: S43972

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-6; MAK

C:Superfamily: classified animal peptides

Query Match 18.2% Score 2; 18.2% Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QA 4

DB 7 QA 8

RESULT 12

114077

Imported from protein N - Methyltransferase methyl tropans (fragment)

C:Species: Morayichthys methyl tropans

C:Date: 16 Jul 1999 #sequence\_revision 16 Jul 1999 #text\_change 23 Jul 2000

C:Accession: 114077

R:Rustafastov, A. V.; Melnik, W. S.; Mathews, F. S.; Lindstrom, M. F.

2; Rustafastov, A. V.; Melnik, W. S.; Mathews, F. S.; Lindstrom, M. F.

A:Title: Purification of the methyltransferase (mtr) genes in Methyltransferase methyl-

A:Reference number: 216945; M010:94,29422; EMBL:08,61342

A:Accession: 114077

A:Status: preliminary; translated from db/08/61342

A:Molecule type: DNA

A:Residues: 1-4; CPH

A:Cross-references: EMBL:126407; M010:94,29422; 216945; 114077; 114077

A:Experimental source: strain WAT

C:Genetic:

A:Gene: mtrN

Query Match 18.2% Score 2; 18.2% Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QA 4

DB 5 QA 5

RESULT 13

PC141

Hypothetical protein B [imported] pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa

C:Date: 20 Apr 2000 #sequence\_revision 20 Apr 2000 #text\_change 20 Apr 2000

C:Accession: PC141

R:Kawashita, S.; Arai, H.; Igarashi, Y.; Kodama, T.

Gene 167; 87-91, 1995

A:Title: Sequencing and characterization of the downstream region of the genes encoding

RESULT 16

S63493

Y: for biosynthesis of heme d1.

A:Reference number: J04552; M010:96,142254; PMID:8566817

A:Accession: PC141

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8; KAW

A:Cross-references: M010:100471; NID:01217594

A:Note: this ORF is not annotated in Genbank entry PSENJRC, release 11.0

Query Match 18.2% Score 2; 18.2% Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KK 7

DB 6 KK 7

RESULT 14

S57141

IPSA protein - Erwinia chrysanthemi

C:Species: Erwinia chrysanthemi

C:Date: 06 Jan 1995 #sequence\_revision 06 Jan 1995 #text\_change 08 Oct 1999

C:Accession: S57141

R:Facillie, A.; Toussaint, A.; Faellen, M.

submitted to the EMBL Data Library, August 1993

A:Description: Identification of the integration host factor genes of E. chrysanthem

A:Reference number: S57139

A:Accession: S57141

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8; KAW

A:Cross-references: EMBL:X74750; NID:0395669; PIDN:CAA52769.1; PID:0581108

Query Match 18.2% Score 2; 18.2% Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AK 5

DB 5 AK 5

RESULT 15

S70727

IPaF protein, Shigella flexneri (fragment)

C:Species: Shigella flexneri

C:Date: 15 Feb 1997 #sequence\_revision 13 Mar 1997 #text\_change 08 Oct 1999

C:Accession: S70727

R:Alam, A.; Sansonetti, P. J.; Mounier, J.; Raiz, S.; Mounier, J.; Philipon, A.; P

del, M.; et al., 1997, 461, 470, 1995

A:Title: Mxlg, a membrane protein required for secretion of Shigella spp. Ipa invasi

A:Reference number: S70727; M010:96,100445; PMID:8559065

A:Accession: S70727

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-8; KAW

A:Cross-references: EMBL:244957; NID:0929880; PIDN:CAA88821.1; PID:0929881

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995

C:Genetic:

A:Gene: ipaF

Query Match 18.2% Score 2; 18.2% Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KK 7

DB 6 KK 7

desulfatase, sulfate reductase, gamma chain, membrane bound and soluble, Desulfatase  
 C-Species: *Desulfohalobium desulfatans*  
 C-Date: 28-Oct-1996 #sequence\_revision 17-Mar-1997 #text\_change 17-Mar-1999  
 C-Accession: S63493; S63494

E-Sequence: 3:1 Atendsen, A.F.; Haged, W.R.; Kierck, F.M.H.  
 Eur. J. Biochem. 255: 873-879, 1999

A-Title: Molecular properties of the desulfatase and sulfate reductase from *Desulfohalobium*  
 A-Reference number: S63489; M0109000102; PMID:9523697

A-Accession: S63493

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

A-Accession: S63494

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KG 9

DB 11

6 KG 7

RESULT 47

S63494

endolysosomal hydrolase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 30-Dec-1991

C-Accession: B4745

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: B4745

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 48

S63495

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63495

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63495

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 49

S63496

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63496

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63496

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 50

S63497

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63497

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63497

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 51

S63498

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63498

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63498

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 52

S63499

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63499

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63499

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 53

S63500

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63500

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63500

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 54

S63501

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63501

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63501

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 55

S63502

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63502

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63502

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 56

S63503

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.

C-Date: 29-Mar-1997 #sequence\_revision 29-Mar-1997 #text\_change 29-Mar-1997

C-Accession: S63503

P-Title: Molecular cloning, characterization, and expression of the gene for the

acid phosphatase of *Desulfohalobium* sp.

A-Title: Acid phosphatase of *Desulfohalobium* sp.

A-Reference number: A45745; M01091102; PMID:134327

A-Accession: S63503

A-Status: preliminary

A-Molecule type: protein

A-Residues: 18 (STE)

C-Keywords: acid phosphatase; hydrolase

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11

DB 12

6 KG 7

RESULT 57

S63504

acid phosphatase (EC 3.2.1.22) in *Desulfohalobium* sp. (Fragment)

C-Species: *Desulfohalobium* sp.





A:Reference number: A28719; M01D:88425920; PMID:1261954  
 A:Accession: A28719  
 A:Molecule type: protein  
 A:Residues: 18<BR>

Query Match 18.2% Score 21.10 21.10 21.10 83  
 Best Local Similarity 100.0% Pred. No. 2.8e+05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 9 KP 10  
 II 11  
 IB 4 KP 5

## RESULT 48

148934

apelinreceptor A II - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision: 02-Jul-1996 #text\_change: 06-Nov-1999

C:Accession: 148934

Riku, M., S. Wang, X. J. Horton, J. H. Burton, M. O. Takahashi, K. Marzaki, Y. Nakam, G. H.

Mamm Genome 5: 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: 148934; M01D:44190621; PMID:804349

A:Accession: 148934

A&gt;Status: Preliminary; translated from GenBank/EMBL.

A:Molecule type: DNA

A:Residues: 18&lt;RES&gt;

A:Access reference: EMBL:025591; NID:147610; PDB: A28719; PDB: 441906

Query Match 18.2% Score 21.10 21.10 21.10  
 Best Local Similarity 100.0% Pred. No. 2.8e+05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 4 AK 5  
 II 1  
 IB 5 AK 8

## RESULT 49

A54824

c-fos-like receptor 17 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 24-Apr-1995 #sequence\_revision: 24-Apr-1995 #text\_change: 17-Mar-1999

C:Accession: A54824

Schmidt, A., J. Schmitt, J. Giedt, H. J. Axelsen, R.

Cell 78: 823-834, 1994

A:Title: Altered induction of Fos family genes by c-fos-like receptor 17.

A:Reference number: A54824; M01D:94438646; PMID:766511

A:Accession: A54824

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 18&lt;RES&gt;

Query Match 18.2% Score 21.10 21.10 21.10 83  
 Best Local Similarity 100.0% Pred. No. 2.8e+05  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 KP 7  
 IB 4 KP 4

## RESULT 50

P10595

c-fos-like receptor beta chain V-loop region (mouse)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision: 17-Jul-1992 #text\_change: 06-Mar-1993

C:Accession: P10595

Reference: A.J.

J. Exp. Med. 174: 125-124, 1991

A:Title: Functional sequences of total c-fos-like receptor beta chains have low N regions.

A:Reference number: P10509; M01D:9127701; PMID:1711109

GeneCore version 5.1.5  
Copyright (c) 1993 - 2002 Compugen Ltd

OM protein protein search, using sw model

Run on: September 30, 2003, 11:06:54 Search file 41-083: Sequents  
(2) local alignment  
42.49% Match on cell updates/sec

Title: US-09-787-443-15

Perfect score: 11

Sequence: 1 ASQAKRKRGR 11

Scoring Table: Gapped  
Gap: 60.0, Gapext: 60.0

Search: 1107663 seqs, 150720533 residues

Word size: 3

Total number of hits satisfying chosen parameters: 278824

Minimum LB seq length: 8

Maximum DB seq length: 35

Post-processing: Testing first 500 summaries

Database: A\_Geneseq\_19Jun03.\*

1:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1981.DAT.*
2:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1982.DAT.*
3:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1983.DAT.*
4:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1984.DAT.*
5:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1985.DAT.*
6:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1986.DAT.*
7:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1987.DAT.*
8:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1988.DAT.*
9:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1989.DAT.*
10:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1990.DAT.*
11:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1991.DAT.*
12:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1992.DAT.*
13:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1993.DAT.*
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16:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1996.DAT.*
17:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA1997.DAT.*
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21:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA2001.DAT.*
22:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA2002.DAT.*
23:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA2003.DAT.*
24:	/SIDSI/gcadata/geneseq/geneseq.cdb//AA2004.DAT.*

Foot. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	21	NCAM Igl binding p
2	11	100.0	11	23	Human neural cell
3	5	45.5	9	17	Human heat shock p
4	5	45.5	10	14	Hepatitis C Ab det
5	5	45.5	13	16	H.V. StV. REV prot
6	5	45.5	13	21	RNA binding peptid
7	5	45.5	13	21	RNA binding peptid
8	5	45.5	13	21	RNA binding peptid
9	5	45.5	13	21	RNA binding peptid

10	5	45.5	13	21	RNA binding peptid
11	5	45.5	13	21	RNA binding peptid
12	5	45.5	13	21	RNA binding peptid
13	5	45.5	13	21	RNA binding peptid
14	5	45.5	13	21	RNA binding peptid
15	5	45.5	13	21	RNA binding peptid
16	5	45.5	13	21	RNA binding peptid
17	5	45.5	13	21	RNA binding peptid
18	5	45.5	13	22	AAU06073
19	5	45.5	13	22	AAU05076
20	5	45.5	13	22	AAU06079
21	5	45.5	13	24	AAU06082
22	5	45.5	13	22	AAU06085
23	5	45.5	13	22	AAU05088
24	5	45.5	13	22	AAU05091
25	5	45.5	13	22	AAU05096
26	5	45.5	13	22	AAU06099
27	5	45.5	13	22	AAU06101
28	5	45.5	13	22	AAU06104
29	5	45.5	13	22	AAU06107
30	5	45.5	15	19	AAU20948
31	5	45.5	15	21	AAU14221
32	5	45.5	15	21	AAU14223
33	4	36.4	8	16	AAU21239
34	4	36.4	8	16	AAU21240
35	4	36.4	8	19	AAU39185
36	4	36.4	8	21	AAU08148
37	4	36.4	8	22	ABP12017
38	4	36.4	8	22	ABP17716
39	4	36.4	8	22	AAU65137
40	4	36.4	8	22	AAU65140
41	4	36.4	8	22	AAU65143
42	4	36.4	8	22	AAU65150
43	4	36.4	8	22	AAU66201
44	4	36.4	8	22	AAU66206
45	4	36.4	8	22	AAU66207
46	4	36.4	8	22	AAU66208
47	4	36.4	8	22	AAU66252
48	4	36.4	8	22	AAU66253
49	4	36.4	8	22	AAU66257
50	4	36.4	8	22	AAU05700
51	4	36.4	8	22	AAU05701
52	4	36.4	8	22	AAU05702
53	4	36.4	8	22	AAU05703
54	4	36.4	8	22	AAU05704
55	4	36.4	8	22	AAU05705
56	4	36.4	8	22	AAU05706
57	4	36.4	8	22	AAU05707
58	4	36.4	8	22	AAU05708
59	4	36.4	8	22	AAU05709
60	4	36.4	8	22	AAU05710
61	4	36.4	8	22	AAU05712
62	4	36.4	8	22	AAU05713
63	4	36.4	8	22	AAU05714
64	4	36.4	8	22	AAU05715
65	4	36.4	8	22	AAU05716
66	4	36.4	8	22	AAU05719
67	4	36.4	8	22	AAU05721
68	4	36.4	8	22	AAU05724
69	4	36.4	8	22	AAU05730
70	4	36.4	8	22	AAU05731
71	4	36.4	8	22	AAU05732
72	4	36.4	8	22	AAU05733
73	4	36.4	8	22	AAU05734
74	4	36.4	8	22	AAU05735
75	4	36.4	8	22	AAU05736
76	4	36.4	8	22	AAU05741
77	4	36.4	8	22	AAU05742
78	4	36.4	8	22	AAU05744
79	4	36.4	8	22	AAU05745
80	4	36.4	8	22	AAU05746
81	4	36.4	8	22	AAU05746
82	4	36.4	8	22	AAU05746

83	4	36.4	8	22	AAH80701	Human glandular ka	156	4	36.4	9	24	ABJ22670	162P1E6 cancer gen
84	4	36.4	8	23	ABH74555	DNA repair protein	157	4	36.4	9	24	ABJ22671	162P1E6 cancer gen
85	4	36.4	8	24	ABH74596	Transcription factor	158	4	36.4	9	24	ABJ22676	162P1E6 cancer gen
86	4	36.4	9	11	AAH23609	Peptide antigen	159	4	36.4	9	24	ABJ22684	162P1E6 cancer gen
87	4	36.4	9	13	AAH27776	Transactivation do	160	4	36.4	9	24	ABJ22688	162P1E6 cancer gen
88	4	36.4	9	14	AAH42217	Anti-herpetic pept	161	4	36.4	9	24	ABJ22693	162P1E6 cancer gen
89	4	36.4	9	14	AAH42225	Anti-herpetic pept	162	4	36.4	9	24	ABJ23456	162P1E6 cancer gen
90	4	36.4	9	14	AAH42225	Anti-herpetic pept	163	4	36.4	9	24	ABJ23456	162P1E6 cancer gen
91	4	36.4	9	16	AAH73562	Anti-cytomegalovir	164	4	36.4	9	24	ABJ23366	162P1E6 cancer gen
92	4	36.4	9	16	AAH73562	Anti-cytomegalovir	165	4	36.4	9	24	ABJ23368	162P1E6 cancer gen
93	4	36.4	9	17	AAH92445	Human stem cell p	166	4	36.4	9	24	ABJ23384	162P1E6 cancer gen
94	4	36.4	9	17	AAH92445	Human stem cell p	167	4	36.4	9	24	ABJ23385	162P1E6 cancer gen
95	4	36.4	9	18	AAH25625	Peptide R10, R10a	168	4	36.4	9	24	ABJ24055	162P1E6 cancer gen
96	4	36.4	9	18	AAH25625	Peptide R10, R10a	169	4	36.4	9	24	ABJ24056	162P1E6 cancer gen
97	4	36.4	9	18	AAH25625	Peptide R10, R10a	170	4	36.4	9	24	ABJ24056	162P1E6 cancer gen
98	4	36.4	9	18	AAH25625	Peptide R10, R10a	171	4	36.4	9	24	ABJ24071	162P1E6 cancer gen
99	4	36.4	9	19	AAH24135	Anti-cytomegalovir	172	4	36.4	9	24	ABJ24079	162P1E6 cancer gen
100	4	36.4	9	21	AAH24708	Human stem cell p	173	4	36.4	9	24	ABJ24082	162P1E6 cancer gen
101	4	36.4	9	21	AAH04055	Cytotoxic T lympho	174	4	36.4	9	24	ABJ24753	162P1E6 cancer gen
102	4	36.4	9	21	AAH51594	MN protein RA doma	175	4	36.4	9	24	ABJ24759	162P1E6 cancer gen
103	4	36.4	9	21	AAH51594	HIV-1 derived GP12	176	4	36.4	9	24	ABJ24766	162P1E6 cancer gen
104	4	36.4	9	22	ABH12154	HIV-1 derived GP12	177	4	36.4	9	24	ABJ24768	162P1E6 cancer gen
105	4	36.4	9	22	ABH12154	HIV-1 derived GP12	178	4	36.4	9	24	ABJ24774	162P1E6 cancer gen
106	4	36.4	9	22	ABH12154	HIV-1 derived GP12	179	4	36.4	9	24	ABJ24777	162P1E6 cancer gen
107	4	36.4	9	22	ABH12154	HIV-1 derived GP12	180	4	36.4	10	15	AAH61362	Bradykinin recepto
108	4	36.4	9	22	ABH12154	HIV-1 derived GP12	181	4	36.4	10	15	AAH61362	Bradykinin recepto
109	4	36.4	9	22	ABH12154	HIV-1 derived GP12	182	4	36.4	10	15	AAH61371	Bradykinin recepto
110	4	36.4	9	22	ABH12154	HIV-1 derived GP12	183	4	36.4	10	15	AAH61372	Bradykinin recepto
111	4	36.4	9	22	ABH12154	HIV-1 derived GP12	184	4	36.4	10	15	AAH61382	Bradykinin recepto
112	4	36.4	9	22	ABH12154	HIV-1 derived GP12	185	4	36.4	10	15	AAH61382	Bradykinin recepto
113	4	36.4	9	22	ABH12154	HIV-1 derived GP12	186	4	36.4	10	15	AAH61391	Bradykinin recepto
114	4	36.4	9	22	ABH12154	HIV-1 derived GP12	187	4	36.4	10	15	AAH61392	Bradykinin recepto
115	4	36.4	9	22	ABH12154	HIV-1 derived GP12	188	4	36.4	10	15	AAH85170	Cell growth peptid
116	4	36.4	9	22	ABH12154	HIV-1 derived GP12	189	4	36.4	10	15	AAH85590	Human leukocyte an
117	4	36.4	9	22	ABH12154	HIV-1 derived GP12	190	4	36.4	10	15	AAH85592	Human leukocyte an
118	4	36.4	9	23	AAH52743	Bradykinin recepto	191	4	36.4	10	15	AAH85592	Bradykinin recepto
119	4	36.4	9	23	AAH52743	Bradykinin recepto	192	4	36.4	10	15	AAH85592	Bradykinin recepto
120	4	36.4	9	23	AAH52743	Bradykinin recepto	193	4	36.4	10	15	AAH85592	Bradykinin recepto
121	4	36.4	9	24	AAH85594	Human cancer relat	194	4	36.4	10	20	AAH47976	Immunogenic peptid
122	4	36.4	9	24	AAH85594	Human cancer relat	195	4	36.4	10	20	AAH47976	Immunogenic peptid
123	4	36.4	9	24	AAH85594	Human cancer relat	196	4	36.4	10	20	AAH47976	Immunogenic peptid
124	4	36.4	9	24	AAH85594	Human cancer relat	197	4	36.4	10	20	AAH47976	Immunogenic peptid
125	4	36.4	9	24	AAH85594	Human cancer relat	198	4	36.4	10	20	AAH47976	Immunogenic peptid
126	4	36.4	9	24	AAH85594	Human cancer relat	199	4	36.4	10	20	AAH47976	Immunogenic peptid
127	4	36.4	9	24	AAH85594	Human cancer relat	200	4	36.4	10	20	AAH47976	Immunogenic peptid
128	4	36.4	9	24	AAH85594	Human cancer relat	201	4	36.4	10	20	AAH47976	Immunogenic peptid
129	4	36.4	9	24	AAH85594	Human cancer relat	202	4	36.4	10	20	AAH47976	Immunogenic peptid
130	4	36.4	9	24	AAH85594	Human cancer relat	203	4	36.4	10	20	AAH47976	Immunogenic peptid
131	4	36.4	9	24	AAH85594	Human cancer relat	204	4	36.4	10	20	AAH47976	Immunogenic peptid
132	4	36.4	9	24	AAH85594	Human cancer relat	205	4	36.4	10	20	AAH47976	Immunogenic peptid
133	4	36.4	9	24	AAH85594	Human cancer relat	206	4	36.4	10	20	AAH47976	Immunogenic peptid
134	4	36.4	9	24	AAH85594	Human cancer relat	207	4	36.4	10	20	AAH47976	Immunogenic peptid
135	4	36.4	9	24	AAH85594	Human cancer relat	208	4	36.4	10	20	AAH47976	Immunogenic peptid
136	4	36.4	9	24	AAH85594	Human cancer relat	209	4	36.4	10	20	AAH47976	Immunogenic peptid
137	4	36.4	9	24	AAH85594	Human cancer relat	210	4	36.4	10	20	AAH47976	Immunogenic peptid
138	4	36.4	9	24	AAH85594	Human cancer relat	211	4	36.4	10	20	AAH47976	Immunogenic peptid
139	4	36.4	9	24	AAH85594	Human cancer relat	212	4	36.4	10	20	AAH47976	Immunogenic peptid
140	4	36.4	9	24	AAH85594	Human cancer relat	213	4	36.4	10	20	AAH47976	Immunogenic peptid
141	4	36.4	9	24	AAH85594	Human cancer relat	214	4	36.4	10	20	AAH47976	Immunogenic peptid
142	4	36.4	9	24	AAH85594	Human cancer relat	215	4	36.4	10	20	AAH47976	Immunogenic peptid
143	4	36.4	9	24	AAH85594	Human cancer relat	216	4	36.4	10	20	AAH47976	Immunogenic peptid
144	4	36.4	9	24	AAH85594	Human cancer relat	217	4	36.4	10	20	AAH47976	Immunogenic peptid
145	4	36.4	9	24	AAH85594	Human cancer relat	218	4	36.4	10	20	AAH47976	Immunogenic peptid
146	4	36.4	9	24	AAH85594	Human cancer relat	219	4	36.4	10	20	AAH47976	Immunogenic peptid
147	4	36.4	9	24	AAH85594	Human cancer relat	220	4	36.4	10	20	AAH47976	Immunogenic peptid
148	4	36.4	9	24	AAH85594	Human cancer relat	221	4	36.4	10	20	AAH47976	Immunogenic peptid
149	4	36.4	9	24	AAH85594	Human cancer relat	222	4	36.4	10	20	AAH47976	Immunogenic peptid
150	4	36.4	9	24	AAH85594	Human cancer relat	223	4	36.4	10	20	AAH47976	Immunogenic peptid
151	4	36.4	9	24	AAH85594	Human cancer relat	224	4	36.4	10	20	AAH47976	Immunogenic peptid
152	4	36.4	9	24	AAH85594	Human cancer relat	225	4	36.4	10	20	AAH47976	Immunogenic peptid
153	4	36.4	9	24	AAH85594	Human cancer relat	226	4	36.4	10	20	AAH47976	Immunogenic peptid
154	4	36.4	9	24	AAH85594	Human cancer relat	227	4	36.4	10	20	AAH47976	Immunogenic peptid
155	4	36.4	9	24	AAH85594	Human cancer relat	228	4	36.4	10	20	AAH47976	Immunogenic peptid



479	4	36.4	13	21	AAV69756	RNA binding peptid	446	4	36.4	14	19	AAW79191	Synthetic peptide
479	4	36.4	13	21	AAV69757	RNA binding peptid	449	4	36.4	14	19	AAW56527	Antigenic HIV-1 pe
479	4	36.4	13	21	AAV69758	RNA binding peptid	450	4	36.4	14	19	AAW56528	Antigenic HIV-1 pe
479	4	36.4	13	21	AAV69759	RNA binding peptid	451	4	36.4	14	19	AAW56529	Myelin basic prote
479	4	36.4	13	21	AAV69760	RNA binding peptid	452	4	36.4	14	19	AAW56530	Type-1 collagen al
480	4	36.4	13	21	AAV69761	RNA binding peptid	453	4	36.4	14	21	AAH13789	HIV-1 gp 120 C5 re
480	4	36.4	13	21	AAV69762	RNA binding peptid	454	4	36.4	14	21	AAH13790	HIV-1 gp 120 C5 re
480	4	36.4	13	21	AAV69763	RNA binding peptid	455	4	36.4	14	21	AAH13791	Carboxy terminal p
480	4	36.4	13	21	AAV69764	RNA binding peptid	456	4	36.4	14	21	AAH14904	Human AARP 79 pept
480	4	36.4	13	21	AAV69765	RNA binding peptid	457	4	36.4	14	21	AAH14905	Mutant peptide AKA
480	4	36.4	13	21	AAV69766	RNA binding peptid	458	4	36.4	14	21	AAH14906	Human secreted pro
480	4	36.4	13	21	AAV69767	RNA binding peptid	459	4	36.4	14	21	AAH14907	Human ORF 45-deri
480	4	36.4	13	21	AAV69768	RNA binding peptid	460	4	36.4	14	21	AAH14908	Human peptide 1488
480	4	36.4	13	21	AAV69769	RNA binding peptid	461	4	36.4	14	21	AAH14909	Human peptide 1487
480	4	36.4	13	21	AAV69770	RNA binding peptid	462	4	36.4	14	21	AAH14910	Human peptide 1486
480	4	36.4	13	21	AAV69771	RNA binding peptid	463	4	36.4	14	21	AAH14911	Human peptide 1485
480	4	36.4	13	21	AAV69772	RNA binding peptid	464	4	36.4	14	21	AAH14912	Synthetic peptide
480	4	36.4	13	21	AAV69773	RNA binding peptid	465	4	36.4	14	21	AAH14913	Synthetic peptide
480	4	36.4	13	21	AAV69774	RNA binding peptid	466	4	36.4	14	21	AAH14914	Protein encoded by
480	4	36.4	13	21	AAV69775	RNA binding peptid	467	4	36.4	14	21	AAH14915	IGFBP-1 displacer
480	4	36.4	13	21	AAV69776	RNA binding peptid	468	4	36.4	14	21	AAH14916	IGFBP-1 displacer
480	4	36.4	13	21	AAV69777	RNA binding peptid	469	4	36.4	14	21	AAH14917	Transcription fact
480	4	36.4	13	21	AAV69778	RNA binding peptid	470	4	36.4	14	21	AAH14918	HBZ cell overexp
480	4	36.4	13	21	AAV69779	RNA binding peptid	471	4	36.4	14	21	AAH14919	Antigenic peptide
480	4	36.4	13	21	AAV69780	RNA binding peptid	472	4	36.4	14	21	AAH14920	Antigenic peptide
480	4	36.4	13	21	AAV69781	RNA binding peptid	473	4	36.4	14	21	AAH14921	HIV500 fusion prot
480	4	36.4	13	21	AAV69782	RNA binding peptid	474	4	36.4	14	21	AAH14922	HIV virus 1 gp120
480	4	36.4	13	21	AAV69783	RNA binding peptid	475	4	36.4	14	21	AAH14923	HTLV-III envelope
480	4	36.4	13	21	AAV69784	RNA binding peptid	476	4	36.4	14	21	AAH14924	BPL16, BPL domain
480	4	36.4	13	21	AAV69785	RNA binding peptid	477	4	36.4	14	21	AAH14925	Murine stromalin-1
480	4	36.4	13	21	AAV69786	RNA binding peptid	478	4	36.4	14	21	AAH14926	Neisseria gonorrho
480	4	36.4	13	21	AAV69787	RNA binding peptid	479	4	36.4	14	21	AAH14927	Neisseria gonorrho
480	4	36.4	13	21	AAV69788	RNA binding peptid	480	4	36.4	14	21	AAH14928	Neisseria gonorrho
480	4	36.4	13	21	AAV69789	RNA binding peptid	481	4	36.4	14	21	AAH14929	SP-22 region of HI
480	4	36.4	13	21	AAV69790	RNA binding peptid	482	4	36.4	14	21	AAH14930	Polymerase epsilon
480	4	36.4	13	21	AAV69791	RNA binding peptid	483	4	36.4	14	21	AAH14931	HIV gp120 envelope
480	4	36.4	13	21	AAV69792	RNA binding peptid	484	4	36.4	14	21	AAH14932	Human heparanase p
480	4	36.4	13	21	AAV69793	RNA binding peptid	485	4	36.4	14	21	AAH14933	Mutant HIV cleavag
480	4	36.4	13	21	AAV69794	RNA binding peptid	486	4	36.4	14	21	AAH14934	HIV DR super motif
480	4	36.4	13	21	AAV69795	RNA binding peptid	487	4	36.4	14	21	AAH14935	HIV DR super motif
480	4	36.4	13	21	AAV69796	RNA binding peptid	488	4	36.4	14	21	AAH14936	HIV DR super motif
480	4	36.4	13	21	AAV69797	RNA binding peptid	489	4	36.4	14	21	AAH14937	Peptide which inhi
480	4	36.4	13	21	AAV69798	RNA binding peptid	490	4	36.4	14	21	AAH14938	Peptide which inhi
480	4	36.4	13	21	AAV69799	RNA binding peptid	491	4	36.4	14	21	AAH14939	HIV-1 gp120 glycop
480	4	36.4	13	21	AAV69800	RNA binding peptid	492	4	36.4	14	21	AAH14940	Guanosine triphosp
480	4	36.4	13	21	AAV69801	RNA binding peptid	493	4	36.4	14	21	AAH14941	DNA repair protein
480	4	36.4	13	21	AAV69802	RNA binding peptid	494	4	36.4	14	21	AAH14942	Transcription fact
480	4	36.4	13	21	AAV69803	RNA binding peptid	495	4	36.4	14	21	AAH14943	Human cancer-relat
480	4	36.4	13	21	AAV69804	RNA binding peptid	496	4	36.4	14	21	AAH14944	Human cancer-relat
480	4	36.4	13	21	AAV69805	RNA binding peptid	497	4	36.4	14	21	AAH14945	Human cancer-relat
480	4	36.4	13	21	AAV69806	RNA binding peptid	498	4	36.4	14	21	AAH14946	Human cancer-relat
480	4	36.4	13	21	AAV69807	RNA binding peptid	499	4	36.4	14	21	AAH14947	Human cancer-relat
480	4	36.4	13	21	AAV69808	RNA binding peptid	500	4	36.4	14	21	AAH14948	Human cancer-relat

ALIGNMENTS

RESULT 1	
AAV69804	
11	AAV69804 vs standard; peptide: 11 AA.
XX	
AC	AAV69804
XX	
UT	01 AUG 2000 (first entry)
XX	
FE	NCAM 141 binding peptide #15.
XX	
KW	NCAM; neural cell adhesion molecule; lq1; immunoglobulin domain 1;
KW	neutrite osteocyte precursor; proliferation; nerve damage; sclerosis;
KW	impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
KW	Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
KW	treatment; prosthetic nerve guide; treatment; nervous system.



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XX RES011.5
XX AAK96626
XX 13 AAK96626 standard, peptide: 9 AA.
XX AC AAK96626;
XX 29 NOV-1996 (first entry)
XX DE Human heat shock protein 47, homologous to N-acetyltransferase (human)
XX 1AA protease precursor: 1991 bacterial polypeptide, anti-immune?
XX viral infection; rheumatoid arthritis; AIDS; mononuclear bacterial
XX human heat shock protein 47, Hsp47; Neisseria gonorrhoeae; MS13
XX OS amino sulfonates.
XX FH Key Location/Qualifiers
XX FI 1.1.7
XX FT /note= "homologous to the sequence AKA5266.1 in
XX Neisseria gonorrhoeae strain MS13"
XX FN W09609435 A2.
XX 26 MAR-1996;
XX 21 SEP-1996; 95960-EP03726.
XX 21 SEP-1996; 945B 4433768.
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTLICH
XX Beck SG, Jose J, Lorenzen DK, Meyer TF, Metzelder KR;
XX Pöschner J, Weick J;
XX WP1: 1996 186456/19.
XX Reagents for treating viral diseases - e.g.
XX substances interfering with bacterial polypeptide function
XX Claim (2): Fig 2: 117pp; German.
XX the present sequence from human heat shock protein hsp47 has homology
XX to a cleavage product from the car-terminal domain of the precursor of
XX hsp47 protease polypeptide (1991 of Neisseria gonorrhoeae strain MS13.
XX The Neisseria hsp has been applied in rheumatoid arthritis and
XX other autoimmune diseases. The polypeptide also activates proteinase
XX including HIV. Substances which interfere with the function of hsp
XX from Neisseria will be useful for treating autoimmune diseases
XX diseases and viral infections. Fig 2: 117pp; the homology region
XX sequences, whether from Neisseria or from human, are claimed.
XX Sequence 9 AA;
XX Query Match 45.5%; Score 5; DB 15; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 82;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX 07 1 ASQAK 5
XX 1111
XX 4 ASQAK 8
XX AAK94419
XX 25 MAR-2003 (updated)
XX 05-AUG-1993 (first entry)
XX Hepatitis C Ab detection peptide #3.

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XX Test reagent: detection; antibody; hepatitis C; virus; HCV; epitope;
XX structural region; diagnosis; SS.
XX Synthetic.
XX W09307488 A1.
XX 15-APR-1993.
XX 02-OCT-1992; 92W03JP01276.
XX 02-OCT-1991; 91JP 0255524.
XX 26 MAR-1992; 92JP 0668695.
XX (EIKE ) EIKEN KAZAKU KK
XX (TANA ) TANAKA SEIYAKU KK.
XX (OSAE ) UNIV OSAKA.
XX Ishibashi K, Ito M, Shibutani T, Takamizawa A, Yoshida I;
XX WP1: 1993-114624/16.
XX Reagent for detecting antibodies to hepatitis C virus - comprises
XX peptide(s) with the same sequence as an epitope of an HCV
XX structural region
XX Disclosure: Page 42; 51pp; Japanese.
XX The sequences given in AAK44417 25 are peptides which can be used in a
XX test reagent for the detection of antibodies against hepatitis C.
XX The peptides represent epitopes of an HCV structural region and they
XX react specifically with antibodies against the HCV structural region.
XX Detection is sensitive and accurate and allows diagnosis of the
XX infection at a very early stage.
XX (updated on 25 MAR-2003 to correct PN field.)
XX Sequence 10 AA;
XX Query Match 45.5%; Score 5; DB 14; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 82;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX 07 7 RKQPR 11
XX 1111
XX 1 RKQPR 5
XX RES011.5
XX AAW21512
XX 10 AAW21512 standard, peptide: 14 AA.
XX AC AAW21512;
XX 30-JUN-1997 (first entry)
XX HIV, HIV, HIV protein derived signal oligopeptide #14.
XX Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; HIV;
XX competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
XX charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
XX hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
XX gonadotropin precursor; plasminogen activator inhibitor 2; prorenin;
XX Alzheimer amyloid A4; corticotropin releasing factor binding protein;
XX apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVNS;
XX herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
XX zeprenone pallidum membrane protein; TMPA; islet amyloid polypeptide;
XX fibroblast MMP1; schistosoma elastase precursor; schistosomin;
XX hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX Human immunodeficiency virus.
XX Simian immunodeficiency virus.

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XX WP99019568-A1.  
 XX  
 XX 20 JUL 1995  
 XX  
 XX 12 JAN 1995; 95WO-0800575.  
 XX  
 XX 14 JAN 1994; 94US 018224W.  
 XX  
 XX (KATP/1) RATH M.  
 XX  
 XX RATH M.  
 XX  
 XX WPI: 1995-253953/34.  
 XX  
 XX Identifying signal oligopeptide(s) in protein sequence(s) is shown as  
 XX regions of max. hydrophobicity, used in calculation of correlation  
 XX between protein(s)  
 XX  
 XX \*Page 5; Page 74; 88pp; English.  
 XX  
 XX The sequences given in AAW21201-566 represent hydrophobic signal oligo-  
 XX peptides. These signal oligopeptides are analysed on the surface  
 XX of the protein and are represented by the hydrophobicity maxima of  
 XX the protein. These peptides are enriched in charged amino acids  
 XX arranged with neutral spacer amino acids. The specific signal  
 XX character of these oligopeptides is determined by a characteristic  
 XX combination of conformation and charge within the signal sequence.  
 XX These oligopeptides may be used as vaccines in the treatment of  
 XX local disease, as competitive inhibitors to prevent or reduce the  
 XX metabolic action or interaction of a selected protein by blocking  
 XX its specific signal sequences, or as fragment peptides to function  
 XX as feedback regulators to reduce synthesis rate of a selected protein.  
 XX These peptides may be modified by omitting one or more amino acids at  
 XX the N- and/or C-terminal, by substituting one or more amino acids  
 XX without consideration of charge and polarity, by substitution and/or  
 XX more amino acids with amino acid residues with similar charge and/or  
 XX polarity, by omitting one or more amino acids or a combination of these.  
 XX  
 XX Sequence 13 AA:  
 XX  
 XX Query Match: 45-58; Score 5; 2H 21; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 18-02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 5 KRRKG 9  
 XX 1 1 1  
 XX 2 KRRKG 11  
 XX  
 XX RESIDUE 7  
 XX AAY6774  
 XX ID AAY6774 standard; peptide: 13 AA.  
 XX  
 XX AC AAY6774;  
 XX  
 XX DE 11 APR 2000 (first entry)  
 XX  
 XX DE RNA binding peptide #6.  
 XX  
 XX KW Antiviral; antibacterial; antitumoral; anticancer; detection; TAK: PRR;  
 XX KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 XX KW autoimmune disease; trans-activation regulatory region.  
 XX  
 XX CS Synthesis.  
 XX  
 XX FH Key Location/Qualifiers  
 XX FI Modified site 1 /note- "conjugated to BAPCYL  
 XX FI (4-(((dimethylamino)phenyl)azo)benzoic acid);"  
 XX FI Modified site 13 /note- "C-terminal amide"  
 XX FI Modified site 13  
 XX PN W09964125-A2.  
 XX  
 XX PO 16 DEC 1999.  
 XX  
 XX

XX 16 DEC 1999.  
 XX  
 XX 04 JUN 1999; 99WO 0101761.  
 XX  
 XX 05 JUN 1998; 98GB 0012195.  
 XX  
 XX 02 MAR 1999; 99GB 0004790.  
 XX  
 XX (RIDE) KHEJASHEETS LTD  
 XX  
 XX Kato J. Present: CH;  
 XX  
 XX WPI: 2000 097545/06.  
 XX  
 XX Identifying compounds that bind to target RNA, potentially useful for  
 XX treating infections, tumors and autoimmune diseases -  
 XX  
 XX Examples: Page 50; 82pp; English.  
 XX  
 XX The invention relates to a method of determining if a compound binds to  
 XX a target RNA by treating a test compound with a reporter (R) labelled  
 XX with a donor or acceptor group and labelled target RNA, labelled with  
 XX the complementary donor or acceptor group, and measuring the  
 XX fluorescence from fluorescent groups associated with a compound; target  
 XX RNA complex in presence of the test compound and comparing the result  
 XX with a standard. This peptide represents a reporter molecule isolated  
 XX from a combinatorial peptide library having the generic sequence  
 XX AAY6774. Detection of the complex is by fluorescence resonance energy  
 XX transfer (FRET). The method is used to identify compounds that interfere  
 XX with interaction between the target RNA and ligands or proteins.  
 XX Compounds that are identified are potentially useful for treating  
 XX infections (viral, bacterial or fungal), cancer and autoimmune diseases.  
 XX The compounds are preferably directed to the TAR and RRE regions of human  
 XX immunodeficiency virus RNA and inhibit viral replication.  
 XX  
 XX Sequence 13 AA:  
 XX  
 XX Query Match: 45-58; Score 5; 2H 21; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 18-02;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 5 KRRKG 9  
 XX 1 1 1  
 XX 2 KRRKG 11  
 XX  
 XX RESIDUE 7  
 XX AAY6774  
 XX ID AAY6774 standard; peptide: 13 AA.  
 XX  
 XX AC AAY6774;  
 XX  
 XX DE 11 APR 2000 (first entry)  
 XX  
 XX DE RNA binding peptide #6.  
 XX  
 XX KW Antiviral; antibacterial; antitumoral; anticancer; detection; TAK: PRR;  
 XX KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 XX KW autoimmune disease; trans-activation regulatory region.  
 XX  
 XX CS Synthesis.  
 XX  
 XX FH Key Location/Qualifiers  
 XX FI Modified site 1 /note- "conjugated to BAPCYL  
 XX FI (4-(((dimethylamino)phenyl)azo)benzoic acid);"  
 XX FI Modified site 13 /note- "C-terminal amide"  
 XX FI Modified site 13  
 XX PN W09964125-A2.  
 XX  
 XX PO 16 DEC 1999.  
 XX  
 XX







PT Treating infections, tumors and autoimmune diseases  
 PS Examples, Page 50: 82pp: English.  
 XX  
 PT The invention relates to a method of determining if a compound binds to  
 a target RNA by treating a test compound with a reporter (R) labelled  
 with a donor or acceptor group and a target RNA, labelled with  
 the complementary donor or acceptor group, and measuring the  
 fluorescence from fluorescent groups associated with a compound:target  
 RNA complex in presence of the test compound and comparing the result  
 with a standard. This peptide represents a reporter molecule isolated  
 from a combinatorial peptide library having the generic sequence  
 AAY69734. Detection of the complex is by fluorescence resonance energy  
 transfer (FRET). The method is used to identify compounds that interfere  
 with interaction between the target RNA and ligands or proteins.  
 Compounds that are identified are potentially useful for treating  
 infections (viral, bacterial or fungal), cancer and autoimmune diseases.  
 The compounds are preferably directed to the TAR and RRE regions of human  
 immunodeficiency virus RNA and inhibit viral replication.  
 XX  
 SQ Sequence: 13 AA:  
 Query Match: 45.5%, Score 53, DB 21, Length 13;  
 Best Local Similarity: 100.0%, Pred. No. 1c+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KRRKG 9  
 1111  
 QL 7 KRRKG 11  
 1111  
 RESUL: 12  
 AAY69734  
 DE AAY69734 standard; peptide: 13 AA  
 A\* AAY69734;  
 XX  
 XX 11-APS 2000 (first entry)  
 DE RNA binding peptide #23.  
 XX  
 XX Antiviral, antibacterial; antifungal; anticancer; detection; TAR; RRE;  
 KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 KW autoimmune disease; trans-activation; regulatory region.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FI Modified-site 1  
 FI /note "conjugated to DABCYL  
 (4-((diethylamino)phenyl)azo)benzoic acid"  
 FI Modified-site 13  
 FI /note "C-terminal amide"  
 FI  
 FI Modified-site 13  
 FI /note "C-terminal amide"  
 FI  
 FI W09064625 A2  
 XX  
 XX 16 JUN 1999;  
 XX  
 XX 04 JUN 1999; 99060301761;  
 XX  
 XX 05 JUN 1998; 98080012196;  
 XX 02 MAR 1999; 99080004790;  
 XX  
 XX (RIBO+) KIBOTARGETS LTD.  
 XX  
 XX Karin J. Prescott CD;  
 XX  
 XX WPI: 2000-097545/08.  
 XX  
 XX Identifying compounds that bind to target RNA, potentially useful for  
 treating infections, tumors and autoimmune diseases  
 XX  
 XX Examples, Page 50: 82pp: English.  
 PS  
 PT The invention relates to a method of determining if a compound binds to  
 a target RNA by treating a test compound with a reporter (R) labelled

XX  
 XX The invention relates to a method of determining if a compound binds to  
 a target RNA by treating a test compound with a reporter (R) labelled  
 with a donor or acceptor group and a target RNA, labelled with  
 the complementary donor or acceptor group, and measuring the  
 fluorescence from fluorescent groups associated with a compound:target  
 RNA complex in presence of the test compound and comparing the result  
 with a standard. This peptide represents a reporter molecule isolated  
 from a combinatorial peptide library having the generic sequence  
 AAY69734. Detection of the complex is by fluorescence resonance energy  
 transfer (FRET). The method is used to identify compounds that interfere  
 with interaction between the target RNA and ligands or proteins.  
 Compounds that are identified are potentially useful for treating  
 infections (viral, bacterial or fungal), cancer and autoimmune diseases.  
 The compounds are preferably directed to the TAR and RRE regions of human  
 immunodeficiency virus RNA and inhibit viral replication.  
 XX  
 SQ Sequence: 13 AA:  
 Query Match: 45.5%, Score 53, DB 21, Length 13;  
 Best Local Similarity: 100.0%, Pred. No. 1c+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KRRKG 9  
 1111  
 QL 7 KRRKG 11  
 1111  
 RESUL: 14  
 AAY69734  
 DE AAY69734 standard; peptide: 13 AA  
 A\* AAY69734;  
 XX  
 XX 11-APS 2000 (first entry)  
 DE RNA binding peptide #23.  
 XX  
 XX Antiviral, antibacterial; antifungal; anticancer; detection; TAR; RRE;  
 KW Fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
 KW autoimmune disease; trans-activation; regulatory region.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FI Modified-site 1  
 FI /note "conjugated to DABCYL  
 (4-((diethylamino)phenyl)azo)benzoic acid"  
 FI Modified-site 13  
 FI /note "C-terminal amide"  
 FI  
 FI W09064625 A2  
 XX  
 XX 16 JUN 1999;  
 XX  
 XX 04 JUN 1999; 99060301761;  
 XX  
 XX 05 JUN 1998; 98080012196;  
 XX 02 MAR 1999; 99080004790;  
 XX  
 XX (RIBO+) KIBOTARGETS LTD.  
 XX  
 XX Karin J. Prescott CD;  
 XX  
 XX WPI: 2000-097545/08.  
 XX  
 XX Identifying compounds that bind to target RNA, potentially useful for  
 treating infections, tumors and autoimmune diseases  
 XX  
 XX Examples, Page 50: 82pp: English.  
 PS  
 PT The invention relates to a method of determining if a compound binds to  
 a target RNA by treating a test compound with a reporter (R) labelled

with a donor or acceptor group and labeled target RNA, labelled with the complementary donor or acceptor group, and measuring the fluorescence from fluorescent groups associated with a compound:target RNA complex in presence of the test compound and comparing the result with a standard. This peptide represents a reporter molecule isolated from a combinatorial peptide library having the generic sequence AAY69733. . Detection of the complex is by fluorescence resonance energy transfer (FRET). The method is used to identify compounds that interfere with interaction between the target RNA and ligands or proteins. Compounds that are identified are potentially useful for treating infections (viral, bacterial or fungal), cancer and autoimmune diseases. The compounds are preferably directed to the TAR and RRE regions of human immunodeficiency virus RNA and inhibit viral replication.

Query Match: 45.5%; Score 5; DB 21; Length 13;  
Best Local Similarity: 100.0%; Pred. No. 1e-02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 5 KRKKG 9  
ID 7 KRKKG 11

RESULT 14  
AAY69762  
ID AAY69762 standard; peptide: 13 AA.  
XX  
AC AAY69762;  
XX  
DT 11 APR 2003 (first entry)  
XX  
DE RNA binding peptide #33.  
XX  
KW Antiviral; antibacterial; antifungal; anticancer; detection; TAR; RRE;  
KW fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
KW autoimmune disease; trans-activation regulatory region.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note "conjugated to DABCYL  
FT Modified-site 13 (4-(((dimethylamino)phenyl)azo)benzoic acid)"  
FT Modified-site 13 /note "C-terminal amide"  
XX  
FN W0964625-A2  
XX  
FD 16-DEC-1999.  
XX  
FD 04-JUN 1999; 99WG-GB01761.  
XX  
FD 05-JUN 1998; 98GB-0012196.  
PR 02-MAR-1999; 99GB-0004790.  
XX  
PA (RIBO-) RIBOTARGETS LTD.  
XX  
PI Karin J. Prescott CD;  
XX  
XX WPI: 2003-097545/08.  
XX  
PT Identifying compounds that bind to target RNA, potentially useful for treating infections, tumors and autoimmune diseases  
XX  
PS Examples: Page 50; 82pp; English.  
XX  
CC The invention relates to a method of determining if a compound binds to a target RNA by treating a test compound with a reporter (R) labelled with a donor or acceptor group and labelled target RNA, labelled with the complementary donor or acceptor group, and measuring the fluorescence from fluorescent groups associated with a compound:target RNA complex in presence of the test compound and comparing the result with a standard. This peptide represents a reporter molecule isolated from a combinatorial peptide library having the generic sequence

CC RNA complex in presence of the test compound and comparing the result with a standard. This peptide represents a reporter molecule isolated from a combinatorial peptide library having the generic sequence AAY69733. . Detection of the complex is by fluorescence resonance energy transfer (FRET). The method is used to identify compounds that interfere with interaction between the target RNA and ligands or proteins. Compounds that are identified are potentially useful for treating infections (viral, bacterial or fungal), cancer and autoimmune diseases. The compounds are preferably directed to the TAR and RRE regions of human immunodeficiency virus RNA and inhibit viral replication.

Query Match: 45.5%; Score 5; DB 21; Length 13;  
Best Local Similarity: 100.0%; Pred. No. 1e-02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 5 KRKKG 9  
ID 7 KRKKG 11

RESULT 15  
AAY69764  
ID AAY69764 standard; peptide: 13 AA.  
XX  
AC AAY69764;  
XX  
DT 11 APR 2003 (first entry)  
XX  
DE RNA binding peptide #33.  
XX  
KW Antiviral; antibacterial; antifungal; anticancer; detection; TAR; RRE;  
KW fluorescence resonance energy transfer; tat; HIV-1; Rev response element;  
KW autoimmune disease; trans-activation regulatory region.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /note "conjugated to DABCYL  
FT Modified-site 13 (4-(((dimethylamino)phenyl)azo)benzoic acid)"  
FT Modified-site 13 /note "C-terminal amide"  
XX  
FN W0964625-A2  
XX  
FD 16-DEC-1999.  
XX  
FD 04-JUN 1999; 99WG-GB01761.  
XX  
FD 05-JUN 1998; 98GB-0012196.  
PR 02-MAR-1999; 99GB-0004790.  
XX  
PA (RIBO-) RIBOTARGETS LTD.  
XX  
PI Karin J. Prescott CD;  
XX  
XX WPI: 2003-097545/08.  
XX  
PT Identifying compounds that bind to target RNA, potentially useful for treating infections, tumors and autoimmune diseases  
XX  
PS Examples: Page 50; 82pp; English.  
XX  
CC The invention relates to a method of determining if a compound binds to a target RNA by treating a test compound with a reporter (R) labelled with a donor or acceptor group and labelled target RNA, labelled with the complementary donor or acceptor group, and measuring the fluorescence from fluorescent groups associated with a compound:target RNA complex in presence of the test compound and comparing the result with a standard. This peptide represents a reporter molecule isolated from a combinatorial peptide library having the generic sequence





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Q7 5 KRKG 5
Q8 111 1
Q9 7 KRKG 11

RESULT 21
AAU06082 standard: peptide: 14 AA
XX AAU06082
XX AAU06082
XX 24-00T-2000 (first entry)
XX RNA binding peptide #14 tested for binding to HIV IRES RNA
XX RNA binding peptide: Hepatitis C virus, HCV 5'-UTR; minimal IRES; IRES;
XX internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX HIV translation initiation; antiviral
XX Synthesized
XX Key Location/Qualifiers
XX Key 4.18
XX Note "Variable pentapeptide core"
XX WF200144266-A2
XX 21 JUN 2001
XX 18 DEC 2000; 2000W0 3003412
XX 18 DEC 1999; 9908 0029820
XX 22 DEC 1999; 9908 0121804
XX (KIB) KIBOTARGETS LTD.
XX Kuhn J. Walker S.
XX WPI: 2001-465550/50
XX Nucleotide sequences derived from Hepatitis C virus, useful for
XX identifying candidate antiviral compounds
XX Disclosed: Page 29; 48pp; English
XX The present sequence represents RNA binding peptide #14 tested for
XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX RNA. A subset of 46 peptides (AAU06071-AAU06110) selected from a
XX library of synthetic peptides with a variable pentapeptide core and
XX constant flanking neutral and basic amino acids were tested for
XX association related to a novel compound comprising nucleotide sequences
XX capable of annealing and which is derived from a 5'-untranslated region
XX (UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX eIF3 (eukaryotic initiation factor 3). The invention particularly
XX relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX IRES (IRES) which can be used to identify drugs which inhibit HCV
XX translation initiation. The compounds of the invention may be used to
XX screen for potential HCV antiviral compounds. Assays based on the
XX IRES enable potential antivirals to be screened in a cheaper and easier
XX way. It allows rapid assaying with a small volume of material and are
XX suitable to parallel processing.
XX Sequence 14 AA:
Query Match 45.0% Score 5; DB 22; Length 13;
Best Local Similarity 100.0%; Fred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q7 5 KRKG 9
Q8 111 1
Q9 7 KRKG 11

RESULT 22
AAU06085 standard: peptide: 14 AA
XX AAU06085
XX AAU06085
XX 24-00T-2000 (first entry)
XX RNA binding peptide #14 tested for binding to HIV IRES RNA
XX RNA binding peptide: Hepatitis C virus, HCV 5'-UTR; minimal IRES; IRES;
XX internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX HIV translation initiation; antiviral
XX Synthesized
XX Key Location/Qualifiers
XX Key 4.18
XX Note "Variable pentapeptide core"
XX WF200144266-A2
XX 21 JUN 2001
XX 18 DEC 2000; 2000W0 3003412
XX 18 DEC 1999; 9908 0029820
XX 22 DEC 1999; 9908 0121804
XX (KIB) KIBOTARGETS LTD.
XX Kuhn J. Walker S.
XX WPI: 2001-465550/50
XX Nucleotide sequences derived from Hepatitis C virus, useful for
XX identifying candidate antiviral compounds
XX Disclosed: Page 29; 48pp; English
XX The present sequence represents RNA binding peptide #14 tested for
XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX RNA. A subset of 46 peptides (AAU06071-AAU06110) selected from a
XX library of synthetic peptides with a variable pentapeptide core and
XX constant flanking neutral and basic amino acids were tested for
XX association related to a novel compound comprising nucleotide sequences
XX capable of annealing and which is derived from a 5'-untranslated region
XX (UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX eIF3 (eukaryotic initiation factor 3). The invention particularly
XX relates to a sub-region of the HCV 5'-UTR which is essential for
XX IRES (IRES) which can be used to identify drugs which inhibit HCV
XX translation initiation. The compounds of the invention may be used to
XX screen for potential HCV antiviral compounds. Assays based on the
XX IRES enable potential antivirals to be screened in a cheaper and easier
XX way. It allows rapid assaying with a small volume of material and are
XX suitable to parallel processing.
XX Sequence 14 AA:
Query Match 45.0% Score 5; DB 22; Length 13;
Best Local Similarity 100.0%; Fred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q7 5 KRKG 9
Q8 111 1
Q9 7 KRKG 11
```

```
Q7 5 KRKG 5
Q8 111 1
Q9 7 KRKG 11

RESULT 21
AAU06082 standard: peptide: 14 AA
XX AAU06082
XX AAU06082
XX 24-00T-2000 (first entry)
XX RNA binding peptide #14 tested for binding to HIV IRES RNA
XX RNA binding peptide: Hepatitis C virus, HCV 5'-UTR; minimal IRES; IRES;
XX internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX HIV translation initiation; antiviral
XX Synthesized
XX Key Location/Qualifiers
XX Key 4.18
XX Note "Variable pentapeptide core"
XX WF200144266-A2
XX 21 JUN 2001
XX 18 DEC 2000; 2000W0 3003412
XX 18 DEC 1999; 9908 0029820
XX 22 DEC 1999; 9908 0121804
XX (KIB) KIBOTARGETS LTD.
XX Kuhn J. Walker S.
XX WPI: 2001-465550/50
XX Nucleotide sequences derived from Hepatitis C virus, useful for
XX identifying candidate antiviral compounds
XX Disclosed: Page 29; 48pp; English
XX The present sequence represents RNA binding peptide #14 tested for
XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX RNA. A subset of 46 peptides (AAU06071-AAU06110) selected from a
XX library of synthetic peptides with a variable pentapeptide core and
XX constant flanking neutral and basic amino acids were tested for
XX association related to a novel compound comprising nucleotide sequences
XX capable of annealing and which is derived from a 5'-untranslated region
XX (UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX eIF3 (eukaryotic initiation factor 3). The invention particularly
XX relates to a sub-region of the HCV 5'-UTR referred to as the minimal
XX IRES (IRES) which can be used to identify drugs which inhibit HCV
XX translation initiation. The compounds of the invention may be used to
XX screen for potential HCV antiviral compounds. Assays based on the
XX IRES enable potential antivirals to be screened in a cheaper and easier
XX way. It allows rapid assaying with a small volume of material and are
XX suitable to parallel processing.
XX Sequence 14 AA:
Query Match 45.0% Score 5; DB 22; Length 13;
Best Local Similarity 100.0%; Fred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q7 5 KRKG 9
Q8 111 1
Q9 7 KRKG 11

RESULT 22
AAU06085 standard: peptide: 14 AA
XX AAU06085
XX AAU06085
XX 24-00T-2000 (first entry)
XX RNA binding peptide #14 tested for binding to HIV IRES RNA
XX RNA binding peptide: Hepatitis C virus, HCV 5'-UTR; minimal IRES; IRES;
XX internal ribosome entry site; eIF3; eukaryotic initiation factor 3;
XX HIV translation initiation; antiviral
XX Synthesized
XX Key Location/Qualifiers
XX Key 4.18
XX Note "Variable pentapeptide core"
XX WF200144266-A2
XX 21 JUN 2001
XX 18 DEC 2000; 2000W0 3003412
XX 18 DEC 1999; 9908 0029820
XX 22 DEC 1999; 9908 0121804
XX (KIB) KIBOTARGETS LTD.
XX Kuhn J. Walker S.
XX WPI: 2001-465550/50
XX Nucleotide sequences derived from Hepatitis C virus, useful for
XX identifying candidate antiviral compounds
XX Disclosed: Page 29; 48pp; English
XX The present sequence represents RNA binding peptide #14 tested for
XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)
XX RNA. A subset of 46 peptides (AAU06071-AAU06110) selected from a
XX library of synthetic peptides with a variable pentapeptide core and
XX constant flanking neutral and basic amino acids were tested for
XX association related to a novel compound comprising nucleotide sequences
XX capable of annealing and which is derived from a 5'-untranslated region
XX (UTR) of the Hepatitis C virus (HCV) which is essential for binding of
XX eIF3 (eukaryotic initiation factor 3). The invention particularly
XX relates to a sub-region of the HCV 5'-UTR which is essential for
XX IRES (IRES) which can be used to identify drugs which inhibit HCV
XX translation initiation. The compounds of the invention may be used to
XX screen for potential HCV antiviral compounds. Assays based on the
XX IRES enable potential antivirals to be screened in a cheaper and easier
XX way. It allows rapid assaying with a small volume of material and are
XX suitable to parallel processing.
XX Sequence 14 AA:
Query Match 45.0% Score 5; DB 22; Length 13;
Best Local Similarity 100.0%; Fred. No. 1e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q7 5 KRKG 9
Q8 111 1
Q9 7 KRKG 11
```





KW Internal ribosome entry site: eIF3; eukaryotic initiation factor 3;  
 KW HCV translation initiation; antiviral;  
 XX Synthetic;  
 XX Key Location/Qualifiers  
 XX Region 4..8  
 XX /note- "Variable pentapeptide core"  
 XX  
 XX WC200144266-A2;  
 XX 21-JUN-2001;  
 XX 18 DEC-2000; 250060-380435-2;  
 XX 16 DEC-1999; 99GB-0029820;  
 XX 22-DEC-1999; 99US-0171804;  
 XX (KIBO ) KIBOTARGETS LTD;  
 XX Karn J, Walker S;  
 XX WPI: 2001-465050/50;  
 XX Nucleotide sequences derived from Hepatitis C virus, useful for  
 XX identifying candidate antiviral compounds  
 XX  
 XX Disclosure: Page 29; 48pp; English  
 XX The present sequence represents RNA binding peptide #28 tested for  
 XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)  
 XX RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a  
 XX library of synthetic peptides with a variable pentapeptide core and  
 XX constant flanking neutral and basic amino acids were tested for  
 XX binding to HCV IRES RNA. The present sequence is described in an  
 XX invention relating to a novel compound comprising nucleotide sequences  
 XX capable of annealing and which is derived from a 5'-untranslated region  
 XX (5'UTR) of the Hepatitis C virus (HCV) which is essential for binding of  
 XX eIF3 (eukaryotic initiation factor 3). The invention particularly  
 XX relates to a sub-region of the HCV 5'-UTR referred to as the minimal  
 XX IRES (mIRES) which can be used to identify drugs which inhibit HCV  
 XX translation initiation. The compounds of the invention may be used to  
 XX screen for potential HCV antiviral compounds. Assays based on the  
 XX mIRES enable potential antivirals to be screened in a cheaper and easier  
 XX way. It allows rapid assaying with a small volume of material and are  
 XX suitable to parallel processing.  
 XX Sequence 13 AA;  
 XX  
 XX Query Match 45.5%; Score 5; DB 22; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 1e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Gaps 0;  
 XX  
 XX 5 KRRKG 9  
 XX 111  
 XX 7 KRRKG 11  
 XX  
 XX RESSET 25  
 XX AAU06096  
 XX 10 AAU06096 standard; peptide: 13 AA  
 XX AC AAU06096;  
 XX 24 OCT-2001 (first entry)  
 XX RNA binding peptide #28 tested for binding to HCV IRES RNA;  
 XX RNA binding peptide; Hepatitis C virus; HCV 5'-UTR; minimal IRES; mIRES;  
 XX Internal ribosome entry site; eIF3; eukaryotic initiation factor 3;  
 XX HCV translation initiation; antiviral;  
 XX Synthetic;  
 XX Key Location/Qualifiers  
 XX Region 4..8  
 XX /note- "Variable pentapeptide core"

XX Key Location/Qualifiers  
 XX Region 4..8  
 XX /note- "Variable pentapeptide core"  
 XX  
 XX WC200144266-A2;  
 XX 21-JUN-2001;  
 XX 18 DEC-2000; 250060-380435-2;  
 XX 16 DEC-1999; 99GB-0029820;  
 XX 22-DEC-1999; 99US-0171804;  
 XX (KIBO ) KIBOTARGETS LTD;  
 XX Karn J, Walker S;  
 XX WPI: 2001-465050/50;  
 XX Nucleotide sequences derived from Hepatitis C virus, useful for  
 XX identifying candidate antiviral compounds  
 XX  
 XX Disclosure: Page 29; 48pp; English  
 XX The present sequence represents RNA binding peptide #28 tested for  
 XX binding to Hepatitis C virus (HCV) internal ribosome entry site (IRES)  
 XX RNA. A subset of 40 peptides (AAU06071-AAU06110) selected from a  
 XX library of synthetic peptides with a variable pentapeptide core and  
 XX constant flanking neutral and basic amino acids were tested for  
 XX binding to HCV IRES RNA. The present sequence is described in an  
 XX invention relating to a novel compound comprising nucleotide sequences  
 XX capable of annealing and which is derived from a 5'-untranslated region  
 XX (5'UTR) of the Hepatitis C virus (HCV) which is essential for binding of  
 XX eIF3 (eukaryotic initiation factor 3). The invention particularly  
 XX relates to a sub-region of the HCV 5'-UTR referred to as the minimal  
 XX IRES (mIRES) which can be used to identify drugs which inhibit HCV  
 XX translation initiation. The compounds of the invention may be used to  
 XX screen for potential HCV antiviral compounds. Assays based on the  
 XX mIRES enable potential antivirals to be screened in a cheaper and easier  
 XX way. It allows rapid assaying with a small volume of material and are  
 XX suitable to parallel processing.  
 XX Sequence 13 AA;  
 XX  
 XX Query Match 45.5%; Score 5; DB 22; Length 13;  
 XX Best Local Similarity 100.0%; Pred. No. 1e+02;  
 XX Matches 5; Conservative 0; Mismatches 0; Gaps 0;  
 XX  
 XX 5 KRRKG 9  
 XX 111  
 XX 7 KRRKG 11  
 XX  
 XX RESSET 26  
 XX AAU06099  
 XX 10 AAU06099 standard; peptide: 13 AA  
 XX AC AAU06099;  
 XX 24 OCT-2001 (first entry)  
 XX RNA binding peptide #31 tested for binding to HCV IRES RNA;  
 XX RNA binding peptide; Hepatitis C virus; HCV 5'-UTR; minimal IRES; mIRES;  
 XX Internal ribosome entry site; eIF3; eukaryotic initiation factor 3;  
 XX HCV translation initiation; antiviral;  
 XX Synthetic;  
 XX Key Location/Qualifiers  
 XX Region 4..8  
 XX /note- "Variable pentapeptide core"





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XX  further, the Grosfeld et al. Van der Woude et al.
XX  WJ 1996 09961/51.
XX  N 5866 AAK5762.
XX
XX  immunising disease by detecting transcribed mutations of a disease
XX  corresponding protein mutations. used to diagnose liver and
XX  neurological diseases, particularly Alzheimer's disease and also
XX  for treatment and prevention with specific mutations of said type
XX  RNA
XX
XX  discussed, Figure 11, 25pp, English.
XX
XX  This invention describes a novel method for the diagnosis of a disease
XX  caused by, or associated with, an RNA molecule that has a frameshift
XX  mutation. The method is used to diagnose and treat diseases, especially
XX  cancer, and a wide range of neurodegenerative disorders (e.g., Alzheimer's
XX  disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
XX  multiple sclerosis, alcoholic liver disease, neurofibrosis type 1)
XX  and many others (listed) or susceptibility to these disorders. The method
XX  allows a definitive diagnosis of Alzheimer's disease in living patients,
XX  at an early stage. It is based on the observation that disease may be
XX  caused by mutations in RNA rather than DNA. The invention describes the
XX  use of central system RNA molecules. Specifically proteins included
XX  beta amyloid precursor protein (beta A42), the microtubule associated
XX  proteins tau and Big Tau, ubiquitin, B, apolipoprotein E, plectin,
XX  associated protein 2 (MAP2), neuronal protein 1, neuronal M,
XX  neurofilament E, presenilin 1, presenilin 2, huntingtin, fibrinolytic
XX  protein (GPA), the cellular tumor antigen 153, growth cone/lymphoma
XX  2 (GCL-2) proto-oncogene, scap, protein 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000.

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XX  Expression cassettes encoding the human immunodeficiency virus (HIV)
XX  Gag containing polypeptide useful for vaccinating against HIV
XX  infections and acquired immunodeficiency syndrome (AIDS) -
XX
XX  Example 1: Page 126; 59pp; English.
XX
XX  The present invention relates to synthetic HIV Gag and Env expression
XX  cassettes. The gag protein of HIV is needed for the assembly of
XX  virus like particles. In addition, the gag protein is involved in many
XX  stages of the HIV life cycle, including assembly, virion maturation,
XX  after particle release and early host entry steps in viral replication.
XX  The expression cassettes of the present invention may be used for the
XX  recombinant expression of HIV gag-polypeptides which may then be used to
XX  vaccinate against HIV infection and acquired immunodeficiency syndrome
XX  (AIDS). The present sequence is the HIV US4 qpl20 cleavage site. This
XX  site was mutated for use in the construction of the HIV Env expression
XX  cassettes (see AAB14223 for the mutant cleavage site).
XX
XX  Sequence 15 AA:
XX
XX  Query Match 45.5% Score 5; DB 21; Length 15;
XX  Best Local Similarity 100.0%; Pred. No. 1.1e-02;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  5' 5 KKKK 9
XX  DE 111
XX  10 10 KKKK 14
XX
XX  RESIDUE 1
XX  AAB14221
XX  ID AAB14221 standard; Peptide: 15 AA
XX  AC AAB14221;
XX  DI 28-N-W-2003 (FIRST entry)
XX  DE Mutant HIV cleavage site qpl40.mut.modUS4.
XX  KW HIV 1, AIDS, Gag; vaccine; expression cassette; Env; cleavage site;
XX  KW mutant; mutant.
XX  XX
XX  OS Human immunodeficiency virus type 1.
XX  OS SYNTACTIC.
XX  FH Key Location/Qualifiers
XX  FI Miscellaneous:
XX  FI /note "With type Arg substituted by Ser"
XX  XX
XX  GN W20030902 A2.
XX  XX
XX  PO 16-200 2000
XX  XX
XX  DE DEC-1999; 9906 US51245.
XX  XX
XX  PR 31-DEC-1998; 9805-0114495.
XX  PR 31-DEC-1999; 9905-0168471.
XX  XX
XX  PA (CHIR ) CHIR-N CORP.
XX  XX
XX  PI Barnett S, Zou Meqede J, Srivastava I, Lian Y, Hartog K, Liu H;
XX  PI Green C, Selby M, Walker C;
XX  XX
XX  GR WPI; 2030 45240/39.
XX  XX
XX  PR Expression cassettes encoding the human immunodeficiency virus (HIV)
XX  PR Gag containing polypeptide useful for vaccinating against HIV
XX  PR infections and acquired immunodeficiency syndrome (AIDS) -
XX  XX
XX  PS Example 1: Page 121; 59pp; English.
XX
XX  The present invention relates to synthetic HIV Gag and Env expression

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CC These oligopeptides may be used as vaccines in the treatment of  
 CC human disease, as competitive inhibitors to prevent or reduce the  
 CC metabolic action of a selected protein by blocking  
 CC its specific signal sequences, or as therapeutic agents to function  
 CC as feedback regulators to reduce synthesis rate of a selected protein.  
 CC These peptides may be modified by adding one or more amino acids at  
 CC the N and/or C-terminal, by substituting one or more amino acids  
 CC without consideration of charge and polarity, by substituting one or  
 CC more amino acids with amino acid residues with a similar charge and/or  
 CC polarity, by omitting one or more amino acids or a substitution of these.  
 XX  
 SQ Sequence: 8 AA;

Query Match: 46.4%; Score 4; DB 19; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KRRK R  
 III  
 DB 5 KRRK R

RESULT 4:  
 AAW791B5  
 ID AAW791B5 standard: peptide: 8 AA;

XX AAW791B5:

XX 25 JAN-1999 (first entry)

XX HIV gp120 C5 region B cell epitope peptide.

XX B cell: T cell; epitope: immunoglobulin heavy chain gp120 C5  
 KW human immune deficiency virus; HIV; tolerance: treatment: therapy;  
 KW prophylaxis: vaccine; chemotherapy; immune response; modified; human;  
 KW microbial infection; autoimmune disease; antibody; apoptosis;  
 KW antiviral: cell immunity;

XX Mos SP;

XX Homo sapiens

XX W0086627-1-1

XX 20-AUG-1998

XX 13-FEB-1994 96WD-0802766

XX 13-FEB-1994 97GS-0040084

XX (AFMA : AMERICAN NAT RES) CROSS

XX 2001 D; Zaididis E;

XX W01: 1996 5.6.615/43.

XX New fusion immunoglobulin heavy chain containing gp120 epitopes and  
 CC related complete antibodies - DNA vectors and transduced cells  
 CC used to induce tolerance to the epitopes for treatment of human  
 CC immune deficiency virus infection

XX Example 11: Page 73; 154pp; English.

XX This sequence is an epitope used in the construction of a novel fusion  
 CC immunoglobulin heavy chain (IGH) protein with a mammalian, especially  
 CC human, IgH chain fused in frame at its N-terminus to one or more human  
 CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or  
 CC transduced cells are used to tolerate subjects to gp120 epitopes and to  
 CC maintain this tolerance, particularly for treatment of HIV infection,  
 CC optionally together with other therapeutic/prophylactic agents such as  
 CC vaccines, chemotherapeutic agents and immune response modifiers. Such  
 CC proteins can be used against other diseases where an immune response is  
 CC deleterious, e.g. microbial infection, cancers or autoimmune disease.  
 CC Induction of tolerance suppresses production of antibodies against gp120.

CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that  
 CC are bound to gp120 protein, maximising induction of protective antiviral  
 CC T cell immunity.  
 XX  
 SQ Sequence: 8 AA;

Query Match: 46.4%; Score 4; DB 19; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AKRR R  
 III  
 DB 5 AKRR R

RESULT 36  
 AAW59607  
 ID AAW59607 standard: peptide: 8 AA;

XX AAW59607:

XX 23-OCT-1998 (first entry)

XX Epitope of the Hepatitis C virus.

XX Epitope: HCV; envelope protein E2; HCV antibody; anti-idiotype;  
 KW vaccine; HCV infection; treatment; diagnosis;

XX Synthetic

XX Hepatitis C virus.

XX W09816647 A1

XX 25-APR-1998

XX 03-OCT-1997 97W0-JP045511

XX 03-MAR-1997 97JP-0065448

XX 14-OCT-1996 96JP-0293359

XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

XX Makizumi K, Mizuno K, Nishihara T, Nishimura S;

XX Sezaki O, Kikuhisa I;

XX W01: 1998 241644/24.

XX Hepatitis C virus envelope antigen epitope peptide(s) useful for,  
 CC e.g. treatment, vaccination and detection of hepatitis C virus  
 CC infection(s)

XX Disclosure: Fig 14; 99pp; Japanese.

XX AAW59504-606 represent epitopes of the Hepatitis C virus (HCV). The  
 CC peptides are derived from the HCV envelope protein E2 (384-414 region)  
 CC and are capable of binding to HCV antibodies. The epitope peptides and  
 CC anti-idiotype antibodies can be used to produce effective vaccines  
 CC against HCV infection. The antibodies recognising the epitope peptides  
 CC can be used in the treatment of HCV infection. The epitope peptides,  
 CC DNA and antibodies can be used for diagnosis of HCV infection, detection  
 CC of the presence of HCV and for HCV neutralising antibody assay.

XX Sequence: 8 AA;

Query Match: 46.4%; Score 4; DB 19; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ASQA 4  
 III  
 DB 1 ASQA 4

```

RESULT 47
AA000148
ID  AA000148 standard; peptide; 8 AA.
XX
XX
XX
XX  04-SEP-2002 (first entry)
XX
XX  peptide mediating activity of hepatitis and other viruses.
XX
XX  glycosaminoglycan; proteoglycan; heparin; heparan sulfate; and chondroitin
XX  cell attachment; cell adhesion; cell migration; tumor cell metastasis;
XX  cartilage differentiation; wound healing
XX
XX  Synthetic.
XX
XX  Key location/Qualifiers
XX  Rise difference 1-8
XX  /note: "this peptide may be related to an
XX  unspecified number of things"
XX
XX  W-2001-45441-A1.
XX
XX  10 AUG-2002.
XX
XX  G2-FEB-2002: 2000W-US02853.
XX
XX  G2-FEB-1999: 990S-0118276.
XX
XX  (UWJE ) UNIV JEFFERSON THOMAS.
XX
XX  San Antonio, TX. Verreccini A. Schick BP.
XX
XX  W-1: 2000-54446/49.
XX
XX  Novel synthetic peptides with high affinity for glycosaminoglycans and
XX  proteoglycans, useful for mediating heparin promoting cell
XX  attachment, modulating tumor metastasis and modulating wound healing.
XX
XX  Chesnut R. Page 24; 76pp; English.
XX
XX  The present sequence represents a synthetic peptide which has a high
XX  affinity for glycosaminoglycans and proteoglycans. The peptide is useful
XX  in methods for modulating repair of other glycosaminoglycans with
XX  antitumoral activity, promoting cell attachment of adenocarcinoma
XX  natural or synthetic surfaces (especially hemostatic), modulation
XX  tumor cell metastasis, modulating cartilage formation, targeting
XX  drugs to epithelial cell surfaces (e.g. tumor cells), expression
XX  proteoglycans, modulating enzymes that degrade glycosaminoglycan
XX  substrates, affinity purification, and other uses. Sequences of a
XX  glycosaminoglycan, modifying endothelial cell permeability, and
XX  anti-coagulant functions mediated through glycosaminoglycans, and
XX  modulation wound healing. The peptide may also be used for blocking
XX  tissue uptake of heparin or other glycosaminoglycans in a normal to
XX  increase heparin half-life in circulation
XX
XX  Sequence 8 AA:
XX
XX  Query Match 36.4%; Score 4; DB 21; Length 8;
XX  Best local Similarity 100.0%; Pred. No. 9, 3e-05;
XX  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  5 RRGK 9
XX  III
XX  2 RRGK 5
XX
XX  RESULT 48
AA012017
ID  AA012017 standard; Peptide; 8 AA.
XX
XX  Asp/2017
XX
XX  Asp/2017:
XX
XX  15-JUL-2002 (first entry)
XX
XX  HIV p24 Super motif env peptide #117.

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D4  15-JUL-2002 (first entry)
XX
XX  HIV AC2 Super motif env peptide #74.
XX
XX  HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX  vpr; vpr; tat; cytochrome b lymphocyte; CTL; immune response; epitope;
XX  antisense; vaccine; HIV infection; immunisation; virucide.
XX
XX  Human immunodeficiency virus type 1.
XX
XX  W-2001-4810-A1
XX
XX  12 APR-2002.
XX
XX  05-JUL-2000: 2000W-US27756.
XX
XX  06-JUL-1999: 990S-0412663.
XX
XX  (EP:9-) ESTIMONE (M).
XX
XX  Sette A, Sidney J. Southwood S, Livingston BD, Chesnut R;
XX  Baker EM, Ellis E, Kubo RT, Grey HM;
XX
XX  W-1: 2001-354827/77.
XX
XX  Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX  peptide groups, useful for vaccinating against HIV-1.
XX
XX  Claim 32; Page 115; 448pp; English.
XX
XX  The present invention describes a composition (1) comprising a prepared
XX  human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX  sequence selected from 91 defined amino acid sequences (AAL25347 to
XX  AAL25397). (1) has virucide activity and can be used in vaccines. (1)
XX  may be used for immunising subjects against HIV-1 infections. The use of
XX  group-based vaccines has several advantages over traditional vaccines,
XX  particularly when compared to the use of whole antigens in vaccine
XX  compositions. There is evidence that the immune response to whole
XX  antigens is directed largely toward variable regions of the antigen,
XX  allowing for immune escape due to mutations. The groups for inclusion in
XX  an group-based vaccine may be selected from conserved regions of viral or
XX  tumor-associated antigens, which therefore reduces the likelihood of
XX  escape mutants. Furthermore, immunosuppressive groups that may be present
XX  in whole antigens can be avoided with the use of group-based vaccines.
XX  An additional advantage of an group-based vaccine approach is the ability
XX  to combine selected groups (CTL and HTL), and further, to modify the
XX  composition of the groups, achieving, for example, enhanced
XX  immunogenicity. Accordingly, the immune response can be modulated, as
XX  appropriate, for the target disease. Similar engineering of the response
XX  is not possible with traditional approaches. AAL1501 to AAL25412
XX  represent peptide sequences used in the exemplification of the present
XX  invention.
XX
XX  Sequence 8 AA:
XX
XX  Query Match 36.4%; Score 4; DB 22; Length 8;
XX  Best local Similarity 100.0%; Pred. No. 9, 3e-05;
XX  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  4 AKRR 7
XX  III
XX  4 AKRR 7
XX
XX  RESULT 49
ABP17716
ID  ABP17716 standard; Peptide; 8 AA.
XX
XX  AC
XX  ABP17716;
XX
XX  15-JUL-2002 (first entry)
XX
XX  HIV p24 Super motif env peptide #117.

```







AA366201

21 NOV 2001 (first entry)

p21 derived cyclin A binding peptide #2

Human p21WAF1, cyclin dependent protein kinase, CDK2, cyclin A, inhibitor, proliferative disorder; cancer; leukaemia; drug screening; mutant; mutant

Host sources:

Synthetic

Key Location/Qualifiers

Modified site 1 /note "Hydrogenated N-terminus"

Misc-difference 2 /note "Optimally substituted N-terminus"

Misc-difference 3 /note "Optimally substituted N-terminus"

Misc-difference 4 /note "Optimally substituted N-terminus"

Misc-difference 5 /note "Optimally substituted N-terminus"

Misc-difference 7 /note "Optimally substituted N-terminus"

Misc-difference 8 /note "Optimally substituted N-terminus"

Modified-site 8 /note "C-terminal amide"

WC200140142 A2.

07 JUN 2001

29 NOV 2001 Z00060-GR04550

30 NOV 1999 9903B-0426424

(CYCLIN) CYCLIN/CDK2

Zheleva D, Fischer PM, McInnes C, Andrews MJ, Chan WC, Atkinson GE

WC200140142 A2.

New p21 derived peptides and their variants, particularly useful as selective inhibitors of CDK2/cyclin interaction for treating proliferative disorders e.g. cancers and leukaemias, and in assays for identifying CDK/cyclin inhibitors

Example 12, Page 53; 102pp; English

The invention relates to peptide and their variants derived from p21WAF1, which are inhibitors of CDK2 activity by binding to G1 and S phase specific cyclins which activate CDK2; selective inhibitors of CDK2/cyclin complexes, particularly CDK2/cyclin A or E complexes. The variants of the peptide may have further amino acids at either end or have up to 7 amino acids deleted, provided the motif XLXF is retained. The peptides are specific regions of p21WAF1 that bind to G1 and S phase specific cyclins, preferably cyclins which activate CDK2. One of the peptide corresponds to p21(149-159). The peptides are used for

combinatorial libraries and single compound collections. The present sequence is a peptide derived from the C-terminus of p21 and used in a cyclin A binding experiment, the effect on cyclin A binding of replacing each residue with its chiral alternative was tested.

Query Match 36.4%; Score 4; DB 22; Length 8;  
Best Label Similarity 100.0%; Pred. No. 9,3e+05;  
Matches 4; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

4 AKKK 2  
111  
2 AKKK 5

RESULT 44

AA366201

ID AA366201 standard; peptide; 8 AA.

XX AA366201

XX 21 NOV 2001 (first entry)

XX p21 derived peptide, p21(152)Ser153Ala.

XX Human; p21WAF1; cyclin dependent protein kinase; CDK2; cyclin A; inhibitor; proliferative disorder; cancer; leukaemia; drug screening; p21(152)Ser153Ala.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /Label: Ala, Ser, CysR

FT /note "Other: 4-pyridylalanine, Thiophenylalanine, Homoserine, 2,4-bisaminobutyric acid or absent and the N-terminus is hydrogenated"

FT Modified site 8 /note "C-terminal amide"

XX WC200140142 A2.

XX 07 JUN 2001

XX 29 NOV 2001 Z00060-GR04550.

XX 30 NOV 1999 9903B-0426424

XX (CYCLIN) CYCLIN/CDK2

XX Zheleva D, Fischer PM, McInnes C, Andrews MJ, Chan WC, Atkinson GE

XX WP1: 2001-48649/53.

New p21 derived peptides and their variants, particularly useful as selective inhibitors of CDK2/cyclin interaction for treating proliferative disorders e.g. cancers and leukaemias, and in assays for identifying CDK/cyclin inhibitors

Example 13; Page 54; 102pp; English.

The invention relates to peptide and their variants derived from p21WAF1, which are inhibitors of CDK2 activity by binding to G1 and S phase specific cyclins which activate CDK2; selective inhibitors of CDK2/cyclin complexes, particularly CDK2/cyclin A or E complexes. The variants of the peptide may have further amino acids at either end or have up to 7 amino acids deleted, provided the motif XLXF is retained. The peptides are specific regions of p21WAF1 that bind to G1 and S phase specific cyclins, preferably cyclins which activate CDK2. One of the peptide corresponds to p21(149-159). The peptides are used for



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XX WP1: 2001-48619/53.
XX
XX New p21 derived peptides and their variants, particularly useful as
XX selective inhibitors of CDK2/cyclin interaction for treating
XX proliferative disorders e.g. cancers and leukaemias, and in assays for
XX identifying CDK/cyclin inhibitors.
XX
XX Example 20: Page 57; 102pp; English.
XX
XX The invention relates to peptide and their variants derived from p21WAF1,
XX which are inhibitors of CDK2 activity by binding to G1 and
XX S phase specific cyclins which activate CDK2; selective inhibitors of
XX CDK2/cyclin complexes, particularly CDK2/cyclin A or E complexes.
XX The variants of the peptide may have further amino acids at either end
XX or have up to 7 amino acids deleted, provided the motif XLRF is retained.
XX The peptides are specific regions of p21WAF1 that bind to G1 and S
XX phase specific cyclins, preferably cyclins which activate CDK2. One
XX of the peptides corresponds to p21(149-159). The peptides are used for
XX treating proliferative disorders, e.g. cancers and leukaemias. The
XX peptides are also for identifying substances which interfere with
XX protein-protein interactions involving cyclins (i.e. cyclin A, E or D),
XX especially CDK2/cyclin interactions, and which are capable of inhibiting
XX CDK2 and/or CDK4 activity. p21 peptides other than p21(149-159)
XX competitively inhibit the binding of peptide p21(149-159) to cyclin and
XX may be used to identify substances that bind to, or inhibit peptide-
XX cyclin interactions. Substances for screening in the assays include
XX antibody products specific for p21 or cyclin binding regions,
XX combinatorial libraries and single compound collections. The present
XX sequence is a peptide derived from the C-terminus of p21 and used in
XX a Cyclin A binding experiment, the effect on cyclin A binding of
XX replacing the Phe residue at position 7 was assessed.
XX
XX Sequence 8 AA:
SQ
Query Match 36.4% Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AKRR 7
SD 11
2b 2 AKRR 5
RESULT 47
AA66208 standard; Peptide: 8 AA
AC AA66208;
XX 21-NOV-2001 (first entry)
XX p21 derived peptide, p21(152)Ser154A #8.
XX Human, p21WAF1; cyclin dependent protein kinase; CDK2; cyclin A;
XX inhibitor; proliferative disorder; cancer; leukaemia;
XX drug screening; p21(152)Ser154A.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX Modified-site 1 /note= "The N-terminus is hydroxylated"
XX Miscellaneous 8 /label= lys, Tyr, Glu, Leu, Trp, 28Al, Phe, Ibal
XX FT /note= "Other: Cyclohexylalanine, norphenylalanine
XX FT para-fluorophenylalanine, meta-fluorophenylalanine
XX FT or biphenylalanine"
XX Modified-site 8
XX FT /note= "C-terminal amide"
XX FT
XX W:2001040:42-AZ.

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GenAge version 5.1.2  
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CM protein: protein search using sw model

Run on: September 30, 2003, 15:07:44 Search file: 418844 Searches  
(with 1000 repetitions)  
42,449 Million cell operations/sec

Title: US-09-787-443-17

Perfect score: 11

Sequences: 1 AKKEPKPNQ 1:

Scoring table: Gaps

Gap: 50.0, Gapext: 60.0

Search: 1107863 seqs, 15072553 residues

Word size: 0

Total number of hits satisfying chosen parameters: 27422

Minimum hit seq length: 8

Maximum hit seq length: 15

Post-processing: testing first 500 similarities

Database: A\_Geneseq\_19Jun03:

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the object having pointed, and is derived by analysts of the total score of all objects.

SCORES

Seq. #	No.	Score	Match	Length	DB	Hit	Description
1	11	100.0	11	21	AA086545	NCAM 141 binding p	
2	11	100.0	11	23	AB0269345	Human neural cell	
3	5	45.5	9	22	AA067918	Formalin for hepari	
4	5	45.5	12	15	AA057069	N tetrahel. fragmen	
5	5	45.5	14	21	AA043548	Hepatic cells virus	
6	5	45.5	14	24	AA047944	HARP derived pepid	
7	5	45.5	15	24	AA043536	Human cancer relat	
8	5	45.5	15	24	AA043719	Human cancer relat	
9	5	45.5	15	24	AA043720	Human cancer relat	

10	5	45.5	15	24	AB030721	Human cancer relat
11	5	45.5	15	24	AB030905	Human cancer relat
12	5	45.5	15	24	AB031339	Human cancer relat
13	5	45.5	15	24	AB031471	Human cancer-relat
14	4	46.4	8	14	AA041244	Cytotoxic T lympho
15	4	46.4	8	15	AA067031	Fibrinolytic ppi
16	4	46.4	8	16	AA070844	P. faicaparum live
17	4	46.4	8	19	AA054665	Peptide from p fal
18	4	46.4	8	20	AA034661	Amino acid sequenc
19	4	46.4	8	21	AA012099	Gl GIPase motif fr
20	4	46.4	8	21	AA023657	Cytotoxic T lympho
21	4	46.4	8	21	AA070286	Plasmodium falcipa
22	4	46.4	8	21	AA056592	HLA-B8-binding HIV
23	4	46.4	8	22	AB011748	HIV A01 super moti
24	4	46.4	8	22	AB011244	HIV A02 super moti
25	4	46.4	8	22	AB015903	HIV A24 super moti
26	4	46.4	8	22	AB017309	HIV B27 super moti
27	4	46.4	8	22	AB019257	HIV B62 super moti
28	4	46.4	8	22	AB019303	HIV B62 super moti
29	4	46.4	8	22	AB021507	HIV A03 motif pol
30	4	46.4	8	22	AB023417	HIV A01 motif pol
31	4	46.4	8	22	AA096771	Human peptide #204
32	4	46.4	8	23	AA078918	Lupinus luteus nuc
33	4	46.4	8	23	AA080841	Rat Rb-interacting
34	4	46.4	9	20	AA052244	HIV pol protein de
35	4	46.4	9	20	AA097781	LEDGF and HDGF com
36	4	46.4	9	21	AA056297	HLA-A3-binding HIV
37	4	46.4	9	22	AB011783	HIV A01 super moti
38	4	46.4	9	22	AB013440	HIV A02 super moti
39	4	46.4	9	22	AB013441	HIV A02 super moti
40	4	46.4	9	22	AB016035	HIV A24 super moti
41	4	46.4	9	22	AB016036	HIV A24 super moti
42	4	46.4	9	22	AB017369	HIV B27 super moti
43	4	46.4	9	22	AB017470	HIV B27 super moti
44	4	46.4	9	22	AB019261	HIV B62 super moti
45	4	46.4	9	22	AB019262	HIV B62 super moti
46	4	46.4	9	22	AB021445	HIV A03 motif pol
47	4	46.4	9	22	AB021380	HIV A01 motif pol
48	4	46.4	9	23	AB054720	Regukin sequence
49	4	46.4	9	23	AB032826	PP2AA-binding pept
50	4	46.4	9	23	AB032828	PP2AA-binding pept
51	4	46.4	9	23	AB036664	Amino acid sequenc
52	4	46.4	9	24	AB004745	Human cancer relat
53	4	46.4	9	24	AB005327	Human cancer relat
54	4	46.4	9	24	AB057270	Regukin, peptide 5
55	4	46.4	10	18	AA061576	Peptide fragment (
56	4	46.4	10	19	AA035336	Human G2NF recepto
57	4	46.4	10	20	AA084175	Human G2NF-alpha
58	4	46.4	10	21	AA097111	Tau conotoxin sequ
59	4	46.4	10	21	AA066279	HLA-A2-binding HIV
60	4	46.4	10	21	AA066323	HLA-A11 binding HI
61	4	46.4	10	22	AB011866	HIV A01 super moti
62	4	46.4	10	22	AB011877	HIV A02 super moti
63	4	46.4	10	22	AB014845	HIV A03 super moti
64	4	46.4	10	22	AB014846	HIV A24 super moti
65	4	46.4	10	22	AB016188	HIV A24 super moti
66	4	46.4	10	22	AB016338	HIV B27 super moti
67	4	46.4	10	22	AB017427	HIV B27 super moti
68	4	46.4	10	22	AB017428	HIV B27 super moti
69	4	46.4	10	22	AB019266	HIV B62 super moti
70	4	46.4	10	22	AB021304	HIV A03 motif pol
71	4	46.4	10	22	AB021468	HIV A03 motif pol
72	4	46.4	10	22	AB023395	HIV A01 motif pol
73	4	46.4	10	22	AA098772	Human peptide #204
74	4	46.4	10	22	AA099355	Vaccine related MH
75	4	46.4	10	22	AA095580	Human complementar
76	4	46.4	10	22	AA086263	Saccharomyces cere
77	4	46.4	10	23	AB099718	Conus sp conotoxin
78	4	46.4	10	23	AB094801	Regukin sequence
79	4	46.4	10	23	AB095666	Amino acid sequenc
80	4	46.4	10	23	AB095667	Amino acid sequenc
81	4	46.4	10	23	AB074808	Nuclear protein nu
82	4	46.4	10	24	AB094976	Human immunodefici





229	8	22	AA098920	Vaccine related ME	302	9	14	AA024666	Immunomodulatory p
230	8	22	AA098921	Peptide encoded by	303	9	14	AA024667	Immunomodulatory p
231	8	22	AA098922	Peptide #24 from 1	304	9	14	AA024668	Immunomodulatory p
232	8	22	AA098923	Peptide #25 from 1	305	9	14	AA024669	Immunomodulatory p
233	8	22	AA098924	Peptide #26 from 1	306	9	14	AA024670	Immunomodulatory p
234	8	22	AA098925	Human leukocyte AN	307	9	14	AA024671	Immunomodulatory p
235	8	22	AA098926	HLA B*07:01:01	308	9	14	AA024672	Immunomodulatory p
236	8	22	AA098927	HLA B*07:01:01	309	9	14	AA024673	Immunomodulatory p
237	8	22	AA098928	HLA B*07:01:01	310	9	14	AA024674	Immunomodulatory p
238	8	22	AA098929	Human immunodeficient	311	9	14	AA024675	Immunomodulatory p
239	8	22	AA098930	Lactylolipase peptid	312	9	14	AA024676	Insulin-like growth
240	8	22	AA098931	Peptide #22, 30id	313	9	14	AA024677	Cytotoxic T lympho
241	8	22	AA098932	Bacillus stearother	314	9	14	AA024678	MHC Class I allele
242	8	22	AA098933	Newcastle disease	315	9	14	AA024679	Haemostatic, bioc
243	8	22	AA098934	Peptide derived fr	316	9	14	AA024680	Protein-kinase inh
244	8	22	AA098935	Polypeptide fragm	317	9	14	AA024681	Peptide (241) inh
245	8	22	AA098936	A polypeptide fra	318	9	14	AA024682	Dynorphin-like pol
246	8	22	AA098937	HLA class I bindin	319	9	14	AA024683	Neurotensin recept
247	8	22	AA098938	Human kallikrein 1	320	9	14	AA024684	Neurotensin recept
248	8	22	AA098939	HLA activation cum	321	9	14	AA024685	Plasmodium falcipa
249	8	22	AA098940	Neurotensin peptid	322	9	14	AA024686	Plasmodium falcipa
250	8	22	AA098941	HLA cytotoxic lymph	323	9	14	AA024687	Plasmodium falcipa
251	8	22	AA098942	Myristoylation ord	324	9	14	AA024688	Plasmodium falcipa
252	8	22	AA098943	HLA class I molecu	325	9	14	AA024689	Templated peptide f
253	8	22	AA098944	Hepatitis B virus	326	9	14	AA024690	Partial sequence f
254	8	22	AA098945	Hepatitis B virus	327	9	14	AA024691	Synthetic HTLV pep
255	8	22	AA098946	Hepatitis B virus	328	9	14	AA024692	Cyclin R/p33(cdc2)
256	8	22	AA098947	Hepatitis B virus	329	9	14	AA024693	Human leucocyte an
257	8	22	AA098948	Hepatitis B virus	330	9	14	AA024694	Compacting peptide
258	8	22	AA098949	Hepatitis B virus	331	9	14	AA024695	Antifungal peptide
259	8	22	AA098950	Hepatitis B virus	332	9	14	AA024696	NS2 receptor alte
260	8	22	AA098951	Hepatitis B virus	333	9	14	AA024697	Bradykinin analogo
261	8	22	AA098952	Hepatitis B virus	334	9	14	AA024698	HPV16 E6 peptide (
262	8	22	AA098953	HLA-1/cyclin A int	335	9	14	AA024699	Anti-fungal peptid
263	8	22	AA098954	CXC chemokine rece	336	9	14	AA024700	Bactericidal/perme
264	8	22	AA098955	Human ADP1 triptic	337	9	14	AA024701	Peptide repeat mot
265	8	22	AA098956	Human Neurotensin	338	9	14	AA024702	Mycobacterium tube
266	8	22	AA098957	Human SLP-76 phosph	339	9	14	AA024703	Mycobacterium tube
267	8	22	AA098958	Classical swine fe	340	9	14	AA024704	HLIV-1a, c.m. deri
268	8	22	AA098959	Endostatin targeti	341	9	14	AA024705	PECAM-1 inhibitor
269	8	22	AA098960	HLV epitope, HIV-1	342	9	14	AA024706	PECAM-1 inhibitor
270	8	22	AA098961	Cysteine-X-cysteine	343	9	14	AA024707	PECAM-1 inhibitor
271	8	22	AA098962	Adenovirus endopep	344	9	14	AA024708	PECAM-1 inhibitor
272	8	22	AA098963	HLV domain binding	345	9	14	AA024709	PECAM-1 inhibitor
273	8	22	AA098964	Simple nuclear loc	346	9	14	AA024710	Epitope C-terminal
274	8	22	AA098965	Transcription fact	347	9	14	AA024711	K4, a nucleic acid
275	8	22	AA098966	Transcription fact	348	9	14	AA024712	Thrombin receptor
276	8	22	AA098967	Transcription fact	349	9	14	AA024713	Peptide GF61: C-9
277	8	22	AA098968	Transcription fact	350	9	14	AA024714	Helicobacter pylor
278	8	22	AA098969	Transcription fact	351	9	14	AA024715	M. tuberculosis po
279	8	22	AA098970	Transcription fact	352	9	14	AA024716	Dengue virus type-
280	8	22	AA098971	Transcription fact	353	9	14	AA024717	Dengue virus type-
281	8	22	AA098972	Transcription fact	354	9	14	AA024718	P. damsela beta-ga
282	8	22	AA098973	Transcription fact	355	9	14	AA024719	Myobacterium tube
283	8	22	AA098974	Transcription fact	356	9	14	AA024720	Yeast MFal peptide
284	8	22	AA098975	Nuclear protein in	357	9	14	AA024721	Peptide motif #1 f
285	8	22	AA098976	Nuclear protein in	358	9	14	AA024722	Peptide motif #1 f
286	8	22	AA098977	Nuclear protein in	359	9	14	AA024723	Peptide from HPV 1
287	8	22	AA098978	NLS containing iso	360	9	14	AA024724	Partial sequence o
288	8	22	AA098979	NLS containing iso	361	9	14	AA024725	Human IEF SSP 9502
289	8	22	AA098980	Proteinase A-2 1	362	9	14	AA024726	DNA-binding peptid
290	8	22	AA098981	CA125/MUC16, Lys81	363	9	14	AA024727	Peptide motif #1 f
291	8	22	AA098982	Adenovirus endopep	364	9	14	AA024728	Peptide motif #1 f
292	8	22	AA098983	Selenoprotein P re	365	9	14	AA024729	HIV-1 gp120 protei
293	8	22	AA098984	Soybean N-terminal	366	9	14	AA024730	HLA binding plu-1
294	8	22	AA098985	MHC binding peptid	367	9	14	AA024731	HLA binding plu-1
295	8	22	AA098986	Human neurodegener	368	9	14	AA024732	HLA binding plu-1
296	8	22	AA098987	cAMP-dependent kin	369	9	14	AA024733	Immunogenic peptid
297	8	22	AA098988	Phospholipase A2 (	370	9	14	AA024734	Immunogenic peptid
298	8	22	AA098989	N terminal peptide	371	9	14	AA024735	Potential T cell e
299	8	22	AA098990	Human SLP-1 epitop	372	9	14	AA024736	Amino acid sequenc
300	9	5	AA098991	Sequence of peptide	373	9	20	AA024737	M. tuberculosis an
301	9	14	AA024738	Immunomodulatory p	374	9	20	AA024738	M. tuberculosis re

435	3	27.3	9	25	AAV447.06	Human, Wilm's tumor
436	3	27.3	9	25	AAV447.07	Human Wilm's tumor
437	3	27.3	9	25	AAV447.08	Human Wilm's tumor
438	3	27.3	9	25	AAV447.09	Human Wilm's tumor
439	3	27.3	9	25	AAV447.10	Human Wilm's tumor
440	3	27.3	9	25	AAV447.11	Human Wilm's tumor
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448	3	27.3	9	25	AAV447.19	Human Wilm's tumor
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451	3	27.3	9	25	AAV447.22	Human Wilm's tumor
452	3	27.3	9	25	AAV447.23	Human Wilm's tumor
453	3	27.3	9	25	AAV447.24	Human Wilm's tumor
454	3	27.3	9	25	AAV447.25	Human Wilm's tumor
455	3	27.3	9	25	AAV447.26	Human Wilm's tumor
456	3	27.3	9	25	AAV447.27	Human Wilm's tumor
457	3	27.3	9	25	AAV447.28	Human Wilm's tumor
458	3	27.3	9	25	AAV447.29	Human Wilm's tumor
459	3	27.3	9	25	AAV447.30	Human Wilm's tumor
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462	3	27.3	9	25	AAV447.33	Human Wilm's tumor
463	3	27.3	9	25	AAV447.34	Human Wilm's tumor
464	3	27.3	9	25	AAV447.35	Human Wilm's tumor
465	3	27.3	9	25	AAV447.36	Human Wilm's tumor
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467	3	27.3	9	25	AAV447.38	Human Wilm's tumor
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472	3	27.3	9	25	AAV447.43	Human Wilm's tumor
473	3	27.3	9	25	AAV447.44	Human Wilm's tumor
474	3	27.3	9	25	AAV447.45	Human Wilm's tumor
475	3	27.3	9	25	AAV447.46	Human Wilm's tumor
476	3	27.3	9	25	AAV447.47	Human Wilm's tumor
477	3	27.3	9	25	AAV447.48	Human Wilm's tumor
478	3	27.3	9	25	AAV447.49	Human Wilm's tumor
479	3	27.3	9	25	AAV447.50	Human Wilm's tumor
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490	3	27.3	9	25	AAV447.61	Human Wilm's tumor
491	3	27.3	9	25	AAV447.62	Human Wilm's tumor
492	3	27.3	9	25	AAV447.63	Human Wilm's tumor
493	3	27.3	9	25	AAV447.64	Human Wilm's tumor
494	3	27.3	9	25	AAV447.65	Human Wilm's tumor
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496	3	27.3	9	25	AAV447.67	Human Wilm's tumor
497	3	27.3	9	25	AAV447.68	Human Wilm's tumor
498	3	27.3	9	25	AAV447.69	Human Wilm's tumor
499	3	27.3	9	25	AAV447.70	Human Wilm's tumor
500	3	27.3	9	25	AAV447.71	Human Wilm's tumor

## ALIGNMENTS

## RESULT 1

AAV88545 standard: peptide: 11 AA.

XX AAV88545

AC AAV88545

XX AAV88545

CT 07-AB5-2000 (first entry)

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12

XX NCAM 141 binding peptide #12





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XX FN W 094 0941 A2.
XX FI 16 JUN 1999.
XX FE 29 JUN 1999. 99W0 US:2929.
XX FR 09 JUN 1999. 98US 0088679.
XX FS 11 JUN 1999. 98US 0089138.
XX GA (GRAN/) KRANCH A D.
XX FA (WALE/) WALEWSKI J L.
XX FA (SUDM/) STUMP D D.
XX FI Bruch A., Walewski JL, Stump D.
XX FS WP: 2000-12641/13.
XX FI Novel hepatitis C virus peptides useful in vaccine compositions for
XX FI diagnosing HCV infection and as therapeutic agents.
XX FS Claim 11: Page 44: 50pp; English.
XX CC The present sequence is a hepatitis C virus (HCV) antigenic
XX CC peptide AEP #1. The novel HCV peptide is
XX CC encoded by a reading frame +1 or +2 relative to the standard HCV open
XX CC reading frame hence not derived from the standard HCV polyprotein.
XX CC The peptide elicits an immune response in patients infected with HCV and
XX CC are produced during HCV infection. The present sequence is used as
XX CC an immunogen to generate antibodies against HCV protein which are
XX CC useful for diagnosing HCV infection. The peptide is also
XX CC useful in vaccine compositions for preventing HCV infection
XX CC and as a target for anti HCV therapy.
XX FS Sequence 14 AA:
XX CC
XX CC Query Match 45.5%; Score 5; DB 22; Length 14;
XX CC Best Local Similarity 100.0%; Pred. No. 49;
XX CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 2 KKEKP 6
XX CC III 1
XX CC DE 2 KKEKP 6
XX CC
XX CC RESULT 7
XX CC ABR30596
XX CC ID ABR30596 standard; peptide: 15 AA.
XX CC AC ABR30596;
XX CC DT 14-MAY-2003 (first entry)
XX CC DE Human cancer-related protein R30488 HLA peptide #1618.
XX CC KW Human cytostatic vaccine; cancer; immune response; HLA;
XX CC human leukocyte antigen.
XX CC CS Homo sapiens.
XX CC FN W0200263421-A2.
XX CC PS 24-DEC-2002.
XX CC FF 10 APR 2003: 2002W0-US11054.
XX CC PP 10 APR 2001: 2001US-242709.
XX CC PR 10-APR-2001: 2001US 26112P.
XX CC PS 25-APR-2001: 2001US-26660P.
XX CC PA (AGEN ) AGENSYS INC.
XX CC PI Jakobovits A, Chaitin-Eld PM, Faris M, Ge W, Hubert RS;
XX CC Morrison K, Morrison RK, Raitano AB;
XX CC WP: 2603-075559/e7
XX CC
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC diagnostic reagents for eliciting cellular or humoral immune response
XX CC in cancer patients.
XX CC Claim 13, Page 47: 102pp; English.
XX CC
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (AB078123-AB278128 and AB01789-AB01861). The genes and

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XX DR WP: 2001-281970/29.
XX FI New Heparin Affinity Regulatory Peptide angiotensin peptides, useful for
XX FI regenerating muscle cells, aiding cicatrization, detecting and
XX FI treating immunosuppressive diseases, stimulate immune response and
XX FI tissue regeneration.
XX FS Disclosure: Page 4: 4pp; French.
XX CC AAB67904-16 represent peptides which rich in basic amino acids. The
XX CC specification describes heparin affinity regulatory peptide (HARP)
XX CC angiogenic peptides that stimulate immune response, cellular growth
XX CC and regeneration. The peptides are useful for regenerating cells, such
XX CC as muscle cells, and in aiding cicatrization, as well as in the
XX CC treatment of immunosuppressive diseases. The peptides amplify the
XX CC replication of human immunodeficiency virus (HIV) in vitro, and are
XX CC useful in the detection of HIV infections. When used with anti-viral
XX CC agents, they render the HIV more accessible to the antiviral agent,
XX CC and therefore are more easily destroyed.
XX FS Sequence 14 AA:
XX CC
XX CC Query Match 45.5%; Score 5; DB 22; Length 14;
XX CC Best Local Similarity 100.0%; Pred. No. 49;
XX CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC QY 2 KKEKP 6
XX CC III 1
XX CC DE 2 KKEKP 6
XX CC
XX CC RESULT 7
XX CC ABR30596
XX CC ID ABR30596 standard; peptide: 15 AA.
XX CC AC ABR30596;
XX CC DT 14-MAY-2003 (first entry)
XX CC DE Human cancer-related protein R30488 HLA peptide #1618.
XX CC KW Human cytostatic vaccine; cancer; immune response; HLA;
XX CC human leukocyte antigen.
XX CC CS Homo sapiens.
XX CC FN W0200263421-A2.
XX CC PS 24-DEC-2002.
XX CC FF 10 APR 2003: 2002W0-US11054.
XX CC PP 10 APR 2001: 2001US-242709.
XX CC PR 10-APR-2001: 2001US 26112P.
XX CC PS 25-APR-2001: 2001US-26660P.
XX CC PA (AGEN ) AGENSYS INC.
XX CC PI Jakobovits A, Chaitin-Eld PM, Faris M, Ge W, Hubert RS;
XX CC Morrison K, Morrison RK, Raitano AB;
XX CC WP: 2603-075559/e7
XX CC
XX CC New composition comprising a substance that modulates the structure of
XX CC proteins and polynucleotides, useful for therapeutic, prognostic and
XX CC diagnostic reagents for eliciting cellular or humoral immune response
XX CC in cancer patients.
XX CC Claim 13, Page 47: 102pp; English.
XX CC
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (AB078123-AB278128 and AB01789-AB01861). The genes and

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XX Proteins are useful for eliciting a protective or cellular immune response.  
 XX The genes are useful as probes and primers for the amplification and/or  
 XX detection of genes, mRNAs or their transcripts as reagents for the  
 XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX directing the expression of the protein, as tools for modulation of  
 XX inhibiting the expression of genes and/or translation of transcripts and  
 XX as therapeutic agents. The proteins and peptides are useful as  
 XX diagnostic and diagnostic reagents for cancer. The present  
 XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX from the invention.

XX Sequence 15 AA:

Query Match 45.5% Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 KKEKP 6  
 XX 1 1 1 1  
 XX 5 KKEKP 12

RESILI 9

ABR03720  
 ID ABR03720 standard; Peptide: 15 AA

XX ABR03719;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein RA789 HLA peptide #1782.

XX Human cytotoxic vaccine; cancer; immune response; HLA

XX human leukocyte antigen;

XX Homo sapiens;

XX W020283921-A2;

XX 24 OCT-2002;

XX 10-APR-2002; 2002W0-US11654;

XX 10-APR-2001; 2001US-2847340;

XX 10-APR-2001; 2001US-2841120;

XX 25-APR-2001; 2001US-2866400;

XX (AGEN) AGENSYS INC;

XX Jakubovits A., Chaillat-Bid PM, Paris M, Ge W, Hubert RS;

XX Morrison K., Morrison RK, Kaitano AB;

XX WPI; 2003 075555/07;

XX New composition comprising a substance that modulates the structure of  
 XX proteins and polynucleotides, useful for therapeutic, prognostic and  
 XX diagnostic reagents for eliciting cellular or humoral immune response  
 XX in cancer patients.

XX claim 13; Page 480; 1021pp; English

XX The present invention relates to novel human cancer-related genes and  
 XX proteins (AB278120-AB278168 and ABR0789-ABR01861). The genes and  
 XX proteins are useful for eliciting a humoral or cellular immune response  
 XX The genes are useful as probes and primers for the amplification and/or  
 XX detection of genes, mRNAs or their transcripts as reagents for the  
 XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX directing the expression of the protein, as tools for modulation of  
 XX inhibiting the expression of genes and/or translation of transcripts and  
 XX as therapeutic agents. The proteins and peptides are useful as  
 XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
 XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX from the invention.

XX Sequence 15 AA:

Query Match 45.5% Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 KKEKP 6  
 XX 1 1 1 1  
 XX 5 KKEKP 9

RESILI 9

ABR03720

ID ABR03720 standard; Peptide: 15 AA

XX ABR03720;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein RA789 HLA peptide #1782.

XX Human cytotoxic vaccine; cancer; immune response; HLA;

XX human leukocyte antigen;

XX Homo sapiens;

XX W0200283921-A2;

XX 24 OCT-2002;

XX 10-APR-2002; 2002W0-US11654;

XX 10-APR-2001; 2001US-2847340;

XX 10-APR-2001; 2001US-2841120;

XX 25-APR-2001; 2001US-2866400;

XX (AGEN) AGENSYS INC;

XX Jakubovits A., Chaillat-Bid PM, Paris M, Ge W, Hubert RS;

XX Morrison K., Morrison RK, Kaitano AB;

XX WPI; 2003 075555/07;

XX New composition comprising a substance that modulates the structure of  
 XX proteins and polynucleotides, useful for therapeutic, prognostic and  
 XX diagnostic reagents for eliciting cellular or humoral immune response  
 XX in cancer patients.

XX claim 13; Page 480; 1021pp; English

XX The present invention relates to novel human cancer-related genes and  
 XX proteins (AB278120-AB278168 and ABR0789-ABR01861). The genes and  
 XX proteins are useful for eliciting a humoral or cellular immune response.  
 XX The genes are useful as probes and primers for the amplification and/or  
 XX detection of genes, mRNAs or their transcripts, as reagents for the  
 XX diagnosis and/or prognosis of cancer, as coding sequences capable of  
 XX directing the expression of the protein, as tools for modulation of  
 XX inhibiting the expression of genes and/or translation of transcripts, and  
 XX as therapeutic agents. The proteins and peptides are useful as  
 XX therapeutic, prognostic and diagnostic reagents for cancer. The present  
 XX sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 XX from the invention.

XX Sequence 15 AA:

Query Match 45.5% Score 5; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 KKEKP 6  
 XX 1 1 1 1  
 XX 4 KKEKP 9







CC unknown cytotoxic T lymphocytes. It may be useful to have data against  
CC related  
CC (Updated on 25-MAR-2003 to correct IN field.)  
XX  
XX  
SQ Sequence 8 AA:

Query Match 46.4%, Score 47, DB 16, Length 8;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPNQ 1;  
DB 1;  
I KPNQ 4

RESULT 16  
AA067042  
ID AAK67042 standard; peptide: 8 AA;  
AC AAK67042;  
XX

DT 25-MAR-2003 (updated)  
DI 26 JUN 1996 (first entry)  
XX

DE Ethanolamine peptide EP-SRPL, modified peptide, peptides  
XX

XX Formylated peptide EP-SRPL, streptokinase treatment;  
KW cardiovascular diseases; clot-fissolved fibrinolytic, hemostatic,  
KW thrombosis; haemostasis; myocardial infarction; stroke; malaria;  
KW constitutive conformation; interaction site  
XX

OS Synthesis  
XX

PR W09522417-A1;  
XX

DT 16 NOV 1994;  
XX

DI 21 APR 1994; 94WO 0504244;  
XX

DE 27 APR 1994; 94US-0051741;  
XX

DI 24 OCT 1993; 93US-0143364;  
XX

PA (UNAK); EVANS J J;  
XX

PA (UNAK); SIKS R M;  
XX

PR Evans J J, SIKS R M;  
XX

WPI: 1994-06186/44;  
XX

XX Peptide homologous or analogous with constitutive conformation; it has  
PT proline residues flanking the interaction site (compare entries)  
XX

XX or more stable, biological activity  
XX

XX Example 2; Page 23; 57pp; English.  
XX

XX AAK67042 is a fibrinolytic peptide derived from a naturally occurring  
XX polypeptides that contain proline at position 7, indicated by brackets. These  
XX peptides are shortened to form tripeptides that contain one or more  
XX interaction sites of interest. AAK67042 is a tripeptide that is a streptokinase  
XX and binds to plasminogen and non-proteinolytically activates plasminogen,  
XX which dissolves fibrin clots. These are the first data  
XX collected demonstrates that interaction sites possess activity when  
XX present in a polypeptide that differs from the native form. Inclusion  
XX of conformation constraining moieties can have dramatic effects on an  
XX interaction site. (Also see AAK67041 and AAK67042 for analogues  
XX of other biologically active peptides that have an invariant site flanked  
XX by conformation constraining groups (see AAK67043).  
XX (Updated on 25-MAR-2003 to correct IN field.)  
XX

SQ Sequence 8 AA:

Query Match 36.4%, Score 47, DB 16, Length 8;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 KKNP 3;  
DB 1;  
I KKNP 2

RESULT 16  
AA078642  
ID AAK78642 standard; peptide: 8 AA;  
AC AAK78642;  
XX

DT 25-MAR-2003 (updated)  
DI 27 MAR 1996 (first entry)  
XX

DE P. talciparum liver Ag 1850-1857 cytotoxic T lymphocyte epitope.  
XX

XX Liver Ag 1850-1857 cytotoxic T cell epitope; helper T cell;  
KW lymphocyte viruses; parasites; tumours; antigens; treatment;  
KW disease prevention; cell;  
XX

OS Plasmodium talciparum  
XX

PR W09522417-A1;  
XX

DT 24-APR 1995;  
XX

DI 16 FEB 1995; 95WO 0502121;  
XX

DI 16 FEB 1994; 94US-1197484;  
XX

PA (CYTE); CYTEL CORP  
XX

PR Vitellio MA, Chaslat RW, Sette AB, Celis E, Grey H;  
XX

WPI: 1995-302545/49;  
XX

XX Compsn. inducing cytotoxic T lymphocyte response to pref. viral,  
PT bacterial, parasite or tumour antigens useful in the treatment  
XX and prevention of diseases associated with the antigen e.g.  
XX hepatitis B  
XX

OS Disclosed: Page 17; 10pp; English.  
XX

XX A peptide which induces a cytotoxic T lymphocyte (CTL) response to  
XX an antigen (Ag) in a minimal comprises, a CTL Ag response inducing  
XX peptide (1-10), AAK78642-188649, and a lipid conjugated helper T cell  
XX inducing peptide, the complex induces a CTL response to bacterial,  
XX viral or tumour Ags, and is therefore useful in the treatment and  
XX prevention of diseases associated with the Ag.  
XX (Updated on 25-MAR-2003 to correct PT field.)  
XX

SQ Sequence 8 AA:

Query Match 46.4%, Score 47, DB 16, Length 8;  
Best Local Similarity 100.0%; Pred. No. 9, 3e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPNQ 1;  
DB 1;  
I KPNQ 4

RESULT 17  
AA054665  
ID AAK54665 standard; peptide: 8 AA;  
XX

AC AAK54665;  
XX

DT 25-SEP-1998 (first entry)  
XX

DE Pp1500-1500 i. talciparum IS 1850-1857;  
XX

[illegible]

USPS : ISTS INN VAIL & LID.

Blanchard P., Gilbert S., Burke I., Hill AVS., McMichael A.J.  
Plebanek M., Schneider J., Smith G.D.  
WFL: 1999-07-24, 5/26,  
X PSLEB: AAAGZAGC

Generating the positive T-cell response to target antigen using recombinant poxvirus for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV  
  
Claim no: Case 18, 85pp: English.

The invention relates to methods and reagents for generating a protective CD8+ T-cell immune response against at least one target antigen. The kits of the invention comprises (i) as priming composition, a source of one or more CD8+ T-cell cytotoxic T lymphocytes (CTL); epitopes of the target antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (i), with this source being a non-replicating or replication impaired recombinant poxvirus vector (PVV) plus a carrier. If the source of CTL epitopes in (ii) is a viral vector, then the vector in (ii) is from a different virus. The kits are used to generate an immune response (primarily active or therapeutic) against pathogens of tumours, specifically against malaria parasites such as *P. falciparum*, or HIV, and also many other bacterial, viral or parasitic pathogens. The kits are also used for protective response against melanoma and cancer of breast or colon, and generally wherever a strong CD8<sup>+</sup> response is protective. The boosting composition may be used alone to boost a naturally primed response against malaria. The specified PVV provide an excellent booster effect, better than that from wild-type poxvirus, resulting in complete rather than partial protection against sporozoite challenge. Also pvv are stated to use than wild-type virus. Sequences AAY03661-680 represent CTL peptide epitopes of the malaria (*M*) string.

XX Sequence: 8 AA;  
SQ Query Match: 39.4%; Score 4; DB 20; Length 8;  
Best Local Similarity: 100.0%; Prev. No. 9, 3e-05;  
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

ZY R KMDL:  
LD LIL  
KMDL:  
R KMDL:

RGS LGT  
AAHLYG  
LG-AAHLYG standard reported: 8 AA.  
A: AAHLYG;  
XX LG-AAH-200: (first entry)  
XX GL GFPase modLT1 InvPat #12.  
XX xD Interacting Zinc Finger; FIZ: retinoblastoma; heart disease;  
KW cell proliferation; cell differentiation; tissue repair;  
KW transcription regulation; breast cancer; gene therapy; melanoma;  
KW neuroblastoma; leukemia; Parkinson's disease; Huntington's disease;  
KW Alzheimer's disease; paralysis; motor neuron disorder;  
KW GL GFPase modLT1: rat;  
XX Rat-S sp.  
XS US6,052,011 A.  
PK W-MAX-ZOOLO  
XX LG-AH-200: (first entry)  
XX LG-AH-200: (first entry)









is not positive with traditional approaches. ABP1501 to ABP2541Z represent peptide sequences used in the exemplification of the present invention.

XX Sequence B AA:  
 Query Match 36.4% Score 47 DB 22 Length 87  
 Best Local Similarity 100.0% Pred. No. 9 3e-05  
 Matches 47 Conservative 0 Mismatches 0 Gaps 0  
 QY 2 KKEK 5  
 DE III  
 4 KKEK 7

REFSEQ: 29

ABP1903

XX ABP1903 standard: peptide; B AA:

AC ABP1903A

XX 15 JUL-2002 (first entry)

XX HIV 562 super motif pol peptide #562

XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; cell; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1  
 XX W02001248:10-A1  
 XX 12 APR-2001  
 XX 05-OCT-2000: 2000WO-US27756  
 XX 05-OCT-1999: 990S-0412863  
 XX (EPIM) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R, Baker DM, Cellis E, Kubo RT, Grey HM, WFL, 2001: 054887/52  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1) peptide groups, useful for vaccinating against HIV-1

XX Claim 32, Page 254: 44pp; English

XX The present invention describes a composition (i) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397); (ii) has virucide activity and can be used in vaccines. (i) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL) and further, to modify the immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response to vaccine selected groups (CTL and HTL) and further, to modify the immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP2541Z represent peptide sequences used in the exemplification of the present invention.

XX Sequence B AA:  
 Query Match 36.4% Score 47 DB 22 Length 87  
 Best Local Similarity 100.0% Pred. No. 9 3e-05  
 Matches 47 Conservative 0 Mismatches 0 Gaps 0  
 QY 2 KKEK 5  
 DE III  
 4 KKEK 6

REFSEQ: 29

ABP21507

XX ABP21507 standard: peptide; B AA:

AC ABP21507

XX 15 JUL-2002 (first entry)

XX HIV AC3 motif pol peptide #562

XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; cell; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1  
 XX W02001248:10-A1  
 XX 12 APR-2001  
 XX 05-OCT-2000: 2000WO-US27756  
 XX 05-OCT-1999: 990S-0412863  
 XX (EPIM) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R, Baker DM, Cellis E, Kubo RT, Grey HM, WFL, 2001: 054887/52  
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1) peptide groups, useful for vaccinating against HIV-1

XX Claim 32, Page 254: 44pp; English

XX The present invention describes a composition (i) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397); (ii) has virucide activity and can be used in vaccines. (i) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL) and further, to modify the immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response to vaccine selected groups (CTL and HTL) and further, to modify the immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP2541Z represent peptide sequences used in the exemplification of the present invention.

XX Sequence B AA:

Query Match: 36.4%, Score 41, DB 22, Length 8;  
 Best Local Similarity: 100.0%, Pred. No. 9, 9e-05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 KKEK 5  
 III  
 DB 3 KKEK 6

RESULT 40  
 ABE24417  
 ID: ABE24417 standard; Peptide: 8 AA;  
 AC: ABE24417;  
 DI: 24-JAN-2002 (first entry)

XX 15-JUL-2002 (first entry)

XX HIV A11 motif: pol peptide #359.

XX HIV, HIV 1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vpr; vif; tat; cytototoxic lymphocyte (CTL) immune response; epitope;  
 KW anti-hepat. vaccine; HIV infection; immunisation; virulence;

XX Human immunodeficiency virus type 1.

XX W240124R12-AA1

XX 12 APR 2001

XX 05 OCT 2002; 2002W-9S27766

XX 05 OCT 1999; 930S-0412864

XX (PEP) EPI-MEYNE INC.

XX Setti A, Schady J, Southwood S, Davidson J, New, Christal R;  
 PI Baker LM, Collins E, Kube PL, Gray HG;  
 XX WFL: 2001-04887/37

XX Vaccine compositions comprising human immunodeficiency virus (HIV) 1 peptide groups, useful for vaccinating and diagnosing HIV 1.  
 PS Claim 42; Page 348; 448pp; English.

XX The present invention describes a composition (i) comprising a prepared human immunodeficiency virus (HIV) 1 protein, including an antigen and sequence selected from 51 defined amino acid residues (ABE25417 to ABE25437); (ii) has virulence activity and can be used in vaccines; (iii) may be used for immunised subjects against HIV infections; the use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from observed regions of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of a group-based vaccine approach is the ability to combine selected groups (vif and vif) and further to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease, such as controlling of the response is not possible with traditional approaches. ABE1190 to ABE25412 represent peptide sequences used in the experimental evaluation of the present invention.

XX Sequence: 8 AA;

Query Match: 36.4%, Score 41, DB 22, Length 8;  
 Best Local Similarity: 100.0%, Pred. No. 9, 9e-05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 KKEK 5  
 III

QY 2 KKEK 5  
 III  
 DB 3 KKEK 6

RESULT 41

AAM98771

ID: AAM98771 standard; Peptide: 8 AA;

AC: AAM98771;

DI: 24-JAN-2002 (first entry)

XX Human peptide #204 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease;

XX Homo sapiens

XX W200147344-AA2

XX 05-JUL-2001

XX 28-DEC-2000; 2000W-9S6498

XX 28-DEC-1999; 990S-0174419

XX 27-DEC-2000; 2000S-0173419

XX (CERA-1) CURAGEN CORP.

XX SHUKKETSU RA, Leach M.

XX WPL: 2001-465216/50

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections.

XX Biosciences; Page 416; 414pp; English.

XX The present invention relates to oligonucleotides (see AAI26793-AA134659) encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is a peptide encoded by one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in: prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.

XX Sequence: 8 AA;

Query Match: 36.4%, Score 41, DB 22, Length 8;  
 Best Local Similarity: 100.0%, Pred. No. 9, 9e-05;  
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





AA925244;  
 US SEP 1999 (first entry)  
 HIV pol protein derived peptide treatment 40;  
 KW heat shock protein (HSP) complex - denatured in 100% ethanol and then  
 XX subjected to various treatments; subsequent entry; heat shock protein  
 XX derivative treatment; additional protein;  
 XX Human immunodeficiency virus;  
 XX W 9904182 A1;  
 XX 17 JUN 1999;  
 XX 04 DEC 1998; 9800 US25764;  
 XX 25 APR 1997; 9705 US956234;  
 XX 25 DEC 1997; 9705 US955548;  
 XX (OYRE ) UNIV NEW MEXICO STATE;  
 XX Massey LL; Wallen ES;  
 XX WI 1999 049612/33;  
 XX Synthesis of heat shock protein complexes using a denatured protein  
 XX matrix;  
 XX Example 1: FIG 1C; 4pp; English;  
 XX This invention describes a novel method for synthesizing heat shock  
 XX protein (HSP) complexes comprising adding a heat shock protein to a  
 XX denatured protein matrix for binding, and adding a complexing solution  
 XX comprising a peptide to elute a heat shock protein-peptide complex. A  
 XX complexing solution is useful as a vehicle for treating an allergic  
 XX disease (in a mammal, preferably a human) to reduce susceptibility to  
 XX the disease response, the complex comprising a HSP and one or more peptide  
 XX complexes, the complex is administered to provide a treatment for an allergic  
 XX reaction to an allergic disease, or administered to a mammal having an  
 XX allergic disease, to reduce the allergic reaction. Allergic diseases  
 XX include asthma and skin rashes. FIG 1C shows a blocked and/or treated  
 XX allergic diseases include allergic rhinitis, asthma, and the symptoms  
 XX and/or diseases which have severe side effects and/or immunosuppression  
 XX therapy which has limited use. The complex is used in a treatment  
 XX therapy of use of peptide-based vaccines and/or an adjuvant  
 XX vaccine for use of peptide-based vaccines and/or an adjuvant. This  
 XX sequence represents a peptide treatment used in the HIV pol protein  
 XX which is used in the method of the invention.  
 XX Sequence 9 AA;  
 Query Match 46.4%; Score 4; 105 20; Length 9;  
 Best Local Similarity 100.0%; Ident. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 57 2 KKKK 5  
 10 100  
 2 KKKK 5  
 RES 12 10  
 AA9774;  
 10 AA97741 standard; Peptide: 9 AA;  
 XX AA97741;  
 XX 21 MAY 1999 (first entry)  
 XX 100 and HSP common peptide;  
 XX heat shock protein derived growth factor; cell derived growth factor;  
 KW cataract; cancer; cell proliferation; restenosis; psoriasis;  
 XX wound healing; vulvectomy; therapy; hepatoma derived growth factor;  
 US Borne sopressin;  
 XX W 9905278 A1;  
 XX 04 FEB 1999;  
 XX 24 JUL 1999; 99W US04961;  
 XX 24 JUL 1997; 97US 058647;  
 XX (PGHM ) BRIGHAM 5 WOMENS HOSPITAL;  
 XX Chylack LT; Shimahara T; Simah D;  
 XX WI 1999 14293/12  
 XX New isolated lens epithelial cell derived growth factor - used to  
 XX develop products for cell increasing cell proliferation; inhibiting  
 XX environmental stress induced cell death; treating cancers of  
 XX inhibiting cataract formation;  
 XX Discloser: Page 79; 92pp; English;  
 XX This continuous sequence of 9 amino acids is common to both  
 XX hepatoma derived growth factor (HDGF) and novel human lens  
 XX epithelial cell derived growth factor (LEDGF, see AA97775). The  
 XX inventors provide fragments of LEDGF that exclude fragments  
 XX which share identity with HDGF (see also AA97780-82). LEDGF is a  
 XX novel protein that stimulates protein synthesis leading to the  
 XX enhanced growth of various cell types, such as those of epithelial,  
 XX epidermal or kidney origin, including lens epithelial cells.  
 XX detection of levels of anti LEDGF antibodies can be used to  
 XX determine an individual's susceptibility to developing cataracts.  
 XX LEDGF can be used to suppress the level of anti-LEDGF antibodies in  
 XX a subject to inhibit the formation of lens opacities.  
 XX Sequence 9 AA;  
 Query Match 46.4%; Score 4; 105 20; Length 9;  
 Best Local Similarity 100.0%; Ident. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 57 2 KKKK 5  
 10 100  
 2 KKKK 5  
 RES 12 10  
 AA96297  
 10 AA96297 standard; Peptide: 9 AA;  
 XX AA96297;  
 XX 24 FEB 2000 (first entry)  
 XX HLA A3 binding HIV 1 pol peptide 199;  
 XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;  
 KW human leukocyte antigen; allele; binding; conserved; genome;  
 XX peptide; target; toxic; drug; antibody; antigen; antiviral;  
 KW molecular conjugate; therapeutic; diagnosis; treatment; pathogen;  
 KW localisation; identification; detection; infection; drug resistance;  
 KW Immune response;  
 XX Human immunodeficiency virus type 1;  
 XX W 990499 A1;  
 XX 07 JUL 1999;

KW cataract; cancer; cell proliferation; restenosis; psoriasis;  
 XX wound healing; vulvectomy; therapy; hepatoma derived growth factor;  
 US Borne sopressin;  
 XX W 9905278 A1;  
 XX 04 FEB 1999;  
 XX 24 JUL 1999; 99W US04961;  
 XX 24 JUL 1997; 97US 058647;  
 XX (PGHM ) BRIGHAM 5 WOMENS HOSPITAL;  
 XX Chylack LT; Shimahara T; Simah D;  
 XX WI 1999 14293/12  
 XX New isolated lens epithelial cell derived growth factor - used to  
 XX develop products for cell increasing cell proliferation; inhibiting  
 XX environmental stress induced cell death; treating cancers of  
 XX inhibiting cataract formation;  
 XX Discloser: Page 79; 92pp; English;  
 XX This continuous sequence of 9 amino acids is common to both  
 XX hepatoma derived growth factor (HDGF) and novel human lens  
 XX epithelial cell derived growth factor (LEDGF, see AA97775). The  
 XX inventors provide fragments of LEDGF that exclude fragments  
 XX which share identity with HDGF (see also AA97780-82). LEDGF is a  
 XX novel protein that stimulates protein synthesis leading to the  
 XX enhanced growth of various cell types, such as those of epithelial,  
 XX epidermal or kidney origin, including lens epithelial cells.  
 XX detection of levels of anti LEDGF antibodies can be used to  
 XX determine an individual's susceptibility to developing cataracts.  
 XX LEDGF can be used to suppress the level of anti-LEDGF antibodies in  
 XX a subject to inhibit the formation of lens opacities.  
 XX Sequence 9 AA;  
 Query Match 46.4%; Score 4; 105 20; Length 9;  
 Best Local Similarity 100.0%; Ident. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 57 2 KKKK 5  
 10 100  
 2 KKKK 5  
 RES 12 10  
 AA96297  
 10 AA96297 standard; Peptide: 9 AA;  
 XX AA96297;  
 XX 24 FEB 2000 (first entry)  
 XX HLA A3 binding HIV 1 pol peptide 199;  
 XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;  
 KW human leukocyte antigen; allele; binding; conserved; genome;  
 XX peptide; target; toxic; drug; antibody; antigen; antiviral;  
 KW molecular conjugate; therapeutic; diagnosis; treatment; pathogen;  
 KW localisation; identification; detection; infection; drug resistance;  
 KW Immune response;  
 XX Human immunodeficiency virus type 1;  
 XX W 990499 A1;  
 XX 07 JUL 1999;





WP: 2001-454887/37.

Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

Claim 42: Page 197: 448pp: English.

The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ARL25347 to AR625497). (1) has virulence activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABL1501 to ARP25412 represent peptide sequences used in the exemplification of the present invention.

Sequence 9 AA:

Query Match 46.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 4e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKK 5  
 1111

DB 4 KKKK 7

RESULT 41

ABP16036

ID ABP16036 standard; Peptide: 9 AA.

XX AC ABP16036;

XX DT 15-JUL-2002 (1st entry)

XX DE HIV A24 super motif pol peptide #163.

XX KW HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; viricide.

XX CS Human immunodeficiency virus type 1.

XX PN W02001248[6-A1].

XX PC 12-APR-2001.

XX PF 05-OCT-1999; 2000WO-0527766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM- ) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R, Baker DM, Cellis E, Kubo RT, Grey HM.

XX CR WP: 2001-454887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

XX PS Claim 42: Page 224: 448pp: English.

PT peptide groups, useful for vaccinating against HIV-1 -

PS Claim 32: Page 197: 448pp: English.

XX

The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ARL25347 to AR625497). (1) has virulence activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABL1501 to ARP25412 represent peptide sequences used in the exemplification of the present invention.

Sequence 9 AA:

Query Match 46.4%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 4e-05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKK 5  
 1111

DB 4 KKKK 5

RESULT 42

ABP17369

ID ABP17369 standard; Peptide: 9 AA.

XX AC ABP17369;

XX DT 15-JUL-2002 (1st entry)

XX DE HIV B27 super motif pol peptide #163.

XX KW HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; viricide.

XX CS Human immunodeficiency virus type 1.

XX PN W02001248[6-A1].

XX PC 12-APR-2001.

XX PF 05-OCT-1999; 2000WO-0527766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM- ) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R, Baker DM, Cellis E, Kubo RT, Grey HM.

XX CR WP: 2001-454887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

XX PS Claim 42: Page 224: 448pp: English.

XX The Present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABL1501 to ABL25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA;  
 CC  
 CC Empty Match 96.4%; Score 4; DB 22; Length 9;  
 CC Best Local Similarity 100.0%; Pred. No. 9.4e+05;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 5  
 DE 1 KKER 4

RESULT 4  
 ABL15261  
 ID ABL15261 standard; peptide: 9 AA  
 AC ABL15261  
 CC  
 CC 15-JUL-2002 (first entry)  
 CC HIV b62 super motif pol peptide #267.  
 CC  
 CC HIV: HIV 1; Human immunodeficiency virus; env; pol; gag; nef; vif;  
 CC vpr; vpr; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 CC antigen; vaccine; HIV infection; immunisation; virucide.  
 CC  
 CC Human immunodeficiency virus Type 1  
 CC  
 CC W0200124810-A1  
 CC  
 CC 12-APR-2001  
 CC  
 CC 05-OCT-2000; 2000WO-US27765.  
 CC  
 CC 05-OCT-1999; 99US-0412853.  
 CC  
 CC (EP100) EPIMUNE INC.  
 CC  
 CC Sette A, Sidney J, Southwood S, Livingston BD, Chestnut R;  
 CC Baker DM, Collins E, Kubo RT, Grey HM;  
 CC WPI: 2001-454887/37.  
 CC  
 CC Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 CC peptide groups, useful for vaccinating against HIV-1  
 CC  
 CC Claim 42; Page 24; 448pp; English.

XX The Present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABL1501 to ABL25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA;  
 CC  
 CC Empty Match 96.4%; Score 4; DB 22; Length 9;  
 CC Best Local Similarity 100.0%; Pred. No. 9.4e+05;  
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 5  
 DE 1 KKER 4

RESULT 4  
 ABL15261  
 ID ABL15261 standard; peptide: 9 AA  
 AC ABL15261  
 CC  
 CC 15-JUL-2002 (first entry)  
 CC HIV b62 super motif pol peptide #267.  
 CC  
 CC HIV: HIV 1; Human immunodeficiency virus; env; pol; gag; nef; vpr;  
 CC vpr; vpr; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 CC antigen; vaccine; HIV infection; immunisation; virucide.  
 CC  
 CC Human immunodeficiency virus Type 1  
 CC  
 CC W0200124810-A1  
 CC  
 CC 12-APR-2001  
 CC  
 CC 05-OCT-2000; 2000WO-US27765.  
 CC  
 CC 05-OCT-1999; 99US-0412853.  
 CC  
 CC (EP100) EPIMUNE INC.  
 CC  
 CC Sette A, Sidney J, Southwood S, Livingston BD, Chestnut R;  
 CC Baker DM, Collins E, Kubo RT, Grey HM;  
 CC WPI: 2001-454887/37.  
 CC  
 CC Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 CC peptide groups, useful for vaccinating against HIV-1  
 CC  
 CC Claim 42; Page 24; 448pp; English.

XX The Present invention describes a composition (1) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (1) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of

CC group based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumour associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HIV), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:  
 SQ Query Match 36.4% Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pos. No. 9; 40-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKEK 5  
 ID 1 1  
 ID 4 KKEK 7

RESULT 4b  
 ABP25445  
 ID ABP25445 Standard; Peptide: 9 AA.  
 AC ABP25445;  
 XX 15 JUL 2002 (first entry)  
 DE HIV A33 motif; pol peptide #440  
 XX  
 KW HIV; HIV 1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vif; tat; cytototoxic T lymphocyte; eff; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 IN W-250134810 A1  
 FI 12-APR 2001  
 XX  
 FF 05-OCT 2000; 2003W0 US27766;  
 XX  
 PR 05-OCT 1999; 99US 0412063;  
 XX  
 PA (EPIM ) EPIMUNE INC.  
 XX  
 FI Scott A, Sidney J, Southwood S, Livingston BD, Chestnut K;  
 FI Baker DM, Curtis E, Kubo RT, Grey HM;  
 XX  
 DR WP1; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 263; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25447 to  
 CC ABP25497). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or

CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HIV), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:  
 SQ Query Match 36.4% Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pos. No. 9; 40-05;  
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKEK 5  
 ID 1 1  
 ID 4 KKEK 7

RESULT 4b  
 ABP25445  
 ID ABP25445 Standard; Peptide: 9 AA.  
 AC ABP25445;  
 XX 15 JUL 2002 (first entry)  
 DE HIV A33 motif; pol peptide #440  
 XX  
 KW HIV; HIV 1; human immunodeficiency virus; env; pol; gag; nef; vif;  
 KW vif; tat; cytototoxic T lymphocyte; eff; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 IN W-250134810 A1  
 FI 12-APR 2001  
 XX  
 FF 05-OCT 2000; 2003W0 US27766;  
 XX  
 PR 05-OCT 1999; 99US 0412063;  
 XX  
 PA (EPIM ) EPIMUNE INC.  
 XX  
 FI Scott A, Sidney J, Southwood S, Livingston BD, Chestnut K;  
 FI Baker DM, Curtis E, Kubo RT, Grey HM;  
 XX  
 DR WP1; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 302; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25447 to  
 CC ABP25497). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or







conclusion that would benefit from down regulation of an immune response, e.g. autoimmune disorders, complemented the fact that the interaction between CTLA4 and B7-2A

### Example 1: $\alpha$ -hydroxy acid

The interaction relates to modulation in the disease model, but not to the host condition, as expressed at least in the following manner: (1) Systemic administration of cyclosporin F, cyclosporin A or related compounds (2) Systemic administration of at least one second molecule having a binding site for cyclosporin F, cyclosporin A or related compounds (3) Administration of cyclosporin A (4) Administration of cyclosporin A and a second molecule which modulates the interaction between the first molecule and the second molecule. Also included are (5) Treatment of a subject having a condition that would benefit from low modulation of an immune response, comprising administering to said subject the cyclosporin and such a first molecule and a second molecule described above; (6) Identifying a compound that modulates the interaction of cyclosporin and pPZA; and (7) Identifying a compound which modulates the interaction of a molecule comprising at least one pPZA system with said cyclosporin and a pPZA molecule comprising a pPZA that interacts with cyclosporin.

The methods are useful for modulating an immune response and treating a subject having a condition that would benefit from down regulation of an immune response, such as a chronic disease (e.g., rheumatoid arthritis, cystic fibrosis, diabetes, a systemic lupus erythematosus, type 1 diabetes, vitiligo, chronic disease, multiple sclerosis), a transplant (e.g., a bone marrow transplant, a stem cell transplant, a heart transplant, a lung transplant, a liver transplant, a kidney transplant, a corneal transplant, or a skin transplant), graft versus host disease, an allergy, or an inflammatory disease. Reduction of an immune response is useful in treating bacterial, viral, or fungal infections. Immuno-deficiency virus, hepatitis B virus, or hepatitis C virus, the present sequence is a pPZA that can be used from a mixture of the

500; 1000; 1500

Category	Match	Similarity	Conservative	Non-conservative
Protein	36.4%	100.0%	100.0%	100.0%
Gene	36.4%	100.0%	100.0%	100.0%

—

•  
✓  
✓  
✓  
✓

[illegible]

Sequence version 5.1.6  
Copyright (c) 1994 - 2003, DePamphilis

1M protein: protein search, using sequence

Run on: September 30, 2003, 1:07:41, Search time: 11.455 seconds  
(with all options)  
98.54% Residue cell updates/sec

Title: US-09-787-443-17

Perfect score: 11

Sequence: 1 AKKKPKPKND 11

Scoring table:  $q_{11} = 1.0$ ,  $g_{11} = 0.5$ ,  $g_{12} = 0.5$

Searched: 28338 seqs, 96158682 residues

Word size: 3

Total number of hits satisfying chosen parameters: 2054

Minimum hit seq length: 8

Maximum hit seq length: 15

FAST processing: listing first 500 summaries

Database: PIR76:

1: PIR1:

2: PIR2:

3: PIR3:

4: PIR4:

Note:  $N$  is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	Description
1	4	45.4	15	2	PROTEIN, Q52000
2	3	27.3	8	2	APOLIPROTEIN A-1
3	3	27.3	9	2	CALLIPERFAMIDE 8
4	3	27.3	10	2	HYPOPHOSPHATE 1
5	3	27.3	11	2	PHYSALACIN, BOV
6	3	27.3	11	2	PHYSALACIN, BOV
7	3	27.3	11	2	PHYSALACIN, BOV
8	3	27.3	12	2	PHYSALACIN, BOV
9	3	27.3	12	2	PHYSALACIN, BOV
10	3	27.3	12	2	PHYSALACIN, BOV
11	3	27.3	13	1	PHYSALACIN, BOV
12	3	27.3	13	2	PHYSALACIN, BOV
13	3	27.3	13	2	PHYSALACIN, BOV
14	3	27.3	13	2	PHYSALACIN, BOV
15	3	27.3	13	2	PHYSALACIN, BOV
16	3	27.3	13	2	PHYSALACIN, BOV
17	3	27.3	13	2	PHYSALACIN, BOV
18	3	27.3	13	2	PHYSALACIN, BOV
19	3	27.3	14	1	PHYSALACIN, BOV
20	3	27.3	14	1	PHYSALACIN, BOV
21	3	27.3	14	1	PHYSALACIN, BOV
22	3	27.3	14	1	PHYSALACIN, BOV
23	3	27.3	14	2	PHYSALACIN, BOV
24	3	27.3	14	2	PHYSALACIN, BOV
25	3	27.3	14	2	PHYSALACIN, BOV
26	3	27.3	14	2	PHYSALACIN, BOV
27	3	27.3	14	2	PHYSALACIN, BOV
28	3	27.3	14	2	PHYSALACIN, BOV
29	3	27.3	14	2	PHYSALACIN, BOV

dehydrin 4.5K poly  
hydrogensulfite re  
cellulase (EC 3.2.  
22K protein pi, mi  
small granule S6 c  
cytochrome-c oxida  
hypertrehalosemic  
hypertrehalosemic  
adipokinetic hormo  
neuropeptide led-C  
hypertrehalosemic  
hypertrehalosemic  
lechemoglobin 111  
rpsA protein - Erw  
glycine reductase  
variant surface ql  
neuropeptide M-1 -  
callipermamide 8 -  
acetylcholinestera  
apolipoprotein A-1  
cytochrome P450 AL  
major postsynaptic  
thymic factor - pi  
thymocyte growth p  
cat gene leader po  
chloramphenicol O-  
quinoline 2-oxid  
orf AB protein - S  
ribosomal protein  
tetrameric protein  
amine oxidase (cop  
hypothetical prote  
callipermamide 10  
cytochrome-c oxida  
118K stomach cance  
lg heavy chain CRD  
macrophage inhibit  
zymogen granule me  
alpha-2-macroglobu  
spectrin alpha cha  
unidentified 48.7K  
52.5K protein - SP  
gonadotrophin - se  
alpha-2-macroglobu  
hypertrehalosemic  
hypertrehalosemic  
caerulein-like pep  
scyllorhinin 1 - s  
phyllomedulin - tw  
hypothetical prote  
urease (EC 3.5.1.5  
bacteriotritin -  
neurotoxin-associ  
glycine reductase  
ribosomal protein  
polyferredoxin - M  
polygalacturonase  
transcription fact  
gonadotropin-relea  
cytochrome-c oxida  
cytochrome-c oxida  
bradykinin-potent  
platelet activatin  
T-cell receptor al  
T-cell receptor ga  
matrix metalloprot  
lg heavy chain Cr  
olfactory receptor  
T-cell receptor al  
olfactory receptor  
cytochrome-c oxida



252	2	18.2	15	2	PA0045	protein for 1 - Arabi	522	2	18.2	15	2	PA0082	protein GA600023 -
250	2	18.2	15	2	PA0116	protein GA600044 -	523	2	18.2	15	2	PA0089	seed storage prote
251	2	18.2	15	2	PA0307	lectin B1 - Isoflav	524	2	18.2	15	2	PA0321	RNA-binding protei
252	2	18.2	15	2	PA0326	phosphogluco 1 - En	525	2	18.2	15	2	PA0008	lectin B2 - psopho
253	2	18.2	15	2	PA0357	phosphogluco 1 - xy	526	2	18.2	15	2	PS0276	phosphotibulokinas
254	2	18.2	15	2	PA0377	phosphogluco 1 - a	527	2	18.2	15	2	PA0057	adenylate isopente
255	2	18.2	15	2	PA0375	phosphogluco 1 - 2	528	2	18.2	15	2	PA0064	cytochrome c3 - 1
256	2	18.2	15	2	PA0363	phosphogluco 1 - 2	529	2	18.2	15	2	PA0087	cytochrome c2 - fu
257	2	18.2	15	2	PA0362	phosphogluco 1 - 2	530	2	18.2	15	2	PA0093	enolase synthetase
258	2	18.2	15	2	PA0362	phosphogluco 1 - 2	531	2	18.2	15	2	PA0076	fructose biphosph
259	2	18.2	15	2	PA0365	28K protein for 3 -	532	2	18.2	15	2	PA0105	heat shock protein
260	2	18.2	15	2	PA0367	28K protein for 3 -	533	2	18.2	15	2	PA0091	methionine adenosy
261	2	18.2	15	2	PA0101	protein GF200020 -	534	2	18.2	15	2	PA0056	protein GF200002 -
262	2	18.2	15	2	PA0369	28K chromatin -	535	2	18.2	15	2	PA0052	protein GF200015 -
263	2	18.2	15	2	PA0371	homodimeric protein E	536	2	18.2	15	2	PA0051	protein GF200016 -
264	2	18.2	15	2	PA0368	homodimeric protein E	537	2	18.2	15	2	PA0086	protein GF200044 -
265	2	18.2	15	2	PA0368	homodimeric protein E	538	2	18.2	15	2	PA0088	protein GF200051 -
266	2	18.2	15	2	PA0368	homodimeric protein E	539	2	18.2	15	2	PA0106	protein GF200076 -
267	2	18.2	15	2	PA0368	homodimeric protein E	540	2	18.2	15	2	PA0097	starch phosphoryla
268	2	18.2	15	2	PA0368	homodimeric protein E	541	2	18.2	15	2	PA0097	starch phosphoryla
269	2	18.2	15	2	PA0368	homodimeric protein E	542	2	18.2	15	2	PA0097	starch phosphoryla
270	2	18.2	15	2	PA0368	homodimeric protein E	543	2	18.2	15	2	PA0097	starch phosphoryla
271	2	18.2	15	2	PA0368	homodimeric protein E	544	2	18.2	15	2	PA0097	starch phosphoryla
272	2	18.2	15	2	PA0368	homodimeric protein E	545	2	18.2	15	2	PA0097	starch phosphoryla
273	2	18.2	15	2	PA0368	homodimeric protein E	546	2	18.2	15	2	PA0097	starch phosphoryla
274	2	18.2	15	2	PA0368	homodimeric protein E	547	2	18.2	15	2	PA0097	starch phosphoryla
275	2	18.2	15	2	PA0368	homodimeric protein E	548	2	18.2	15	2	PA0097	starch phosphoryla
276	2	18.2	15	2	PA0368	homodimeric protein E	549	2	18.2	15	2	PA0097	starch phosphoryla
277	2	18.2	15	2	PA0368	homodimeric protein E	550	2	18.2	15	2	PA0097	starch phosphoryla
278	2	18.2	15	2	PA0368	homodimeric protein E	551	2	18.2	15	2	PA0097	starch phosphoryla
279	2	18.2	15	2	PA0368	homodimeric protein E	552	2	18.2	15	2	PA0097	starch phosphoryla
280	2	18.2	15	2	PA0368	homodimeric protein E	553	2	18.2	15	2	PA0097	starch phosphoryla
281	2	18.2	15	2	PA0368	homodimeric protein E	554	2	18.2	15	2	PA0097	starch phosphoryla
282	2	18.2	15	2	PA0368	homodimeric protein E	555	2	18.2	15	2	PA0097	starch phosphoryla
283	2	18.2	15	2	PA0368	homodimeric protein E	556	2	18.2	15	2	PA0097	starch phosphoryla
284	2	18.2	15	2	PA0368	homodimeric protein E	557	2	18.2	15	2	PA0097	starch phosphoryla
285	2	18.2	15	2	PA0368	homodimeric protein E	558	2	18.2	15	2	PA0097	starch phosphoryla
286	2	18.2	15	2	PA0368	homodimeric protein E	559	2	18.2	15	2	PA0097	starch phosphoryla
287	2	18.2	15	2	PA0368	homodimeric protein E	560	2	18.2	15	2	PA0097	starch phosphoryla
288	2	18.2	15	2	PA0368	homodimeric protein E	561	2	18.2	15	2	PA0097	starch phosphoryla
289	2	18.2	15	2	PA0368	homodimeric protein E	562	2	18.2	15	2	PA0097	starch phosphoryla
290	2	18.2	15	2	PA0368	homodimeric protein E	563	2	18.2	15	2	PA0097	starch phosphoryla
291	2	18.2	15	2	PA0368	homodimeric protein E	564	2	18.2	15	2	PA0097	starch phosphoryla
292	2	18.2	15	2	PA0368	homodimeric protein E	565	2	18.2	15	2	PA0097	starch phosphoryla
293	2	18.2	15	2	PA0368	homodimeric protein E	566	2	18.2	15	2	PA0097	starch phosphoryla
294	2	18.2	15	2	PA0368	homodimeric protein E	567	2	18.2	15	2	PA0097	starch phosphoryla
295	2	18.2	15	2	PA0368	homodimeric protein E	568	2	18.2	15	2	PA0097	starch phosphoryla
296	2	18.2	15	2	PA0368	homodimeric protein E	569	2	18.2	15	2	PA0097	starch phosphoryla
297	2	18.2	15	2	PA0368	homodimeric protein E	570	2	18.2	15	2	PA0097	starch phosphoryla
298	2	18.2	15	2	PA0368	homodimeric protein E	571	2	18.2	15	2	PA0097	starch phosphoryla
299	2	18.2	15	2	PA0368	homodimeric protein E	572	2	18.2	15	2	PA0097	starch phosphoryla
300	2	18.2	15	2	PA0368	homodimeric protein E	573	2	18.2	15	2	PA0097	starch phosphoryla
301	2	18.2	15	2	PA0368	homodimeric protein E	574	2	18.2	15	2	PA0097	starch phosphoryla
302	2	18.2	15	2	PA0368	homodimeric protein E	575	2	18.2	15	2	PA0097	starch phosphoryla
303	2	18.2	15	2	PA0368	homodimeric protein E	576	2	18.2	15	2	PA0097	starch phosphoryla
304	2	18.2	15	2	PA0368	homodimeric protein E	577	2	18.2	15	2	PA0097	starch phosphoryla
305	2	18.2	15	2	PA0368	homodimeric protein E	578	2	18.2	15	2	PA0097	starch phosphoryla
306	2	18.2	15	2	PA0368	homodimeric protein E	579	2	18.2	15	2	PA0097	starch phosphoryla
307	2	18.2	15	2	PA0368	homodimeric protein E	580	2	18.2	15	2	PA0097	starch phosphoryla
308	2	18.2	15	2	PA0368	homodimeric protein E	581	2	18.2	15	2	PA0097	starch phosphoryla
309	2	18.2	15	2	PA0368	homodimeric protein E	582	2	18.2	15	2	PA0097	starch phosphoryla
310	2	18.2	15	2	PA0368	homodimeric protein E	583	2	18.2	15	2	PA0097	starch phosphoryla
311	2	18.2	15	2	PA0368	homodimeric protein E	584	2	18.2	15	2	PA0097	starch phosphoryla
312	2	18.2	15	2	PA0368	homodimeric protein E	585	2	18.2	15	2	PA0097	starch phosphoryla
313	2	18.2	15	2	PA0368	homodimeric protein E	586	2	18.2	15	2	PA0097	starch phosphoryla
314	2	18.2	15	2	PA0368	homodimeric protein E	587	2	18.2	15	2	PA0097	starch phosphoryla
315	2	18.2	15	2	PA0368	homodimeric protein E	588	2	18.2	15	2	PA0097	starch phosphoryla
316	2	18.2	15	2	PA0368	homodimeric protein E	589	2	18.2	15	2	PA0097	starch phosphoryla
317	2	18.2	15	2	PA0368	homodimeric protein E	590	2	18.2	15	2	PA0097	starch phosphoryla
318	2	18.2	15	2	PA0368	homodimeric protein E	591	2	18.2	15	2	PA0097	starch phosphoryla
319	2	18.2	15	2	PA0368	homodimeric protein E	592	2	18.2	15	2	PA0097	starch phosphoryla
320	2	18.2	15	2	PA0368	homodimeric protein E	593	2	18.2	15	2	PA0097	starch phosphoryla
321	2	18.2	15	2	PA0368	homodimeric protein E	594	2	18.2	15	2	PA0097	starch phosphoryla



[illegible]





CiDate: 05-Jun-1997 #sequence\_revision 05-Jun-1997 #text\_change 16-Aug-2000  
 CiAccession: A05174

R:Kawagoe, Y.; Gozzini, L.; Espasador, V.

Int. J. Pept. Protein Res. 27, 176-182, 1996

A:Reference number: A05174

A:Accession: A05174

A:Molecule type: Protein

A:Residues: 1-13 <MW>

CiSpecies: family: classified animal peptides

CiKeywords: pyrrolidone carboxylic acid; skin

CiTitle: Pyrrolidone carboxylic acid (PAC) ester as experimental

Query Match: 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEK 6

DB 11

DB 2 KEK 4

RESULT 14

QJ2419

hypothetical protein X - Enterobacter aerogenes (strain ATCC 29424)

CiSpecies: Enterobacter aerogenes

CiDate: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

CiAccession: J02419

R:Kawagoe, Y.; Shih, D.S.; McCarthy, B.; Koster, J.M.; Thomas, C.M.

Plant Dis. 75, 95-111, 1996

A:Title: Characterization of the cloned X gene involved in replication and transfer across of

A:Reference number: J16434; MUID:97116920; PMID:8944861

A:Accession: J02419

A:Status: preliminary; translated from db/EMBL/GenBank

A:Molecule type: DNA

A:Residues: 1-13 <TR>

A:Cross references: EMBL:067194; MUID:9725423; PDB:1A064477; 1; PMID:1572582

CiGenetics:

CiKeywords: plasmid; K751

Query Match:

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 4

DB 6 AKK 8

RESULT 15

SZ2995

hypothetical protein X (traj 5' region) - Escherichia coli (strain ATCC 8739)

CiSpecies: Escherichia coli

CiDate: 11-Jun-1993 #sequence\_revision 02-Aug-1994 #text\_change 08-Oct-1999

CiAccession: SZ2995

R:Zhou, C.; Pansegrau, W.; Strack, B.; Hultner, L.; Knecht, M.; Kott, V.; Lanka, E.

Int. J. Med. Microbiol. 189, 403-427, 1991

A:Title: Nucleotide sequence and organization of genes flanking the transfer origin of

A:Reference number: SZ2992; MUID:9239548; PMID:1645677

A:Accession: SZ2995

A:Molecule type: DNA

A:Residues: 1-13 <21E>

A:Cross references: EMBL:X54459; MUID:842656; PDB:1A064477; 1; PMID:9561411

CiGenetics:

CiKeywords: plasmid

A:Start codon: TTG

Query Match:

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

DB 11

DB 6 AKK 8

RESULT 16

JQ2409

hypothetical 1.6K protein - Tomato chloroplast (strain Toka)

CiSpecies: chloroplast; Cytopsisium esculentum (tomato)

CiDate: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 24-Mar-1995

CiAccession: JQ2409

R:Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.)

A:Reference number: JQ2405

A:Accession: JQ2409

A:Molecule type: DNA

A:Residues: 1-13 <KAW>

A:Experimental source: Strain: Tokyo

CiGenetics:

A:Genome: chloroplast

CiKeywords: chloroplast

Query Match:

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEK 5

DB 11

DB 2 KEK 4

RESULT 17

JQ2419

hypothetical 1.6K protein - potato chloroplast

CiSpecies: chloroplast; Solanum tuberosum (potato)

CiDate: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Jan-1996

CiAccession: JQ2419; JQ2314

R:Kawagoe, Y.; Kikuta, Y.

Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.)

A:Reference number: JQ2406

A:Accession: JQ2419

A:Molecule type: DNA

A:Residues: 1-13 <KAW>

A:Experimental source: cv. W554 4

A:Accession: JQ2414

A:Molecule type: DNA

A:Residues: 1-13 <KAW>

A:Experimental source: cv. W554 4

CiGenetics:

A:Genome: chloroplast

CiKeywords: chloroplast

Query Match:

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEK 5

DB 11

DB 2 KEK 4

RESULT 18

A86126

hypothetical protein 75883 [imported] - Escherichia coli (strain O157:H7, substrain

CiSpecies: Escherichia coli

CiDate: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

CiAccession: A86126

R:Perna, N.J.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; M

iller, L.; Gottlieb, E.; Davis, N.W.; Lim, A.; Dimaianta, E.; Polamoussis, K.; Apo

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A86126; MUID:21074935; PMID:11206551

A:Accession: A86126

A:Status: preliminary





CAC accession: P7974  
Kikushima, A., Kawakuchi, T., Seki, T., Kano, R., Matsuda, Y.  
Electrophoresis 21, 185-187, 1980  
A.Literature reference analysis of mouse brain two-dimensional electrophoretic patterns of  
A.Sequence marker: P6792  
A.Accession: P7974  
A.Molecular type: protein  
A.Residues: 114 amino acids  
A.Experimental source: Strain C3H/HeJ Stockholder: Dr. Saito  
Keywords: brain

Query Match: 27.3% Score: 100.0 Length: 114  
Best Local Similarity: 100.0% Pred. Residue Cons.: 100.0%  
Matches: 0 Conservative 0 Miscellaneous 0 Gaps 0

DY 2 KKE 4  
+ + +  
SD 2 KKE 5

KESUJL 30  
194 382  
Subunit 4 OK polypeptide Soybean trypsin inhibitor  
K.Altitude: nomenclature acid soluble 26K protein  
Species: glycine max  
Created: Nov 1997 Sequence revision: N/A Date: 1997  
CAC accession: P4382  
Kikushima, M., Hatakeyama, K., Saito, M., Chikushi, K., Hatada, K.  
Biochim. Biophys. Acta 1246, 221-227, 1992  
A.Literature reference analysis of chicken egg yolk and soybean trypsin inhibitor from  
A.Sequence marker: P4380; MDID:9446521; 1992010101  
A.Accession: P4382  
A.Molecular type: protein  
A.Residues: 124 amino acids  
A.Experimental source: seed  
Comments: this protein is rich in hydrophobic residues and highly heat stable.

Query Match: 27.3% Score: 100.0 Length: 114  
Best Local Similarity: 100.0% Pred. Residue Cons.: 100.0%  
Matches: 0 Conservative 0 Miscellaneous 0 Gaps 0

DY 3 KKK 5  
+ + +  
PD 3 KKK 7

KESUJL 31  
222 304  
Soybean alpha-galactosyl transferase (EC 2.6.1.99) of bean (*Vicia faba*) contains six identical  
N-glycosylated subunits (monomers). Each monomer has a molecular mass of 26 kDa and  
specifically desulfates various substrates.  
Created: 19 Mar 1997 Sequence revision: N/A Date: 1997  
CAC accession: S2129  
Fukui, A., Ochi, T., Yoshizawa, M., Ochi, T., van Halbeek, H., Watanabe, K., Hoshino, W.  
Eur. J. Biochem. 255, 111-115, 1992  
A.Literature reference analysis of desulfotransferase type I from soybean subunit compounds  
A.Sequence marker: S2119; MDID:922694; 1992010101  
A.Accession: S2129  
A.Molecular type: protein  
A.Residues: 115 amino acids  
A.Experimental source: strain H-14600001  
Comments:  
A.Name: dsSB  
A.Complex: heterohexameric: two alpha, two beta and two gamma chains  
C.Funct: 001  
A.Description: catalyzes the six-electron reduction of sulfate to sulfite  
A.Pathway: the terminal oxidase in the sulfate reduction pathway  
Keywords: heterohexamer; oxidoreductase

Query Match: 27.3% Score: 100.0 Length: 115  
Best Local Similarity: 100.0% Pred. Residue Cons.: 100.0%  
Matches: 0 Conservative 0 Miscellaneous 0 Gaps 0

Query Match 27.3% Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3 Acc. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 EKP 6  
 IL 1 EKP 3

RESULT 15  
 S77987  
 cytochrome c oxidase (EC 1.9.3.1) chain V10.2 Lipase (14-peptides)  
 C:Species: Thaumodes (bigeye tuna)  
 C:Date: 17 Sep 1997 #sequence\_revision 17-Sep 1997 #text\_change 04 Sep 1998  
 C:Accession: S77987  
 R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Lindell, D.; Gottschalk, F.; Kadenbach, B.  
 submitted to the Protein Sequence Database, June 1997  
 A:Reference number: S77980  
 A:Accession: S77987  
 A:Molecule type: protein  
 A:Residues: 18;9-15 <ARN>  
 A:Experimental source: heart  
 A:Genetics:  
 A:Genome: nuclear  
 A:Function:  
 A:Pathway: oxidative phosphorylation, respiratory chain  
 C:Keywords: electron transfer; membrane-associated complex; mitochondria; inner membrane

Query Match 27.3% Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3 Acc. 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AKK 4  
 IL 7 AKK 3

RESULT 16  
 S80995  
 hyperreninogenic hormone 1 - oriental cockroach  
 N:Alternate names: P6A-CAH-1  
 C:Species: Blatta orientalis (oriental cockroach)  
 C:Date: 30 Jan 1992 #sequence\_revision 24-Oct 1997 #text\_change 30 Oct 1997  
 C:Accession: S08995  
 R:Gaede, G.; Rinehart, K.L.  
 and L. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A:Title: Primary structures of hyperreninogenic peptides isolated from the cockroach entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
 A:Reference number: S08995; M010:90253659; PMID:2340112  
 A:Accession: S08995  
 A:Molecule type: protein  
 A:Residues: 18 <GAE>

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2 Acc. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PN 7  
 IL 6 PN 7

RESULT 17  
 S08996  
 hyperreninogenic hormone 1 - oriental cockroach  
 N:Alternate names: P6A-CAH-1  
 C:Species: Blatta orientalis (oriental cockroach)  
 C:Date: 30 Jan 1992 #sequence\_revision 24-Oct 1997 #text\_change 30 Oct 1997  
 C:Accession: S08996  
 R:Gaede, G.; Rinehart, K.L.  
 and L. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A:Title: Primary structures of hyperreninogenic peptides isolated from the cockroach entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
 A:Reference number: S08995; M010:90253659; PMID:2340112  
 A:Accession: S08996  
 A:Molecule type: protein  
 A:Residues: 18 <GAE>

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2 Acc. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PN 7  
 IL 6 PN 7

C:Date: 30-Jan 1992 #sequence\_revision 24-Oct-1997 #text\_change 31-Oct-1997  
 C:Accession: S08996  
 R:Gaede, G.; Rinehart, K.L.  
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990  
 A:Title: Primary structures of hyperreninogenic peptides isolated from the cockroach entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment  
 A:Reference number: S08995; M010:90253659; PMID:2340112  
 A:Accession: S08996  
 A:Molecule type: protein  
 A:Residues: 18 <GAE>  
 A:Note: the amino terminal residue forms pyrrolidone carboxylic acid; therefore, we  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid  
 F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F18/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2 Acc. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PN 7  
 IL 6 PN 7

RESULT 38  
 A49823  
 adipokinetic hormone 1 - American cockroach  
 N:Alternate names: periplanetin CC-1  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
 C:Accession: A49823  
 R:Scarborough, K.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory and  
 A:Reference number: A49823; M010:84298179; PMID:6591205  
 A:Accession: A49823  
 A:Molecule type: protein  
 A:Residues: 18 <SCA>  
 A:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic acid  
 F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F18/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2 Acc. 0;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 PN 7  
 IL 6 PN 7

RESULT 39  
 B49923  
 adipokinetic hormone 1 - American cockroach  
 N:Alternate names: neuropeptide M-11; periplanetin CC-1  
 C:Species: Periplaneta americana (American cockroach)  
 C:Date: 03-May-1994 #sequence\_revision 03-May 1994 #text\_change 07-May 1999  
 C:Accession: B49923; A05170  
 R:Scarborough, K.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller  
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984  
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory and  
 A:Reference number: A49823; M010:84298179; PMID:6591205  
 A:Accession: B49923  
 A:Molecule type: protein  
 A:Residues: 18 <SCA>  
 R:Witten, J.L.; Schaffer, M.H.; Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr.,  
 Biochem. Biophys. Res. Commun. 124, 350-358, 1984  
 A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment  
 A:Reference number: A99118; M010:85045530; PMID:6548628  
 A:Accession: A05170  
 A:Molecule type: protein

A:Residues: 76-228 (WIT)  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut  
 P1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 P18/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e-05;  
 Matches: 2; Conservative 0; Mismatches 0; Gaps 0;

QY 6 PN 7  
 1  
 4 PN 7

DB 6 PN 7

RESULT 4:  
 A44960  
 neuropeptide isolated from Colorado potato beetle  
 C:Species: Leptinotarsa decemlineata (Colorado potato beetle)  
 C:Date: 14 Sep 1993 #sequence\_revision 40 Sep 1993 #text\_change 07 May 1999  
 C:Accession: A44960  
 R:Gaede, G., Kotsinski, R.  
 Peptides 11, 455-459, 1990  
 A:Title: The metabolic neuropeptides of the corpora cardiaca from the potato beetle and  
 A:Reference number: A44960; M010:90161081; PMID:2381871  
 A:Accession: A44960  
 A:Molecule type: protein  
 A:Residues: 1-8 (GAE)  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut  
 P1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 P18/Modified site: blocked carboxyl end (Trp) (indicatedly amidated) #status experimental

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e-05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 PN 7  
 1  
 4 PN 7

DB 6 PN 7

RESULT 4:  
 B43976  
 hypertrichalosemic hormone beetle (Zophobas rufipes)  
 C:Species: Zophobas rufipes  
 C:Date: 03-Feb-1993 #sequence\_revision 03 Feb-1993 #text\_change 07-May-1999  
 C:Accession: B43976  
 R:Gaede, G., Kotsinski, G.  
 Peptides 11, 455-459, 1990  
 A:Title: The primary structure of the hypertrichalosemic neuropeptide from tenebrion  
 A:Reference number: A43976; M010:90341081; PMID:2381871  
 A:Accession: B43976  
 A:Molecule type: protein  
 A:Residues: 1-8 (GAE)  
 C:Superfamily: adipokinetic hormone  
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut  
 P1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
 P18/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e-05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 PN 7  
 1  
 4 PN 7

DB 6 PN 7

RESULT 44  
 S20162  
 leghemoglobin III - Sesbania rostrata (fragment)  
 C:Species: Sesbania rostrata  
 C:Date: 10-Jun-1992 #sequence\_revision 10 Jun-1992 #text\_change 04-Mar-2000  
 C:Accession: S20162  
 R:Metz, E.A., Weickers, P., Bettmann, H.J., Jensen, E.O., Scheil, J., de Bruijn, F.J.  
 Mol. Gen. Genet. 214, 181-191, 1988  
 A:Title: Primary structure and promoter analysis of leghemoglobin genes of the stem  
 A:Reference number: S20162; M010:89181515; PMID:3237206  
 A:Accession: S20162  
 A:Molecule type: DNA  
 A:Residues: 1-8 (MET)  
 A:CROSS-references: EMBL:X11504; NID:q21184; PID:CAA31858.1; PID:q579482  
 C:Genetics:  
 A:Gene: glib  
 C:Superfamily: globin; soluble hemology  
 C:Keywords: heme; oxygen carrier

Query Match: 18.2%, Score 2; DB 2; Length 8;  
 Best Local Similarity: 100.0%; Pred. No. 2.8e-05;  
 Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 PN 7  
 1  
 4 PN 7

DB 6 PN 7

RESULT 42  
 A44976  
 hypertrichalosemic hormone yellow mealworm  
 C:Species: Tribolium castaneum (yellow mealworm)







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CM protein - protein search, using SW method

Run on: September 30, 2003, 09:33:01, 1 iteration, time 5.25 seconds

(with gap extension penalty 10, gap opening/extension  
costs of 40/10)

Title: US-09-787-443-17

Perfect score: 11

Sequence: 1 AKKEKPKNPQ 11

Scoring table: 95306

Gap: 60.0, Gapext: 60.0

Searched: 127863 seqs, 4702635 residues

Word size: 0

Total number of hits satisfying chosen parameters: 737

Minimum hit seq length: 8

Maximum hit seq length: 15

Fast processing: Lasting first 500 summaries

Database: SwissProt\_41\*

Prod. No. is the number of results produced by database search.  
Score greater than or equal to the score of the result being plotted,  
and is derived by analysis of the total score distribution.

# SUMMARY

Rank	Score	Query	Match	Length	DB	Id	Description
1	6	27.3	9	1	FABP_CALVO	P14869	Fatty acid-binding protein, caliphora
2	5	27.3	10	1	XNPF_PICG	P01290	Protein, xanthophyll
3	5	27.3	11	1	TKNA_RANCA	P22688	Rana catesbeiana
4	5	27.3	11	1	TKNA_RANCA	P22688	Rana catesbeiana
5	5	27.3	11	1	TKNA_RANCA	P22688	Rana catesbeiana
6	5	27.3	12	1	TKNA_RANCA	P22688	Rana catesbeiana
7	5	27.3	13	1	TKNA_RANCA	P22688	Rana catesbeiana
8	5	27.3	14	1	TKNA_RANCA	P22688	Rana catesbeiana
9	5	27.3	14	1	TKNA_RANCA	P22688	Rana catesbeiana
10	5	27.3	14	1	TKNA_RANCA	P22688	Rana catesbeiana
11	5	27.3	14	1	TKNA_RANCA	P22688	Rana catesbeiana
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13	5	27.3	14	1	TKNA_RANCA	P22688	Rana catesbeiana
14	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
15	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
16	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
17	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
18	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
19	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
20	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
21	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
22	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
23	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
24	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
25	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
26	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
27	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
28	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
29	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
30	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
31	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
32	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana
33	5	27.3	15	1	TKNA_RANCA	P22688	Rana catesbeiana

107	2	18.2	13	1	RSL1_ASHBP	245542 ash yellowes	180	1	9.1	8	1	CAD1_ENTFA	P13268 entecococu
108	2	18.2	13	1	TEJA_RANJA	P80002 rana ranja	181	1	9.1	8	1	CKK1_MACSU	P30369 macropus eu
109	2	18.2	14	1	CALL_CAGLI	P20128 calloripus	182	1	9.1	8	1	CLP1_THICU	P80488 thioaciliu
110	2	18.2	14	1	ETUL_CANFA	P48635 euliparis lami	183	1	9.1	9	1	CMW2_CONPU	P58785 conus purpu
111	2	18.2	14	1	KPPL_SEIMI	P225933 selosteichia	184	1	9.1	8	1	COXG_RAT	P80440 rattus norv
112	2	18.2	14	1	CRGB1_SGSG	P225963 psopocarpia	185	1	9.1	8	1	FAR1_PENNO	P83316 penaeus mon
113	2	18.2	14	1	MASI_TAPIT	P412715 psopocarpia	186	1	9.1	8	1	FAR2_MACRS	P83275 macrobrachi
114	2	18.2	14	1	MASI_TAPIT	P412715 psopocarpia	187	1	9.1	8	1	FAR3_HUMAM	P41486 homarus ame
115	2	18.2	14	1	MASI_VESUM	P412728 psopocarpia	188	1	9.1	8	1	FAR4_HUMAM	P41487 homarus ame
116	2	18.2	14	1	KPKX_KETIM	P412815 psopocarpia	189	1	9.1	8	1	FAR4_MACRS	P83277 macrobrachi
117	2	18.2	14	1	RSL1_TAPIT	P412815 psopocarpia	190	1	9.1	8	1	FAR7_ASCSU	P43171 ascaris suu
118	2	18.2	14	1	RSL1_TAPIT	P412815 psopocarpia	191	1	9.1	8	1	FUSS_FUSSO	P81010 fusarium so
119	2	18.2	14	1	RSL1_TAPIT	P412815 psopocarpia	192	1	9.1	8	1	GLUR_BUMAM	P02729 homo sapien
120	2	18.2	14	1	RSL1_TAPIT	P412815 psopocarpia	193	1	9.1	8	1	LCK1_LEUMA	P21140 leucophaea
121	2	18.2	14	1	TAL_HVWZ	P12509 psopocarpia	194	1	9.1	8	1	LCK2_LEUMA	P21141 leucophaea
122	2	18.2	14	1	TAL_HVWZ	P12509 psopocarpia	195	1	9.1	8	1	LCK3_LEUMA	P21142 leucophaea
123	2	18.2	14	1	TAL_HVWZ	P12509 psopocarpia	196	1	9.1	8	1	LCK4_LEUMA	P21143 leucophaea
124	2	18.2	14	1	UN47_TAPIT	P81362 psopocarpia	197	1	9.1	8	1	LCK7_LEUMA	P19989 leucophaea
125	2	18.2	14	1	UN46_TAPIT	P81362 psopocarpia	198	1	9.1	8	1	LCK8_LEUMA	P19990 leucophaea
126	2	18.2	15	1	ABZ2_PUSE	P22565 psopocarpia	199	1	9.1	8	1	LMT2_LCKMI	P22396 locusta mig
127	2	18.2	15	1	ASPL_LACSN	P82648 psopocarpia	200	1	9.1	8	1	LCK1_LEUMA	P13049 leucophaea
128	2	18.2	15	1	COA1_RAT	P412815 psopocarpia	201	1	9.1	8	1	LPM5_STAEP	P23211 staphylococ
129	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	202	1	9.1	8	1	NFB_BOVIN	P15507 bos taurus
130	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	203	1	9.1	8	1	ORMY_ORCMI	P82455 orconectes
131	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	204	1	9.1	8	1	PKK2_PERAM	P82692 periplaneta
132	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	205	1	9.1	8	1	PKK3_PERAM	P82618 periplaneta
133	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	206	1	9.1	8	1	PKK4_PERAM	P82618 periplaneta
134	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	207	1	9.1	8	1	PKK5_PERAM	P82618 periplaneta
135	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	208	1	9.1	8	1	PKK6_PERAM	P82618 periplaneta
136	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	209	1	9.1	8	1	PKK7_PERAM	P82618 periplaneta
137	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	210	1	9.1	8	1	PKK8_PERAM	P82618 periplaneta
138	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	211	1	9.1	8	1	PKK9_PERAM	P82618 periplaneta
139	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	212	1	9.1	8	1	PKK10_PERAM	P82618 periplaneta
140	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	213	1	9.1	8	1	PKK11_PERAM	P82618 periplaneta
141	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	214	1	9.1	8	1	PKK12_PERAM	P82618 periplaneta
142	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	215	1	9.1	8	1	PKK13_PERAM	P82618 periplaneta
143	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	216	1	9.1	8	1	PKK14_PERAM	P82618 periplaneta
144	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	217	1	9.1	8	1	PKK15_PERAM	P82618 periplaneta
145	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	218	1	9.1	8	1	PKK16_PERAM	P82618 periplaneta
146	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	219	1	9.1	8	1	PKK17_PERAM	P82618 periplaneta
147	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	220	1	9.1	8	1	PKK18_PERAM	P82618 periplaneta
148	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	221	1	9.1	8	1	PKK19_PERAM	P82618 periplaneta
149	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	222	1	9.1	8	1	PKK20_PERAM	P82618 periplaneta
150	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	223	1	9.1	8	1	PKK21_PERAM	P82618 periplaneta
151	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	224	1	9.1	8	1	PKK22_PERAM	P82618 periplaneta
152	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	225	1	9.1	8	1	PKK23_PERAM	P82618 periplaneta
153	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	226	1	9.1	8	1	PKK24_PERAM	P82618 periplaneta
154	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	227	1	9.1	8	1	PKK25_PERAM	P82618 periplaneta
155	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	228	1	9.1	8	1	PKK26_PERAM	P82618 periplaneta
156	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	229	1	9.1	8	1	PKK27_PERAM	P82618 periplaneta
157	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	230	1	9.1	8	1	PKK28_PERAM	P82618 periplaneta
158	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	231	1	9.1	8	1	PKK29_PERAM	P82618 periplaneta
159	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	232	1	9.1	8	1	PKK30_PERAM	P82618 periplaneta
160	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	233	1	9.1	8	1	PKK31_PERAM	P82618 periplaneta
161	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	234	1	9.1	8	1	PKK32_PERAM	P82618 periplaneta
162	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	235	1	9.1	8	1	PKK33_PERAM	P82618 periplaneta
163	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	236	1	9.1	8	1	PKK34_PERAM	P82618 periplaneta
164	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	237	1	9.1	8	1	PKK35_PERAM	P82618 periplaneta
165	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	238	1	9.1	8	1	PKK36_PERAM	P82618 periplaneta
166	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	239	1	9.1	8	1	PKK37_PERAM	P82618 periplaneta
167	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	240	1	9.1	8	1	PKK38_PERAM	P82618 periplaneta
168	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	241	1	9.1	8	1	PKK39_PERAM	P82618 periplaneta
169	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	242	1	9.1	8	1	PKK40_PERAM	P82618 periplaneta
170	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	243	1	9.1	8	1	PKK41_PERAM	P82618 periplaneta
171	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	244	1	9.1	8	1	PKK42_PERAM	P82618 periplaneta
172	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	245	1	9.1	8	1	PKK43_PERAM	P82618 periplaneta
173	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	246	1	9.1	8	1	PKK44_PERAM	P82618 periplaneta
174	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	247	1	9.1	8	1	PKK45_PERAM	P82618 periplaneta
175	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	248	1	9.1	8	1	PKK46_PERAM	P82618 periplaneta
176	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	249	1	9.1	8	1	PKK47_PERAM	P82618 periplaneta
177	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	250	1	9.1	8	1	PKK48_PERAM	P82618 periplaneta
178	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	251	1	9.1	8	1	PKK49_PERAM	P82618 periplaneta
179	2	18.2	15	1	CHIL_FEA	P21225 psopocarpia	252	1	9.1	8	1	PKK50_PERAM	P82618 periplaneta

253	1	9.1	9	1	KNLS_HUMAN	P84058 boletia var	326	1	9.1	10	1	CAJU_HUMAN	P01358 homo sapien
254	1	9.1	9	1	LITR_LITAE	P08945 litocria var	327	1	9.1	10	1	GLEM_HUMAN	P02728 homo sapien
255	1	9.1	9	1	LITR_PHRP	P08946 pyllomedus	328	1	9.1	10	1	GONI_ALLMI	P37041 alligator m
256	1	9.1	9	1	LMF_PHRP	P41759 locusta miq	329	1	9.1	10	1	GONI_CUPA	P81749 cupea pall
257	1	9.1	9	1	LMF_PHRP	P41463 locusta miq	330	1	9.1	10	1	GON2_CHPR	P80678 chelyosoma
258	1	9.1	9	1	MDM_BOVIN	P29177 bos taurus	331	1	9.1	10	1	GUN2_CHCK	P37043 gallus gall
259	1	9.1	9	1	MOSE_CLEA	P39653 clypeaster	332	1	9.1	10	1	GUN2_ONCK	P20357 oncorhynch
260	1	9.1	9	1	MOSH_CLEA	P39652 clypeaster	333	1	9.1	10	1	GUNI_SQUA	P27429 squalus aca
261	1	9.1	9	1	NEF_BOVIN	P12441 human tauru	334	1	9.1	10	1	GRP_RANR1	P23260 rana ridibu
262	1	9.1	9	1	NEUF_GAVO	P43925 gavia pavo	335	1	9.1	10	1	GS09_BACSU	P80243 bacillus su
263	1	9.1	9	1	NEUX_HUMAN	P04272 homo sapien	336	1	9.1	10	1	HTF_HEIZE	P16353 heliothis z
264	1	9.1	9	1	NSK1_SARCA	P41142 sarcophaga	337	1	9.1	10	1	HTF_NAUC1	P10939 nauphoeta c
265	1	9.1	9	1	OXVA_SQVA	P42295 squalus aca	338	1	9.1	10	1	HTF_IARAT	P14596 tabanus atr
266	1	9.1	9	1	OXVE_SQVA	P42297 squalus aca	339	1	9.1	10	1	LABA_JATMU	P13270 jatrophia mu
267	1	9.1	9	1	OXYT_SQPE	P42945 bala redilu	340	1	9.1	10	1	LCMS_LEUMA	P21144 leucophaea
268	1	9.1	9	1	OXYT_SYCA	P43875 tyrannus ca	341	1	9.1	10	1	LSK2_LOCM1	P41488 locusta miq
269	1	9.1	9	1	OXYT_EISFG	P42928 elisenia toe	342	1	9.1	10	1	LSK2_LEUMA	P09039 leucophaea
270	1	9.1	9	1	OXYT_GCTV1	P40327 octopus vol	343	1	9.1	10	1	MALE_KLEPN	P05564 klebsiella
271	1	9.1	9	1	OXYT_KAB11	P42478 cyctolagus	344	1	9.1	10	1	MOSE_CLEJA	P19362 clypeaster
272	1	9.1	9	1	OXYT_KAB11	P42478 cyctolagus	345	1	9.1	10	1	NO40_TUBAC	P55962 nicotiana t
273	1	9.1	9	1	OXYT_SQVA1	P42944 raja clavi	346	1	9.1	10	1	ODP2_BOVIN	P11180 bos taurus
274	1	9.1	9	1	OXVE_SQVA1	P43066 squalus aca	347	1	9.1	10	1	PAP1_PARMA	P81863 pardachirus
275	1	9.1	9	1	PEH1_LYCES	P83386 lycopersico	348	1	9.1	10	1	PNEU_HUMAN	P22103 homo sapien
276	1	9.1	9	1	PEH1_PERAM	P82591 peripanca	349	1	9.1	10	1	PNEU_RAT	P21996 rattus norv
277	1	9.1	9	1	PESP_BOMBO	P82003 bombyx mori	350	1	9.1	10	1	POBH_METIM	P80901 methanobact
278	1	9.1	9	1	PE42_CLEA1	P82475 litoria cit	351	1	9.1	10	1	PPCK_FASHE	P80525 fasciola he
279	1	9.1	9	1	PSL1_SARCA	P45936 serralia ma	352	1	9.1	10	1	PSBF_CAPAN	P03367 capsicum an
280	1	9.1	9	1	SAMP_MUSCA	P19595 musclopente	353	1	9.1	10	1	PVK_LOCM1	P83382 locusta miq
281	1	9.1	9	1	SAP2_SQVA	P43047 squalopente	354	1	9.1	10	1	Q2OB_COMTE	P80465 comamonas t
282	1	9.1	9	1	TAL3_PICJA	P17441 picula fadi	355	1	9.1	10	1	RL16_ACHLA	P29221 acholepiasm
283	1	9.1	9	1	TKC1_GALVO	P41517 galiphora	356	1	9.1	10	1	RRPL_PHOOV	P35946 phoxine dis
284	1	9.1	9	1	TKL1_BOVM	P16224 locusta miq	357	1	9.1	10	1	R02_BOVIN	P82923 bos taurus
285	1	9.1	9	1	TRP4_LEUMA	P41746 leucophaea	358	1	9.1	10	1	SLAP_BACTG	P49325 bacillus th
286	1	9.1	9	1	UFZ2_KOJSE	P86640 mus muscu	359	1	9.1	10	1	TKL2_LOCM1	P16224 locusta miq
287	1	9.1	9	1	UH42_HUMAN	P41929 homo sapien	360	1	9.1	10	1	TKL3_LOCM1	P30249 locusta miq
288	1	9.1	9	1	ULAH_HUMAN	P41944 homo sapien	361	1	9.1	10	1	TKL4_LOCM1	P30250 locusta miq
289	1	9.1	9	1	ULAK_MJOSE	P99041 mus muscu	362	1	9.1	10	1	TKNB_CHICK	P19851 gallus gall
290	1	9.1	9	1	UN19_CLEA	P81355 clypeaster	363	1	9.1	10	1	TKNB_ONCMY	P28500 oncorhynch
291	1	9.1	9	1	UPA3_HUMAN	P40084 homo sapien	364	1	9.1	10	1	TKNB_RANCA	P22889 rana catesb
292	1	9.1	9	1	UPA6_HUMAN	P40092 homo sapien	365	1	9.1	10	1	TKNB_RANR1	P22690 rana catesb
293	1	9.1	9	1	UPA7_HUMAN	P40093 homo sapien	366	1	9.1	10	1	TKNC_RANR1	P22690 rana catesb
294	1	9.1	9	1	YBFR_AZAV1	P59149 streptomyce	367	1	9.1	10	1	TKNK_PIC	P01292 sus scrofa
295	1	9.1	9	1	YBFR_AZAV1	P59149 streptomyce	368	1	9.1	10	1	TKSL_AEDAE	P42634 aedes aegypt
296	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	369	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
297	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	370	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
298	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	371	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
299	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	372	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
300	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	373	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
301	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	374	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
302	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	375	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
303	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	376	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
304	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	377	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
305	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	378	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
306	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	379	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
307	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	380	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
308	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	381	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
309	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	382	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
310	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	383	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
311	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	384	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
312	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	385	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
313	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	386	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
314	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	387	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
315	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	388	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
316	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	389	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
317	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	390	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
318	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	391	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
319	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	392	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
320	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	393	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
321	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	394	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
322	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	395	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
323	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	396	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
324	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	397	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt
325	1	9.1	10	1	AB3_PROSE	P84455 aarocybe ae	398	1	9.1	10	1	TKS2_AEDAE	P42635 aedes aegypt

399	CA32_11001	1	9.1	1	472	1	9.1	1	TKN2_KASMA	P08614	kassina mac
400	CA32_11001	1	9.1	1	473	1	9.1	1	TKN_KASSE	P08611	kassina sen
401	CA41_11001	1	9.1	1	474	1	9.1	1	UH31_RAT	P56572	rattus norv
402	CA42_11001	1	9.1	1	475	1	9.1	1	UH31_RAT	P31144	homo sapien
403	CA42_11001	1	9.1	1	476	1	9.1	1	UH31_RAT	P99032	mus musculu
404	CA42_11001	1	9.1	1	477	1	9.1	1	UH31_RAT	P81359	clatridium
405	CA42_11001	1	9.1	1	478	1	9.1	1	UH31_RAT	P04558	catostomus
406	CA42_11001	1	9.1	1	479	1	9.1	1	UH31_RAT	P04559	catostomus
407	CA42_11001	1	9.1	1	480	1	9.1	1	UH31_RAT	P04561	cyprinus ca
408	CA42_11001	1	9.1	1	481	1	9.1	1	UH31_RAT	P01147	quillichthys
409	CA42_11001	1	9.1	1	482	1	9.1	1	UH31_RAT	P81022	polyodon sp
410	CA42_11001	1	9.1	1	483	1	9.1	1	UH31_RAT	P35490	scyllorhinu
411	CA42_11001	1	9.1	1	484	1	9.1	1	UH31_RAT	P82006	white spot
412	CA42_11001	1	9.1	1	485	1	9.1	1	UH31_RAT	P82005	white spot
413	CA42_11001	1	9.1	1	486	1	9.1	1	UH31_RAT	P82004	white spot
414	CA42_11001	1	9.1	1	487	1	9.1	1	UH31_RAT	P14405	streptomyce
415	CA42_11001	1	9.1	1	488	1	9.1	1	UH31_RAT	P1776	escherichia
416	CA42_11001	1	9.1	1	489	1	9.1	1	UH31_RAT	P15987	glycine max
417	CA42_11001	1	9.1	1	490	1	9.1	1	UH31_RAT	P29622	prunus sero
418	CA42_11001	1	9.1	1	491	1	9.1	1	UH31_RAT	P81173	streptomyce
419	CA42_11001	1	9.1	1	492	1	9.1	1	UH31_RAT	P42991	pseudophryn
420	CA42_11001	1	9.1	1	493	1	9.1	1	UH31_RAT	P81754	leucophaea
421	CA42_11001	1	9.1	1	494	1	9.1	1	UH31_RAT	P01020	bothrops ja
422	CA42_11001	1	9.1	1	495	1	9.1	1	UH31_RAT	P42717	parapolybia
423	CA42_11001	1	9.1	1	496	1	9.1	1	UH31_RAT	P82051	litoria ewi
424	CA42_11001	1	9.1	1	497	1	9.1	1	UH31_RAT	P42718	parapolybia
425	CA42_11001	1	9.1	1	498	1	9.1	1	UH31_RAT	Q10998	aplysia cal
426	CA42_11001	1	9.1	1	499	1	9.1	1	UH31_RAT	P17237	icaria sp.
427	CA42_11001	1	9.1	1	500	1	9.1	1	UH31_RAT	P01518	vespa crabr
428	CA42_11001	1	9.1	1							
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467	CA42_11001	1	9.1	1							
468	CA42_11001	1	9.1	1							
469	CA42_11001	1	9.1	1							
470	CA42_11001	1	9.1	1							
471	CA42_11001	1	9.1	1							

ALIGNMENTS

RESULTS 1  
FAR4\_CALV: 1  
ID FAR4\_CALV: 1  
AC P41859: 1  
BT 01-NOV-1995 (Rev. 12, Created)  
BT 01-NOV-1995 (Rev. 12, Last sequence update)  
BT 01-NOV-1995 (Rev. 12, Last annotation update)  
DE Call:FMRFamide 4.  
GS Calliphora vomitoria (Blue blowfly).  
GC Eukaryota: Metazoa: Arthropoda: Insecta: Pterygota:  
GC Neoptera: Megaloptera: Diptera: Brachycera: Muscomorpha: Oestroidea:  
GC Calliphoridae: Calliphora.  
CX NCBI TaxID: 27454;  
RN 111  
SEQUENCE:  
TISSUE: Tissue: gizzard.  
RX MEDLINE: 32796111; PubMed: 149595;  
RA Dave H. Johnson A.B.; Sewell J.C.; Scott A.G.; Orchard J.;  
RA Reffeld J.F.; Thorpe A.;  
RT \*Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callifemRFamides) from the blowfly  
RT Calliphora vomitoria.\*  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1 SIMILARITY: BELONGS TO THE FARE (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY  
DR PIR: E41978; 041978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES: 9  
SQ SEQUENCE 9 AA: 1182 MW: 31730699GABD457 CRC64:  
27 18: Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match: 27 18: Score 3; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 KIN 7  
DB 1 KIN 5







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RP STRUCTURE BY NMR.
RX MEDLINE 9626894. PubMed:9537994.
RA Kasuoka H., Kakutani K., Sato K., Miyazawa T., Kanno T.
RI "G Protein-bound conformation of mastoparan-A1 is critical for
RI multidimensional transferred nuclear overhauser effect analysis of
RI peptide uniformly enriched with 13C and 15N".
RL Biochemistry 37:4782-4790(1998)
CC -1 FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
CP PIR: A01798; QMWHX.
CR PUB: 1411; 16-FEB-99.
KW Mast cell degranulation; Activation; G structure.
FT MISC_RES 14 34 AMYLATION
SQ SEQUENCE 14 AA: 1557 MW: 1696 MW: 434566C7A40294 CRC64;

Query Match 27.4% Score 3; BB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1; 80-03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3
DB 11
DB 7 AKK 12

RESULT 13
TSNK_RANXA STANDARD; PRI: 14 AA.
AC P40551
DI 01-FEB-1995 (Rev. 31; Created)
DI 01-FEB-1995 (Rev. 31; Last sequence update)
DI 15-SEP-2003 (Rev. 42; Last annotation update)
DE Rana maculata.
DE Rana maculata (Chinese frog).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
CX NCBI_TaxID:121156;
RN [1]
RP SEQUENCE.
TSNK_RANXA STANDARD; PRI: 14 AA.
AC P40551
DI 01-FEB-1995 (Rev. 31; Created)
DI 01-FEB-1995 (Rev. 31; Last sequence update)
DI 15-SEP-2003 (Rev. 42; Last annotation update)
DE Rana maculata.
DE Rana maculata (Chinese frog).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
CX NCBI_TaxID:121156;
RN [1]
RP SEQUENCE.

Query Match 27.4% Score 3; BB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1; 80-03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 3
DB 11
DB 7 AKK 12

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RESULT 14
COXI_THUOB STANDARD; PRI: 15 AA.
AC P80978;
DI 01-NOV-1997 (Rev. 35; Created)
DI 01-NOV-1997 (Rev. 35; Last sequence update)
DI 01-NOV-1997 (Rev. 35; Last annotation update)
DE Cytochrome c oxidase polypeptide Vie-2 (EC 1.9.3.1) (Fragments)
OS Thunnus obesus (Bluefin tuna).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygia; Teleostei; Neoteleostei;
CC Acanthopterygia; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
CC Scombridae; Thunnus
CX NCBI_TaxID:8243;
RN [1]
RP SEQUENCE.
TSNK_THUOB STANDARD; PRI: 15 AA.
AC P80978;
DI 01-NOV-1997 (Rev. 35; Created)
DI 01-NOV-1997 (Rev. 35; Last sequence update)
DI 01-NOV-1997 (Rev. 35; Last annotation update)
DE Cytochrome c oxidase polypeptide Vie-2 (EC 1.9.3.1) (Fragments)
OS Thunnus obesus (Bluefin tuna).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygia; Teleostei; Neoteleostei;
CC Acanthopterygia; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
CC Scombridae; Thunnus
CX NCBI_TaxID:8243;
RN [1]
RP SEQUENCE.

Query Match 27.4% Score 3; BB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; 9e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 11
DB 7 AKK 9

RESULT 15
EFIA_MISCP STANDARD; PRI: 15 AA.
AC P81267;
DI 15-JUL-1996 (Rev. 36; Created)
DI 15-JUL-1996 (Rev. 36; Last sequence update)
DI 15-DEC-1998 (Rev. 37; Last annotation update)
DE Elongation factor 1-alpha (EF-1-alpha) (fragment).
OS Microplitis croceipes.
CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
CC Braconidae; Microgasterinae; Microplitis.
CX NCBI_TaxID:72115;
RN [1]
RP SEQUENCE.
TSNK_MISCP STANDARD; PRI: 15 AA.
AC P81267;
DI 15-JUL-1996 (Rev. 36; Created)
DI 15-JUL-1996 (Rev. 36; Last sequence update)
DI 15-DEC-1998 (Rev. 37; Last annotation update)
DE Elongation factor 1-alpha (EF-1-alpha) (fragment).
OS Microplitis croceipes.
CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
CC Braconidae; Microgasterinae; Microplitis.
CX NCBI_TaxID:72115;
RN [1]
RP SEQUENCE.

Query Match 27.4% Score 3; BB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; 9e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 11
DB 7 AKK 9

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DE PROSTIE; PS00461; EFATOR GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
FT N_K_TER 15
SQ SEQUENCE 15 AA: 1670 MW: 187640.800H-751 (Ref:4)

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 5
DE 111
2 KKK 4

RESULT 18
UP02_METAN STANDARD; PRT: 15 AA.
AC B83439;
DT 28-FEB-2003 (Ref. 4); Created
DT 28-FEB-2003 (Ref. 4); Last sequence update
DE Unknown 70 kDa protein (Fragment).
OS Metathelium anisopliae.
GC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae;
OC Clavicipitaceae; Clavicipitaceae; Metarhizium.
OX NCBI_TaxID 5530;
RN [1]
RP SEQUENCE
RC STRAIN:54A-1b;
RX MEDLINE:22341006; PubMed:12455610;
RT "Protein analysis in a pleomorphic strain of the
insect pathogenic fungus Metarhizium anisopliae."
RL Can. J. Microbiol. 48:787-792(2002).
SQ 1- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
protein is 70 kDa.
FT N_K_TER 15
SQ SEQUENCE 15 AA: 148; MW: 20474.0706H153 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PND 1;
DE 111
8 PND 10

RESULT 19
FAR1_PANRE STANDARD; PRT: 8 AA.
AC P41872;
DT 01-NOV-1995 (Ref. 32); Created
DT 01-NOV-1995 (Ref. 32); Last sequence update
DE PNFamide-like neuropeptide PFI (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE:93027659; PubMed:1408999;

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SA GARY MATH. 18.2% Score 2: DB 1, Length 8;  
 RA GARDISON R.D., WILLIAMS C.F., FRIEDMAN A.K. 1  
 SC "Two PEPAMIDE-like peptides from the free-living nematode  
 SC PANDORINUS TEDIUM." 1  
 SC PEPTIDES 14:209-214(1992).  
 SC 1 FUNCTION: MYOACTIVE.  
 SC 1 TISSUE SPECIFICITY: NERVE CELLS AND LIVER OF CELLS TO CALCIUM  
 SC 1 CAPABLY TO THE BASE OF THE PEAK.  
 SC 1 SIMILARITY: BELONGS TO THE PEPAMIDE PEPTIDE FAMILY.  
 KW Neuro-peptide: Amidation.  
 FI MCD-RES 8 5 AMIDATION.  
 SQ SEQUENCE 8 AA: 995 MW: 6140/2345/941 05-04-94  
 Query Match: 18.2% Score 2: DB 1, Length 8;  
 Best Local Similarity 100.0% Pred. No. 1.3e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 6 PN 7  
 EB 1  
 DB 6 PN 4  
 RESULT 20  
 HFF2\_PERAM STANDARD; PRI: 8 AA.  
 AC 104546  
 DE 01-FEB-1997 (Rel. 05, Created)  
 DE 28-FEB-1994 (Rel. 28, Last Sequence Update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertetrahaseic factor I (Neuropeptide M I) (Extracellular)  
 DE (Pep. AB-1) (Ich-CC-1) (Hypertetrahaseic factor I)  
 DE PANDORINUS TEDIUM (Nematode)  
 DE Septentaria decemlineata (Colorado potato beetle)

SA GARY MATH. 18.2% Score 2: DB 1, Length 8;  
 RA GARDISON R.D., WILLIAMS C.F., FRIEDMAN A.K. 1  
 SC "Two PEPAMIDE-like peptides from the free-living nematode  
 SC PANDORINUS TEDIUM." 1  
 SC PEPTIDES 14:209-214(1992).  
 SC 1 FUNCTION: MYOACTIVE.  
 SC 1 TISSUE SPECIFICITY: NERVE CELLS AND LIVER OF CELLS TO CALCIUM  
 SC 1 CAPABLY TO THE BASE OF THE PEAK.  
 SC 1 SIMILARITY: BELONGS TO THE PEPAMIDE PEPTIDE FAMILY.  
 KW Neuro-peptide: Amidation.  
 FI MCD-RES 8 5 AMIDATION.  
 SQ SEQUENCE 8 AA: 995 MW: 6140/2345/941 05-04-94  
 Query Match: 18.2% Score 2: DB 1, Length 8;  
 Best Local Similarity 100.0% Pred. No. 1.3e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 6 PN 7  
 EB 1  
 DB 6 PN 4  
 RESULT 20  
 HFF2\_PERAM STANDARD; PRI: 8 AA.  
 AC 104546  
 DE 01-FEB-1997 (Rel. 05, Created)  
 DE 28-FEB-1994 (Rel. 28, Last Sequence Update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertetrahaseic factor I (Neuropeptide M I) (Extracellular)  
 DE (Pep. AB-1) (Ich-CC-1) (Hypertetrahaseic factor I)  
 DE PANDORINUS TEDIUM (Nematode)  
 DE Septentaria decemlineata (Colorado potato beetle)

SA GARY MATH. 18.2% Score 2: DB 1, Length 8;  
 RA GARDISON R.D., WILLIAMS C.F., FRIEDMAN A.K. 1  
 SC "Two PEPAMIDE-like peptides from the free-living nematode  
 SC PANDORINUS TEDIUM." 1  
 SC PEPTIDES 14:209-214(1992).  
 SC 1 FUNCTION: MYOACTIVE.  
 SC 1 TISSUE SPECIFICITY: NERVE CELLS AND LIVER OF CELLS TO CALCIUM  
 SC 1 CAPABLY TO THE BASE OF THE PEAK.  
 SC 1 SIMILARITY: BELONGS TO THE PEPAMIDE PEPTIDE FAMILY.  
 KW Neuro-peptide: Amidation.  
 FI MCD-RES 8 5 AMIDATION.  
 SQ SEQUENCE 8 AA: 995 MW: 6140/2345/941 05-04-94  
 Query Match: 18.2% Score 2: DB 1, Length 8;  
 Best Local Similarity 100.0% Pred. No. 1.3e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 6 PN 7  
 EB 1  
 DB 6 PN 4  
 RESULT 20  
 HFF2\_PERAM STANDARD; PRI: 8 AA.  
 AC 104546  
 DE 01-FEB-1997 (Rel. 05, Created)  
 DE 28-FEB-1994 (Rel. 28, Last Sequence Update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypertetrahaseic factor I (Neuropeptide M I) (Extracellular)  
 DE (Pep. AB-1) (Ich-CC-1) (Hypertetrahaseic factor I)  
 DE PANDORINUS TEDIUM (Nematode)  
 DE Septentaria decemlineata (Colorado potato beetle)

OS Blatta orientalis (Oriental cockroach).  
 SC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 SC Neoptera; Orthoptera; Blattellidae; Blattaria; Blattelloidea;  
 SC Blattidae; Periplaneta.  
 SC NCHI\_TaxID: 6978, 7539, 6976;  
 RN 11  
 RP SEQUENCE  
 SC SPECIES: B. americana;  
 RX MEDLINE: 6504563; PubMed: 6549628;  
 RA Witten C.L., Schaller M.H., O'Shea M., Cook J.C., Hemling M.E.,  
 RA Kinkel R.L. 1  
 SC "Structures of two cockroach neuropeptides assigned by fast atom  
 RI bombardment mass spectrometry."  
 RI Biochem. Biophys. Res. Commun. 124: 450-458(1984).  
 RN 12  
 RP SEQUENCE  
 SC SPECIES: B. americana;  
 RX MEDLINE: 84298179; PubMed: 6591205;  
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,  
 RA Miller G.A., Schooley D.A. 1  
 SC "Isolation and primary structure of two peptides with  
 RI cardioacceleratory and hyperglycemic activity from the corpora  
 RI cardiaca of Periplaneta americana."  
 RI Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).  
 RN 13  
 RP SEQUENCE  
 SC SPECIES: B. decemlineata; TISSUE: Corpora cardiaca;  
 RX MEDLINE: 90160533; PubMed: 2576128;  
 RA Gaede G., Kellner R. 1  
 SC "The metabolic neuropeptides of the corpora cardiaca from the potato  
 RI beetle and the American cockroach are identical."  
 RI Peptides 10:1247-1250(1989).  
 RN 14  
 RP SEQUENCE  
 SC SPECIES: B. orientalis; TISSUE: Corpora cardiaca;  
 RX MEDLINE: 90253559; PubMed: 2440112;  
 RA Gaede G., Kinkel R.L. 1  
 SC "Primary structures of hypertetrahaseic neuropeptides isolated from  
 RI the corpora cardiaca of the cockroaches Leucophaea maderae,  
 RI Onophodina portosa, Blattella germanica and Blatta orientalis  
 RI and of the stick insect Ectatomma tarantula assigned by tandem fast  
 RI atom bombardment mass spectrometry."  
 RI Biol. Chem. Hoppe Seyler 371:445-454(1990).  
 SC 1 FUNCTION: HYPERTETRAHAASEIC FACTORS ARE NEUROPEPTIDES THAT  
 SC EVALUATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS  
 SC THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).  
 SC 1 SIMILARITY: BELONGS TO THE AKH / HRTB / RPCH FAMILY.  
 LR PIR: A44560; A44560  
 LR PIR: A49843; A49843  
 LR PIR: S08995; S08995  
 DP Unclipped: IP8002347; AKH  
 DR PROSITE: P500256; AKH: 1  
 KW Neuropeptide: Amidation; Pyroglutamic carboxylic acid.  
 FI MCD-RES 1 1 PYROGLUTAMIC CARBOXYLIC ACID.  
 FI MCD-RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA: 99, MW: 85745775B9C452D6 CRC64;  
 Query Match: 18.2% Score 2: DB 1, Length 8;  
 Best Local Similarity 100.0% Pred. No. 1.3e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 6 PN 7  
 EB 1  
 DB 6 PN 7  
 RESULT 24  
 HFF2\_PERAM STANDARD; PRI: 8 AA.  
 AC 104549  
 DE 13-AUG-1997 (Rel. 05, Created)  
 DE 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)





EX 2 Biochem. 248:99-103(1997)  
 CC 1 FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-ENCODED PEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.

CC 1 CATALYTIC ACTIVITY: 4 ferrihydroxide + 2 H<sup>+</sup> → 4 ferrihydron + 2 H<sub>2</sub>O

CC 1 SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC 1 SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.

DE PIR: S77984; S77984.  
 DE InterPro: IPR001049; COX6A.  
 DE PROSITE: PS0129; COX6A; PARTIAL.

KW Oxidoreductase; Inner membrane; Mitochondrion.

PI NON\_TOX 1  
 PI NON\_TOX 1  
 SQ SEQUENCE 9 AA: 1136 MW: 62E3/2763774R 764.

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4  
 DB 1 KE 2

## RESULT 24

PARA\_PANKE ID PARA\_PANKE STANDARD; PRT; 9 AA.

AC P41873;  
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRFamide-like neuropeptide #2 (SALPNFLR amide).

OS Panagrellus redivivus.

CC Eukaryota; Metazoa; Nemertoda; Chordodonta; Rhabditida;

CC Panagrellidae; Panagrellinae; Panagrellini; Rhabditiidae;

CC NCBI\_TaxID-6233;

KN 111  
 KE SEQUENCE

RC KELLING 9226769; PubMed:1408999

RA Garry T.G., Price D.A., Bowman J.W., Winterford C.A., Mackenzie J.L.,

RA Garrison K.B., Williams J.F., Fricker A.K.

RA "Two FMRFamide-like peptides from the free living nematode

RI Panagrellus redivivus."

RL Peptides 13:209-214(1992).

CC 1 FUNCTION: MOACTIVE.

CC 1 TISSUE SPECIFICITY: NERVE DORSAL AND VENTRAL ROOTS OF SPINAL CORD

CC 1 CATALYTIC ACTIVITY: BELONGS TO THE FMRF (FMRFamide) FAMILY.

CC 1 SIMILARITY: BELONGS TO THE FMRF (FMRFamide) FAMILY.

CC 1 TISSUE SPECIFICITY: NERVE DORSAL AND VENTRAL ROOTS OF SPINAL CORD

CC 1 CATALYTIC ACTIVITY: BELONGS TO THE FMRF (FMRFamide) FAMILY.

CC 1 TISSUE SPECIFICITY: NERVE DORSAL AND VENTRAL ROOTS OF SPINAL CORD

CC 1 CATALYTIC ACTIVITY: BELONGS TO THE FMRF (FMRFamide) FAMILY.

CC 1 TISSUE SPECIFICITY: NERVE DORSAL AND VENTRAL ROOTS OF SPINAL CORD

CC 1 CATALYTIC ACTIVITY: BELONGS TO THE FMRF (FMRFamide) FAMILY.

CC 1 TISSUE SPECIFICITY: NERVE DORSAL AND VENTRAL ROOTS OF SPINAL CORD

CC 1 CATALYTIC ACTIVITY: BELONGS TO THE FMRF (FMRFamide) FAMILY.

CC Ascarididae; Ascaris.

CC NCBI\_TaxID-6253;

CC 11

RP SEQUENCE.

EX MEDLINE-95380362; PubMed-7651904;

RA Cowden C., Stetson A.O.W.

RA "Eight novel FMRFamide-like neuropeptides isolated from the nematode

RI Ascaris suum."

RL Peptides 16:491-503(1995).

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

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CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

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CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

CC 1- SIMILARITY: BELONGS TO THE FMRF (FMRFamide RELATED PEPTIDE)

SS Streptococcus agalactiae.  
 CC Plasmid pPS56, Plasmid pPS57, Plasmid pPS12, and plasmid pPS15.  
 CC Bacteria: Firmicutes; Bacillales; Streptococcaceae.  
 CC NCBI\_TaxID: 1280, 1311;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC SPECIES: Streptococcus STRAIN-4 (6); PLASMID-pPS57.  
 CC MEDLINE 92027692; PubMed 1929426.  
 CC Schwarz S., Cardoso M.  
 CC "Nucleotide sequence and phylogeny of a 9 kb plasmid from  
 CC acetyltransferase encoded by the plasmid pPS57 in Streptococcus  
 CC aureus".  
 CC Antimicrob. Agents Chemother. 45:1031-1036 (1992).  
 CC [2]  
 CC SEQUENCE FROM N.A.  
 CC SPECIES: Streptococcus PLASMID-pPS57.  
 CC MEDLINE 92386047; PubMed 1517173.  
 CC Cardoso M., Schwarz S.  
 CC "Nucleotide sequence and structural relationships of a  
 CC chloramphenicol acetyltransferase encoded by the plasmid pPS56 from  
 CC Streptococcus aureus".  
 CC J. Appl. Bacteriol. 72:287-293 (1992).  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC SPECIES: Streptococcus PLASMID-pPS112.  
 CC MEDLINE 86281759; PubMed 3865770.  
 CC Broekman R., Matzura H.  
 CC "Activation of the inducible chloramphenicol acetyltransferase gene  
 CC of the Streptococcus aureus plasmid pPS112".  
 CC EMBO J. 4:2295-2300 (1985).  
 CC [4]  
 CC SEQUENCE FROM N.A.  
 CC SPECIES: Streptococcus PLASMID-pPS112.  
 CC MEDLINE 94966667; PubMed 1461422.  
 CC Truesdell P., de Cespedes G., Horz F.  
 CC "Nucleotide sequence of the chloramphenicol resistance determinant of  
 CC the streptococcal plasmid pPS112".  
 CC Plasmid 28:272-276 (1992).  
 CC [5]  
 CC SwissProt entry is copyrighted. It is provided through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL database.  
 CC The European Bioinformatics Institute (EMBL) is not responsible for  
 CC use by non-profit institutions as long as the EMBL database is not way  
 CC modified and this statement is not removed. EMBL is not responsible  
 CC for any damage or loss of data caused by any use of the EMBL database.  
 CC For more information, please contact the EMBL database administrator  
 CC or send an email to: [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
 CC [6]  
 CC EMBL: M08533; AAA26632.1  
 CC EMBL: M08533; AAA16526.1  
 CC EMBL: X02672; AAA26630.1  
 CC EMBL: X00627; AAA43217.1  
 CC EMBL: X05462; AAA46454.1  
 CC EMBL: B24362; B24362  
 CC EMBL: S0494; S0494.  
 CC Leader peptide, Antibiotic resistance, Plasmid.  
 CC SEQUENCE 9 AA: 1074 MW: 50508.66065835 CP 54  
 CC  
 CC Query Match 16.2% Score 2; DB 1; Length 9;  
 CC Best Local Similarity 100.0% Pred. No. 1.9e+05;  
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY : 2 KK 3  
 CC II :  
 CC DE : 2 KK 3  
 CC  
 CC RESULT 17  
 CC ID: RT51-ROVIN STANDARD; PRT: 9 AA.  
 CC AC: P82923;  
 CC DT: 28 FEB 2003 (Rel. 41, Created)  
 CC DI: 28 FEB 2003 (Rel. 41, Last sequence update)  
 CC DJ: 28 FEB 2003 (Rel. 41, Last annotation update)

DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).  
 CC MRPS33  
 CC Bos taurus (Bovine).  
 CC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 CC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:  
 CC Bovidae: Bovinae: Bos.  
 CC NCBI\_TaxID: 9914;  
 CC [1]  
 CC SEQUENCE  
 CC Tissue: Liver;  
 CC MEDLINE 21276494; PubMed 11279227;  
 CC Koz E.C., Burkhardt W., Bickelstein K., Moseley A., Spremulli L.L.;  
 CC "The small subunit of the mammalian mitochondrial ribosome:  
 CC identification of the full complement of ribosomal proteins present".  
 CC J. Biol. Chem. 266:19463-19474 (1991).  
 CC [2]  
 CC SUBUNIT: Component of the mitochondrial ribosome small subunit  
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
 CC 1. SUBCELLULAR LOCATION: Mitochondrial.  
 CC Ribosomal protein; Mitochondrion.  
 CC NON\_TER 1 1  
 CC N-TER 9 9  
 CC SEQUENCE 9 AA: 1042 MW: 10413.777680589 CMC64;  
 CC  
 CC Query Match 19.2% Score 2; DB 1; Length 9;  
 CC Best Local Similarity 100.0% Pred. No. 1.9e+05;  
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY : AK 2  
 CC II :  
 CC DE : 6 AK 9  
 CC  
 CC RESULT 34  
 CC ID: THYF-F10 STANDARD; PRT: 9 AA.  
 CC AC: P01255;  
 CC DT: 21 JUL 1986 (Rel. 01, Created)  
 CC DI: 21 JUL 1986 (Rel. 01, Last sequence update)  
 CC DJ: 28 FEB 2003 (Rel. 41, Last annotation update)  
 CC DE: Thymic factor.  
 CC Sus scrofa (Pig).  
 CC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 CC Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.  
 CC NCBI\_TaxID: 9824;  
 CC [1]  
 CC SEQUENCE  
 CC MEDLINE 78926571; PubMed 914862;  
 CC Plean J.-M., Bardenne M., Blomquist Y., Bach J.-F.;  
 CC "Structural study of circulating thymic factor: a peptide isolated  
 CC from pig serum. II. Amino acid sequence.";  
 CC J. Biol. Chem. 252:8045-8047 (1977).  
 CC [2]  
 CC MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL  
 CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.  
 CC PIR: A01523; YEPG.  
 CC Pyroglutamine carboxylic acid.  
 CC MCQ-RES 1  
 CC SEQUENCE 9 AA: 876 MW: 105008.786605833 CMC64;  
 CC  
 CC Query Match 19.2% Score 2; DB 1; Length 9;  
 CC Best Local Similarity 100.0% Pred. No. 1.9e+05;  
 CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY : AK 2  
 CC II :  
 CC DE : 2 AK 3  
 CC  
 CC RESULT 35  
 CC ID: UJAD\_HUMAN STANDARD; PRT: 9 AA.  
 CC AC: P31929;  
 CC DT: 31 JUL 1993 (Rel. 26, Created)  
 CC DI: 31 JUL 1993 (Rel. 26, Last sequence update)

16 CC 2001 (Ref. 40, Last annotation update)  
 17 Unknown protein from 20-page of liver tissue (Spad. 199) (Fragment).  
 18 Homo sapiens (Human).  
 19 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 20 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 21 NCBI TaxID 9606;  
 22 [1]  
 23 TISSUE: Liver;  
 24 MEDLINE 9414799; PubMed 8414874;  
 25 Bader G, Frutiger S, Pappert N, Pospisil C, Sanchez J, C...  
 26 Lissot J, B, Bairoch A, Appel K, B, Bairoch A, B...  
 27 Human liver protein map: update 1999.  
 28 Electrophoresis 14:1216-1222(1999).  
 29 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE PROTEIN W...  
 30 PROTEIN IS: 6, 115 MW IS: 15 KDa;  
 31 SWISS-2DPAGE: P11949;  
 32 NON\_TER 9  
 33 SEQUENCE 9 AA: 1129 MW: 102204 IPI: 1322 CRC64;  
 34  
 35 Query Match 18.2%; Score 2; DB 1; Length 9;  
 36 Best Local Similarity 100.0%; Pred. No. 1.3e-04;  
 37 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 38  
 39 2 KK 4  
 40 3 KK 4  
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US Bothrops insularis (Island Jararaca) (Queimada Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalidae; Bothrops.  
 CX NCBI TaxID 8723;  
 RN [1]  
 RP SEQUENCE;  
 RC TISSUE: Venom;  
 RX MEDLINE 9451557; PubMed 2496615;  
 RA Centro A, Centro V, Centro A, Centro A, Centro A, R...  
 RI Primary structure and biological activity of bradykinin potentiating  
 PT peptides from Bothrops insularis snake venom.\*;  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 CX PIR: H37195; H37196;  
 KW Hypotensive agent; Pyroglutamate; PYROGLUTAMIC ACID.  
 FT MOD\_RES;  
 SQ SEQUENCE 10 AA: 1174 MW: 2583554576165D8 CRC64;  
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10 NOV 1995 (rel. 42, last sequence update)  
 11 16-OCT 2001 (rel. 40, last annotation update)  
 12 quinolone 2-oxidoreductase, guinea chain (rel. 33-99.1) (fragment)  
 13 Camamonas testosterone (Pseudomonas testosterone)  
 14 bacterium; Proteobacteria; Betaproteobacteria; workholobactales;  
 15 Gammaproteobacteria; Comamonas  
 16 NCBI TaxID: 255  
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CC - SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.  
 KW CHLOROPLAST: ATP BINDING.  
 FT NON\_TER 1  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA: 1171 MW: 60450602672B1EA6 CRC64:  
 Query Match: 10.2%, Score 2; DB 1; Length 10;  
 Best Local Similarity: 100.0%; Prod No. 1.3e+04;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0;  
 07 1 AK 2  
 1  
 9 AK 10  
 DB  
 Search completed: September 30, 2003, 10:26:07  
 Job time: 7.25 secs



90	2	18.2	9	12	07.064	Q91066 polyomavirus	163	2	18.2	10	12	Q900X1
91	2	18.2	9	13	Q91067	Q900X9 polyomavirus	164	2	18.2	10	12	Q900X9
92	2	18.2	9	13	Q91068	Q91067 polyomavirus	165	2	18.2	10	12	Q91072
93	2	18.2	10	1	Q91069	Q91068 polyomavirus	166	2	18.2	10	14	Q91074
94	2	18.2	10	2	Q91070	Q91069 polyomavirus	167	2	18.2	10	14	Q91074
95	2	18.2	10	2	Q91071	Q91070 polyomavirus	168	2	18.2	11	2	Q91075
96	2	18.2	10	2	Q91072	Q91071 polyomavirus	169	2	18.2	11	2	Q91076
97	2	18.2	10	2	Q91073	Q91072 polyomavirus	170	2	18.2	11	2	Q91077
98	2	18.2	10	2	Q91074	Q91073 polyomavirus	171	2	18.2	11	2	Q91078
99	2	18.2	10	2	Q91075	Q91074 polyomavirus	172	2	18.2	11	2	Q91079
100	2	18.2	10	2	Q91076	Q91075 polyomavirus	173	2	18.2	11	2	Q91080
101	2	18.2	10	2	Q91077	Q91076 polyomavirus	174	2	18.2	11	2	Q91081
102	2	18.2	10	2	Q91078	Q91077 polyomavirus	175	2	18.2	11	2	Q91082
103	2	18.2	10	2	Q91079	Q91078 polyomavirus	176	2	18.2	11	2	Q91083
104	2	18.2	10	2	Q91080	Q91079 polyomavirus	177	2	18.2	11	2	Q91084
105	2	18.2	10	2	Q91081	Q91080 polyomavirus	178	2	18.2	11	2	Q91085
106	2	18.2	10	2	Q91082	Q91081 polyomavirus	179	2	18.2	11	2	Q91086
107	2	18.2	10	2	Q91083	Q91082 polyomavirus	180	2	18.2	11	2	Q91087
108	2	18.2	10	2	Q91084	Q91083 polyomavirus	181	2	18.2	11	2	Q91088
109	2	18.2	10	2	Q91085	Q91084 polyomavirus	182	2	18.2	11	2	Q91089
110	2	18.2	10	2	Q91086	Q91085 polyomavirus	183	2	18.2	11	2	Q91090
111	2	18.2	10	2	Q91087	Q91086 polyomavirus	184	2	18.2	11	2	Q91091
112	2	18.2	10	2	Q91088	Q91087 polyomavirus	185	2	18.2	11	2	Q91092
113	2	18.2	10	2	Q91089	Q91088 polyomavirus	186	2	18.2	11	2	Q91093
114	2	18.2	10	2	Q91090	Q91089 polyomavirus	187	2	18.2	11	2	Q91094
115	2	18.2	10	2	Q91091	Q91090 polyomavirus	188	2	18.2	11	2	Q91095
116	2	18.2	10	2	Q91092	Q91091 polyomavirus	189	2	18.2	11	2	Q91096
117	2	18.2	10	2	Q91093	Q91092 polyomavirus	190	2	18.2	11	2	Q91097
118	2	18.2	10	2	Q91094	Q91093 polyomavirus	191	2	18.2	11	2	Q91098
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124	2	18.2	10	2	Q91100	Q91099 polyomavirus	197	2	18.2	11	2	Q91104
125	2	18.2	10	2	Q91101	Q91100 polyomavirus	198	2	18.2	11	2	Q91105
126	2	18.2	10	2	Q91102	Q91101 polyomavirus	199	2	18.2	11	2	Q91106
127	2	18.2	10	2	Q91103	Q91102 polyomavirus	200	2	18.2	11	2	Q91107
128	2	18.2	10	2	Q91104	Q91103 polyomavirus	201	2	18.2	11	2	Q91108
129	2	18.2	10	2	Q91105	Q91104 polyomavirus	202	2	18.2	11	2	Q91109
130	2	18.2	10	2	Q91106	Q91105 polyomavirus	203	2	18.2	11	2	Q91110
131	2	18.2	10	2	Q91107	Q91106 polyomavirus	204	2	18.2	11	2	Q91111
132	2	18.2	10	2	Q91108	Q91107 polyomavirus	205	2	18.2	11	2	Q91112
133	2	18.2	10	2	Q91109	Q91108 polyomavirus	206	2	18.2	11	2	Q91113
134	2	18.2	10	2	Q91110	Q91109 polyomavirus	207	2	18.2	11	2	Q91114
135	2	18.2	10	2	Q91111	Q91110 polyomavirus	208	2	18.2	11	2	Q91115
136	2	18.2	10	2	Q91112	Q91111 polyomavirus	209	2	18.2	11	2	Q91116
137	2	18.2	10	2	Q91113	Q91112 polyomavirus	210	2	18.2	11	2	Q91117
138	2	18.2	10	2	Q91114	Q91113 polyomavirus	211	2	18.2	11	2	Q91118
139	2	18.2	10	2	Q91115	Q91114 polyomavirus	212	2	18.2	11	2	Q91119
140	2	18.2	10	2	Q91116	Q91115 polyomavirus	213	2	18.2	11	2	Q91120
141	2	18.2	10	2	Q91117	Q91116 polyomavirus	214	2	18.2	11	2	Q91121
142	2	18.2	10	2	Q91118	Q91117 polyomavirus	215	2	18.2	11	2	Q91122
143	2	18.2	10	2	Q91119	Q91118 polyomavirus	216	2	18.2	11	2	Q91123
144	2	18.2	10	2	Q91120	Q91119 polyomavirus	217	2	18.2	11	2	Q91124
145	2	18.2	10	2	Q91121	Q91120 polyomavirus	218	2	18.2	11	2	Q91125
146	2	18.2	10	2	Q91122	Q91121 polyomavirus	219	2	18.2	11	2	Q91126
147	2	18.2	10	2	Q91123	Q91122 polyomavirus	220	2	18.2	11	2	Q91127
148	2	18.2	10	2	Q91124	Q91123 polyomavirus	221	2	18.2	11	2	Q91128
149	2	18.2	10	2	Q91125	Q91124 polyomavirus	222	2	18.2	11	2	Q91129
150	2	18.2	10	2	Q91126	Q91125 polyomavirus	223	2	18.2	11	2	Q91130
151	2	18.2	10	2	Q91127	Q91126 polyomavirus	224	2	18.2	11	2	Q91131
152	2	18.2	10	2	Q91128	Q91127 polyomavirus	225	2	18.2	11	2	Q91132
153	2	18.2	10	2	Q91129	Q91128 polyomavirus	226	2	18.2	11	2	Q91133
154	2	18.2	10	2	Q91130	Q91129 polyomavirus	227	2	18.2	11	2	Q91134
155	2	18.2	10	2	Q91131	Q91130 polyomavirus	228	2	18.2	11	2	Q91135
156	2	18.2	10	2	Q91132	Q91131 polyomavirus	229	2	18.2	11	2	Q91136
157	2	18.2	10	2	Q91133	Q91132 polyomavirus	230	2	18.2	11	2	Q91137
158	2	18.2	10	2	Q91134	Q91133 polyomavirus	231	2	18.2	11	2	Q91138
159	2	18.2	10	2	Q91135	Q91134 polyomavirus	232	2	18.2	11	2	Q91139
160	2	18.2	10	2	Q91136	Q91135 polyomavirus	233	2	18.2	11	2	Q91140
161	2	18.2	10	2	Q91137	Q91136 polyomavirus	234	2	18.2	11	2	Q91141
162	2	18.2	10	2	Q91138	Q91137 polyomavirus	235	2	18.2	11	2	Q91142





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Query Match: 36.48; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 9; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 5
ID 7 KKK 10

RESULT 2
Q9R735 PRELIMINARY: PRT: 8 AA.
ID Q9R735
AC Q9R735
DT 01-MAY-2000 (EMBLrel. 13, Created)
DT 01-MAY-2000 (EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (EMBLrel. 19, Last annotation update)
DE FKBP-12 (Fragment)
GN FKBP1
OS Mus musculus (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartida; Haplorhina; Homi-
OC NCBI_TaxID 9606;
SN 111
SN 111
RX MEDLINE 9215747; PubMed 104426;
RA White G.R.M., Varley J.M., Hargway J.,
RI "Genomic structure and expression profile of a 71K gene
RI variably expressed in breast cancer cell lines."
RI Biochem. Biophys. Acta 1491:75-92(2000).
ER EMBL: A244569; CAB60204.1;
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 1025 MW: 4559076344AAB6 CB664;

Query Match: 27.3%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKK 9
ID 111
ID 4 KKK 6

RESULT 3
Q9R735 PRELIMINARY: PRT: 8 AA.
ID Q9R735
AC Q9R735
DT 01-JUN-1998 (EMBLrel. 36, Created)
DT 01-JUN-1998 (EMBLrel. 36, Last sequence update)
DT 01-NOV-1999 (EMBLrel. 12, Last annotation update)
DE Apoptoprotein A-II (APO-AII) (Fragment)
GN APCA2
OS Mus musculus (Western wild mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus-
OC NCBI_TaxID 10096;
SN 111
SN 111
RX MEDLINE 94319082; PubMed 8043949;
RA Ko M.S., Wang X., Horton J.H., Hagen M.L., Takahashi Y.,
RA Nadeau J.H.,
RI "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."
RI Mamm. Genome 5:349-355(1994).

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Query Match: 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EXP 6
ID 111
ID 5 EXP 5

RESULT 4
Q9EZ14 PRELIMINARY: PRT: 9 AA.
ID Q9EZ14
AC Q9EZ14
DT 01-MAR-2001 (EMBLrel. 16, Created)
DT 01-MAR-2001 (EMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (EMBLrel. 19, Last annotation update)
DE SPAS (Fragment)
GN SPAS
OS Sodalis glossinidius
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis
OC NCBI_TaxID 63612;
SN 111
SN 111
RX MEDLINE 2117142; PubMed 11172045;
RA Dale C., Young S.A., Haydon D.T., Welburn S.C.,
RI "The insect endosymbiont Sodalis glossinidius utilizes a type III
RI secretion system for cell invasion."
RI Proc. Natl. Acad. Sci. U.S.A. 98:1883-1888(2001).
ER EMBL: AF06650; AAG48607.1;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA: 1035 MW: 8185633801A33455 CRC64;

Query Match: 27.3%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EXP 6
ID 111
ID 6 EXP 8

RESULT 5
Q9R735 PRELIMINARY: PRT: 9 AA.
ID Q9R735
AC Q9R735
DT 01-MAY-2000 (EMBLrel. 13, Created)
DT 01-MAY-2000 (EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (EMBLrel. 19, Last annotation update)
DE FKBA protein (Fragment)
GN FKBA
OS Streptomyces chrysomallus
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces
OC NCBI_TaxID 1899;
SN 111
SN 111
RX MEDLINE 94341259; PubMed 8062824;
RA Pahl A., Keller U.;
RI "Streptomyces chrysomallus FKBP-13 is a novel immunophilin consisting
RI of two FK506-binding domains with its gene transcriptionally coupled
RI to the FKBP-12 gene."
RI EMBO J. 13:472-480(1994).
ER EMBL: Z44523; CAA84282.1;

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20 090037 2 EXP 9
RESULT 9
Q90037 PRELIMINARY: PRI: 12 AA.
AC Q90037
DE 01-MAY-2000 (EMBLrel. 13, last sequence update)
DI 01-MAY-2000 (EMBLrel. 13, last sequence update)
ID 01-JUN-2002 (EMBLrel. 21, last annotation update)
DE Alpha B crystallin (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Kladogram: Metazoa; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI TaxID 9606;
RN 1;
RP SEQUENCE
PP RECLINE 2218444; PubMed 146006;
RA Kato K., Shimada H., Goto S., Inaguma Y., Morishita K., Asano F.,
RI "Purification of small heat shock protein with alpha B crystallin
RI from human skeletal muscle."
RL 5. Biol. Chem. 267:7718-7725(1992).
FT NON-TER 1 12
FT NON-TER 12 12
SQ SEQUENCE 12 AA: 1268 MW: 1476052900018205 CRC64;
Query Match 27.9% Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EXP 5
DI 2 EXP 4

RESULT 12
P82325 PRELIMINARY: PRI: 12 AA.
AC P82325
DE 01-JUN-2000 (EMBLrel. 14, created)
DI 01-JUN-2000 (EMBLrel. 14, last sequence update)
ID 01-JUL-2000 (EMBLrel. 15, last annotation update)
DE Unknown protein from 20 pair of thylakoid (SPOT106) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
CX NCBI TaxID 3886;
RN 1;
RP SEQUENCE
PP SEQUENCE SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RA STRAIN 09. DE GRAY, TISSUE LEAF;
RX MEDLINE 2018728; PubMed 10715420;
RA Bellini M., Friso G., Kalme U.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk R.J.;
RI "Proteomics of the chloroplast: systematic identification and
RI targeting analysis of internal and peripheral thylakoid proteins."
RL Plant Cell 12:419-443(2000).
OC 1 SUBCELLULAR LOCATION CHLOROPLAST; THYLAKOID MEMBRANE LUMEN (W
OC PERIPHERY.
OC 1- DEVELOPMENTAL STAGE UNDEVELOPED AND FULLY DEVELOPED LEAVES
OC 1- MISCELLANEOUS ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
OC PROTEIN IS: 5.0, 11S MW IS: 18.2 KDA.
KW Chloroplast; Thylakoid membrane
FT NON-TER 12 12
FT NON-TER 12 12
SQ SEQUENCE 12 AA: 1236 MW: 14627950305405452 CRC64;
Query Match 27.9% Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EXP 9
DI 6 EXP 8

RESULT 13
P82325

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20 090037 2 EXP 9
RESULT 9
Q90037 PRELIMINARY: PRI: 12 AA.
AC Q90037
DE 01-MAY-2000 (EMBLrel. 13, last sequence update)
DI 01-MAY-2000 (EMBLrel. 13, last sequence update)
ID 01-JUN-2002 (EMBLrel. 21, last annotation update)
DE Alpha B crystallin (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Kladogram: Metazoa; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI TaxID 9606;
RN 1;
RP SEQUENCE
PP RECLINE 2218444; PubMed 146006;
RA Kato K., Shimada H., Goto S., Inaguma Y., Morishita K., Asano F.,
RI "Purification of small heat shock protein with alpha B crystallin
RI from human skeletal muscle."
RL 5. Biol. Chem. 267:7718-7725(1992).
FT NON-TER 1 12
FT NON-TER 12 12
SQ SEQUENCE 12 AA: 1268 MW: 1476052900018205 CRC64;
Query Match 27.9% Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EXP 5
DI 2 EXP 4

RESULT 12
P82325 PRELIMINARY: PRI: 12 AA.
AC P82325
DE 01-JUN-2000 (EMBLrel. 14, created)
DI 01-JUN-2000 (EMBLrel. 14, last sequence update)
ID 01-JUL-2000 (EMBLrel. 15, last annotation update)
DE Unknown protein from 20 pair of thylakoid (SPOT106) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
CX NCBI TaxID 3886;
RN 1;
RP SEQUENCE
PP SEQUENCE SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RA STRAIN 09. DE GRAY, TISSUE LEAF;
RX MEDLINE 2018728; PubMed 10715420;
RA Bellini M., Friso G., Kalme U.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk R.J.;
RI "Proteomics of the chloroplast: systematic identification and
RI targeting analysis of internal and peripheral thylakoid proteins."
RL Plant Cell 12:419-443(2000).
OC 1 SUBCELLULAR LOCATION CHLOROPLAST; THYLAKOID MEMBRANE LUMEN (W
OC PERIPHERY.
OC 1- DEVELOPMENTAL STAGE UNDEVELOPED AND FULLY DEVELOPED LEAVES
OC 1- MISCELLANEOUS ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN
OC PROTEIN IS: 5.0, 11S MW IS: 18.2 KDA.
KW Chloroplast; Thylakoid membrane
FT NON-TER 12 12
FT NON-TER 12 12
SQ SEQUENCE 12 AA: 1236 MW: 14627950305405452 CRC64;
Query Match 27.9% Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EXP 9
DI 6 EXP 8

RESULT 13
P82325

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ID Q66746 PRELIMINARY: PRT: 13 AA.
AC Q66746
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DI 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Analogue of IIN-2B (Fragment).
GN Analogue of IIN-2B.
OS Insect softens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID: 9606.
RN 1.
RP SEQUENCE FROM N.A.
RX MEDLINE 20422911; PubMed 10964117.
RA Mezquita J., Mezquita P., Montserrat P., Mezquita B., Francisco V.,
RA Villarasa X., Mezquita C.
RT "Genomic structure and alternative splicing of chicken antioprotein
RT 2."
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DB EMBL: A028780; CAC08179.1.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1548 MW: 334196A1G4F9P02 CRF64;

Query Match: 27.3%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKK 4
DB 1
2 KKK 4

RESULT 18
Q66743
ID Q66743 PRELIMINARY: PRT: 13 AA
AC Q66743
DT 01-MAR-2001 (TrEMBLrel. 24, Created)
DI 01-MAR-2001 (TrEMBLrel. 24, Last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 24, Last annotation update)
DE Myosin in (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Saurimordia; Muridae; Mus.
OX NCBI_TaxID: 10090.
RN 11.
RP SEQUENCE FROM N.A.
RX STRAIN BALB/c; TISSUE-Kidney;
RX MEDLINE 20444280; PubMed 1087616.
RA Al-Jel P.M., Seddiq N., Gaudin N., Gaudin A., Gaudin N.,
RA Velasco P., Seddiq N., Gaudin N., Gaudin A., Gaudin N.,
RT "Myosin is a novel member of the myosin family and is highly
RT expressed in human muscle."
RL Biochem. Biophys. Res. Commun. 275:643-651(2000).
DB EMBL: AF545444; AAN28707.1.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1445 MW: 309506A1P0F0E CRF64;

Query Match: 27.3%; Score 4; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 4 KKK 6
DB 1
1 KKK 4

RESULT 19
Q66746
ID Q66746 PRELIMINARY: PRT: 13 AA.
AC Q66746
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Polymerase (Fragment).
OS Equine infectious anemia virus.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID: 11655.
RN 11.
RP SEQUENCE FROM N.A.
RX MEDLINE 90204701; PubMed 21570667.
RA Naiman S., Yaniv A., Sherman L., Ironack S.R., Garit A.,
RT "Pattern of transcription of the genome of equine infectious anemia
RT virus."
RL J. Virol. 64:1819-1843(1990).
DB EMBL: M33845; AAG6411.1.
FT NON_TER 1
SQ SEQUENCE 13 AA: 1493 MW: 97803905A92321 CRF64;

Query Match: 27.4%; Score 3; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KPN 7
DB 11
11 KPN 13

RESULT 20
Q6X4F5
ID Q6X4F5 PRELIMINARY: PRT: 13 AA.
AC Q6X4F5
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DI 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein z5883.
OS Escherichia.
GN z5883.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID: 83344.
RN 11.
RP SEQUENCE FROM N.A.
RX STRAIN 0157:H7 / HUS-05 / APEC 760927;
RX MEDLINE 21074945; PubMed 11201511.
RA Perna N.J., Plunkett G., III, Hargill V., Mau R., Glasner J.B.,
RA Rose G.J., Mayhew G.E., Evans P.S., Gregor J., Kirkpatrick B.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.F., Polamoussis K.,
RA Apodaca J., Anantharaman I.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,
RT "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
RL Nature 409:529-533(2001).
DB EMBL: AE005659; AAG59469.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 13 AA: 1526 MW: 4145922739041877 CRF64;

Query Match: 27.4%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 6
6 AKK 10

RESULT 21
Q56750

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RA Cooperand N.G., Potter S.S.:  
RT "Identification of 10 murine hemebox genes."  
RC Proc. Natl. Acad. Sci. U.S.A. 86:10766-10770(1989).  
Q9 InterPro: IPSC01456; Hemebox.  
Q9 Pfam: PF00046; Hemebox_1.  
Q9 PROSITE: PS00071; HEMEBOX_2; 1.  
FT NON TER 1 1  
FT NON TER 14 14  
SQ SEQUENCE 14 AA: 1859 MW: 7818000A:9AD04 (8974)  
  
Query Match: 27.4%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 KEK 5  
DB 1  
+ KEK 1;  
  
RESULT 26  
P22801 PRELIMINARY: PRT: 14 AA.  
AC P22801  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE Temporalin TBR.  
OS Rana temporaria.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana;  
OX NCBI_TaxID:5817;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RX MEDLINE:2217703; PubMed:10651828;  
RA Carey J., Ward V., Li Z., Griffiths R., Knapp A., Pate J.E.,  
RA Garton J.M.  
RT "Peptides with antimicrobial activity from four different families  
isolated from the skins of the North American frogs Rana intermedia,  
Rana berlandieri, and Rana pipiens."  
RL Exp. J. Biochem. 267:894-900(2000).  
Q9 FUNCTION: ANTI-BACTERIAL ACTIVITY AGAINST GRAM POSITIVE BACTERIA  
Q9 Q9 FUNCTION: WEAK ACTIVITY AGAINST GRAM NEGATIVE BACTERIUM ESCHERICHIA  
Q9 Q9 THE YEAST CALICANS.  
Q9 Q9 MASS SPECTROMETRY: MW:1576; METHOD: ELECTRIC SPRAY  
Q9 Q9 SIMILARITY: BELONGS TO THE SEVININ/ESTULENTIN/GABDIN/RN/SN  
Q9 Q9 FAMILY.  
KW Anticleral Acidation; Fungicide.  
FT MOWS 14 14 AMIGADIN.  
SQ SEQUENCE 14 AA: 1576 MW: 15470000:94044 (8974)  
  
Query Match: 27.4%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AKK 3  
DB 1  
+ AKK 1;  
  
RESULT 27  
Q47612 PRELIMINARY: PRT: 15 AA.  
AC Q47612  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE KPSG protein (Fragment).  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI_TaxID:562;
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RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K-12;  
RX MEDLINE:85267249; PubMed:4894886;  
RA Schrier J., Isom S., Cumberledge A.G., Isom K.,  
RT "Unstable mutations caused by regional tandem multiplications in the  
K1 gene for ribosomal protein S4 show thermosensitivity in Escherichia  
K1 coli."  
RL Mol. Gen. Genet. 199:265-276(1985).  
DK EMBL: M25824; AAA2454.1; 1.  
FT NON TER 1 1  
SQ SEQUENCE 15 AA: 1545 MW: 7456155A:4A8EU05 CRC64;  
  
Query Match: 27.4%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AKK 4  
DB 1  
+ AKK 5  
  
RESULT 28  
Q9UBK0 PRELIMINARY: PRT: 15 AA.  
AC Q9UBK0  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Retal tissue-specific alkaline phosphatase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID:9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE:94092415; PubMed:14585452;  
RA Nishihara Y., Hayashi Y., Adachi I., Koyama I., Stigbrand T.,  
RA Hirano K.  
RT "Chemical nature of intestinal-type alkaline phosphatase in human  
RT kidney."  
RL Clin. Chem. 38:2539-2542(1992).  
SQ SEQUENCE 15 AA: 1931 MW: 9A28FDE13F01F716 CRC64;  
  
Query Match: 27.4%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 KEK 5  
DB 1  
+ KEK 7  
  
RESULT 29  
Q9UC07 PRELIMINARY: PRT: 15 AA.  
AC Q9UC07  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE Midline (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID:9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE:94059921; PubMed:8241100;  
RA Novotny W.F., Matti T., Mehta R.L., Milner P.G.,  
RT "Identification of novel heparin-releasable proteins, as well as the  
RT cytokines midline and pleiotrophin, in human postheparin plasma."  
RC Arterioscler. Thromb. 13:1798-1805(1993).  
SQ SEQUENCE 15 AA: 1527 MW: C34B6B97878474AC CRC64;
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Query Match      27.3%  Score 3;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 AKK 3
DB      1 1
      2 AKK 4

RESULT 40
Q9U0N2
ID Q9U0N2 PRELIMINARY: PRT: 15 AA
AC Q9U0N2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 15, Last annotation update)
DE Fructose-1,6-bisphosphate aldolase A (EC 4.1.2.13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN 11
RP SEQUENCE
RX MEDLINE:92453128; PubMed:1359685;
RA Lee K.N., Maxwell M.D., Patterson M.K. et al., Borekshahler P.O.,
RA Conway E.
RT "Identification of transaminase substrates in HT29 colon cancer
RT cells: use of 5-(biotinamido)pentylamine as a transaminase-
RT specific probe."
KL Biochim. Biophys. Acta 1136:12-16(1992).
DR HSSP: P04075; ZALD.
SQ SEQUENCE 15 AA; 1805 MW; 8D07546D7FC04F6; CRC64;

Query Match      27.3%  Score 3;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      2 KKE 4
DB      1 1
      12 KKE 14

RESULT 41
Q81ZQ0
ID Q81ZQ0 PRELIMINARY: PRT: 15 AA
AC Q81ZQ0
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase A catalytic subunit beta (Fragment).
GN PKA-B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN 11
RP SEQUENCE FROM N.A.
RA Wu K.-J., Mattioli M., Morse H.C., Dalla-Favera R.
RT "c-MYC activates protein kinase A (PKA) by direct transcriptional
RT activation of the PKA catalytic subunit beta (PKA-Cb) gene."
KL Oncogene 0:0(2002).
DR ENBL: AF538872; AAN16454.1; -.
KW Kinase.
FT NON-TER 15 15
SQ SEQUENCE 15 AA; 1480 MW; 52FE5695C19870A; CRC64;

Query Match      27.3%  Score 3;  DB 4;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 AKK 3
DB      1 1
      1 AKK 3
      13 AKK 15

RESULT 44
Q9AT15
ID Q9AT15 PRELIMINARY: PRT: 15 AA
AC Q9AT15
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Plasma membrane H+-ATPase (Fragment).
GN LHA1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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DT Spermatophyta: Magnoliophyta: eudicotyledons: euro eudicots:
DE Asteridiales: Solanales: Solanaceae: Solanum
OX NCBI_taxid:4081;
GN Sol
RN SEQUENCE FROM N.A.
RC STRAIN:cv. VFNT Cherry;
RA Bawa N.N., Wermers L.E., Meyer L.D., Chetelat A.L., Bonnet A.B.;
RT "Molecular cloning of tomato plasma membrane H+-ATPase";
RL Life Sci. Adv. Plant Physiol. 94:11-14 (1994);
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN:cv. VFNT Cherry;
RA Bawa N.N., Bonnet A.B.;
RT "Assessment of the number and expression of P-type H+-ATPase genes
in tomato";
RL Life Sci. Adv. Plant Physiol. 106:547-557 (1994);
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN:cv. VFNT Cherry;
RA Bahmani Z., Bawa N.N.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF355103; AAC31206.1;
FT NON_TER 15
SQ SEQUENCE 15 AA: 1673 MW: 55704775.20858096 P1:64;

Query Match 27.3% Score 4 DB 10 Length 15;
Best Local Similarity 100.0% Pred. No. 1.3e+05;
Matches 37 Conservative 0 Mismatches 0 Indels 0 Gaps 0;

QY 4 KK 5
DB 3 EXP 5

RESULT 35
Q9SG16 PRELIMINARY: PRT: 15 AA
ID Q9SG16
DT 03-MAY-2003 (TrEMBLrel. 13, Created)
ET 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
ET 01-JUL-2002 (TrEMBLrel. 22, Last annotation update)
DE Translation elongation factor (Fragment).
OS Oryza sativa (rice).
OC Eukaryota: Viridiplantae: Streptophyta: Erythropbyt: Eriophyta:
OC Spermatophyta: Magnoliophyta: Eudicotyledons: Eurosid: Eudicots:
OC Asteridiales: Myrtales: Myrtaceae: Myrtaceae:
OX NCBI_taxid:4530;
GN Sol
RN SEQUENCE FROM N.A.
RC STRAIN:cv. VFNT Cherry;
RT "Predictable expression of translation elongation factor in a model plant
system";
RL Acta Bot. Sin. 47:800-806 (1999);
DR EMBL: AF067195; AAC79991.1;
DE Characterization of Q9SG16;
KW Elongation factor;
FT NON_TER 1
SQ SEQUENCE 15 AA: 1514 MW: 9255456.0969795 P1:61;

Query Match 27.4% Score 4 DB 10 Length 15;
Best Local Similarity 100.0% Pred. No. 1.3e+05;
Matches 37 Conservative 0 Mismatches 0 Indels 0 Gaps 0;

QY 1 KK 5
DB 12 KK 14

RESULT 36
Q9F712 PRELIMINARY: PRT: 15 AA
ID Q9F712
DT 03-MAY-2003 (TrEMBLrel. 13, Created)

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DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
DE Hypothetical: 1.0 kDa protein (fragment).
GN YCFG.
OS Escherichia coli.
OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales;
OC Enterobacteriaceae: Escherichia.
OX NCBI_taxid:562;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN K12;
RX MEDLINE-97061202; PubMed-6255242;
RA Oshata T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Ikada T., Itoh T., Kajiura M., Kanai K., Kashimoto K.,
RA Kimura S., Katagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiechi T.;
RT "A 718-kD DNA sequence of Escherichia coli K-12 Genome Corresponding
to the 12.7-28.0 min Region on the Linkage Map.";
RL DNA Res. 3:137-155 (1996);
DR EMBL: D90705; BAA3410.1;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA: 964 MW: 261335BD0048476A CRC64;

Query Match 18.2% Score 2 DB 2 Length 8;
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 27 Conservative 0 Mismatches 0 Indels 0 Gaps 0;

QY 3 KK 4
DB 7 KK 8

RESULT 37
Q9AGP4 PRELIMINARY: PRT: 8 AA
ID Q9AGP4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
ET 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Serine hydroxymethyltransferase (Fragment).
GN GlyA.
OC Archaea: Crenarchaeota: Thermococcales: Thermococcus.
OC Bacteria: Actinobacteria: Actinomycetales: Actinomycetales;
OC Micrococcales: Micrococcales: Actinobacter.
OX NCBI_taxid:153502;
GN GlyA.
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN:LIN;
RA Meskys R., Bartis R., Casallo V., Bosian J., Scrutton N.S.;
RT "Genetic organization of the genes involved in dimethylglycine and
PI sarcosine degradation in Actinobacter spp.: implications for glycine
RT betaine catabolism";
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF22478; AAC36465.1;
KW Methyltransferase; Transferrase;
FT NON_TER 1
SQ SEQUENCE 8 AA: 896 MW: 651870533372457 CRC64;

Query Match 18.2% Score 2 DB 2 Length 8;
Best Local Similarity 100.0% Pred. No. 8.3e+05;
Matches 27 Conservative 0 Mismatches 0 Indels 0 Gaps 0;

QY 2 KK 3
DB 4 KK 5

RESULT 38
Q9AG64 PRELIMINARY: PRT: 8 AA
ID Q9AG64
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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Q94954:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P120 (Fragment).
GN P120.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatidae; Mycoplasma.
OX NCBI_TaxID:2098;
RN [1].
RC STRAIN:VZ785;
RC STRAIN:FROM N.A.
RC STRAIN:VZ785;
RA Nyvold G., Hixkeld S., Christensen G.
RT "The Mycoplasma hominis p120 membrane protein encodes a 100 base
RT pair hypervariable domain."
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL:U22025; AAA67455.1;
FT NON_TER 1
SQ SEQUENCE 8 AA: 869 MW: 91445.945062550 CRC64:
      Query Match      18.2%  Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 6 FN 7
Q8 5 FN 7

RESULT 19
Q94954:
ID Q94954 PRELIMINARY: PRI: 8 AA
AC Q94954
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE beta lactamase repressor Blar (Fragment).
GN Blar.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
OX NCBI_TaxID:1292;
RN [1].
RC STRAIN 6;
RC STRAIN:FROM N.A.
RA Sidhu M.S., Heir E., Sorum H., Helvik A.L.
RT "Genetic linkage between quaternary ammonium compound and beta lactam
RT resistance in Staphylococci isolated from food."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL:AF028779; AAK38453.1;
KW Phasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA: 930 MW: 48325.805766372 CRC64:
      Query Match      18.2%  Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
QZ 7 KK 8

RESULT 40
Q55429:
ID Q55429 PRELIMINARY: PRI: 8 AA
AC Q55429
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAPDH (Fragment).
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermaceae;

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OC Thermus.
OX NCBI_TaxID 274;
RN [1].
RC STRAIN:FROM N.A.
RC STRAIN:HH-8;
RX MEDLINE:89025722; PubMed:8952437;
RA Bowen D., Littlechild J.A., Forthright J.E., Watson H.C., Hall T.
RT "Nucleotide sequence of the phosphoglycerate kinase gene from the
RT extreme thermophile, Thermus thermophilus."
RC Biochem. J. 254:539-547(1988).
DR EMBL:X12464; CAA1105.1;
FT NON_TER 1
SQ SEQUENCE 8 AA: 845 MW: 90673.3332572B CRC64:
      Query Match      18.4%  Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
QZ 5 KK 5

RESULT 41
Q9R9E3:
ID Q9R9E3 PRELIMINARY: PRI: 8 AA
AC Q9R9E3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Stage V sporulation protein E (Fragment).
GN SpvE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1424;
RN [1].
RC STRAIN:FROM N.A.
RC STRAIN 168;
RX MEDLINE 93003529; PubMed 1451853;
RA Henriques A.G., de Lencastre H., Plagiot P.J.
RT "A bacillus subtilis morphotype cluster that includes spvE is
RT homologous to the rfa region of Escherichia coli."
RL Biochimie 74:735-748(1992).
DR EMBL:X64258; CAA45556.1;
FT NON_TER 8
SQ SEQUENCE 8 AA: 893 MW: 88754.1A33321B1A6 CRC64:
      Query Match      18.2%  Score 2: DB 2: Length 8;
      Best Local Similarity 100.0%  Pred. No. 8.3e+05;
      Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
QZ 4 KK 5

RESULT 42
Q9R5R0:
ID Q9R5R0 PRELIMINARY: PRI: 8 AA
AC Q9R5R0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11-500 DA product of ORFA (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID:622;
RN [1].
RX MEDLINE:92085268; PubMed 1660923;
RA Polard P., Pierre M.F., Chaudier M., Fayet O.
RT "Programmed translational frameshifting and initiation at an AUG codon

```

57 In gene expression of bacterial insertion sequence IS911.";  
 RL J. Mol. Biol. 222:465-477(1991).  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA: 935 MW: 94559CA5AF4346 CRC64:

Query Match 18.2% Score 2: 05 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3  
 DB 2 KK 3

RESULT 44  
 Q90BN9 ID Q90BN9 PRELIMINARY: PRT: 8 AA  
 AC Q90BN9  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DE Hypothetical 1.0 kDa protein (Fragment).  
 OS Coxiella burnetii.  
 GC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
 OC Coxiellaceae; Coxiella.  
 CX NCBI\_TaxID:777;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN Nine Mile Phase 1;  
 RX MEDLINE 98348442; PubMed-9683477;  
 RA Williams H., Jaeger C., Baljer G.  
 RT "Physical and genetic map of the obligate intracellular bacterium  
 Coxiella burnetii.";  
 RC J. Bacteriol. 180:3816-3822(1998).  
 DR EMBL: AF064961; AAC09947.1;  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 993 MW: 04665AAM5172227 CRC64:

Query Match 18.2% Score 2: 18 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ND 11  
 DB 1 ND 6

RESULT 44  
 Q90BN9 ID Q90BN9 PRELIMINARY: PRT: 8 AA  
 AC Q90BN9  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 21, Last annotation update)  
 DE Anticapsidase B (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 GC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.  
 CX NCBI\_TaxID:4942;  
 RN 1;  
 RP SEQUENCE  
 RX MEDLINE-92088139; PubMed-1750699;  
 RA Kassel D.B., Williams K.P., Musselman B.D., Smith A.J.  
 RT "Optimization of the fragmentation in a first-last atom bombardment ion  
 source for the sequencing of peptides at the picomole level.";  
 RL Anal. Chem. 64:1978-1983(1991).  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 772 MW: 7830DAAR2074208 CRC64:

Query Match 18.2% Score 2: 18 21 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AK 2  
 DB 7 AK 8

## RESULT 45

Q15888 ID Q15888 PRELIMINARY: PRT: 8 AA  
 AC Q15888  
 DT 01-NOV-1995 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1995 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE (Clone XPI548A) (Fragment).  
 OS Homo sapiens (Human).  
 GC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID:9606;  
 RN 1;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Placenta;  
 RA Lee C.-C., Yazdani A., Weinert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.L., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
 RA Caskey C.T.H.;  
 RT "Isolation of chromosome specific genes by reciprocal probing of  
 arrayed cDNAs and cosmid libraries.";  
 RC Hum. Mol. Genet. 0:0-0(1995).  
 DR EMBL: L32059; AAA74878.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA: 1568 MW: 0315A47EAB580763 CRC64:

Query Match 18.2% Score 2: 18 4 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KP 6  
 DB 1 KP 2

## RESULT 46

Q90CN4 ID Q90CN4 PRELIMINARY: PRT: 8 AA  
 AC Q90CN4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Cell-surface heparin/HeparanSULFATE-binding protein peptide 3  
 (Fragment).  
 OS Homo sapiens (Human).  
 GC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CX NCBI\_TaxID:9606;  
 RN 1;  
 RP SEQUENCE  
 RX MEDLINE-92291065; PubMed-1601862;  
 RA Raboudi N., Julien J., Rohde L.H., Carson D.D.;  
 RT "Identification of cell-surface heparin/heparan sulfate-binding  
 proteins of a human uterine epithelial cell line (RL95).";  
 RL J. Biol. Chem. 267:11930-11939(1992).  
 SQ SEQUENCE 8 AA: 689 MW: 808733DD33DD87D CRC64:

Query Match 18.2% Score 2: 18 4 Length 8;  
 Best Local Similarity 100.0% Pred. No. 8.3e+05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AK 2  
 DB 3 AK 4

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RESULT 47
Q9H4D3      PRELIMINARY:      PRT:      8 AA.
AC Q9H4D3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE LIM domain only 1 protein (Fragment).
GN LIM
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Bruckmann T., Winterpacht A., Hankeln T., Schmidt E.R., Zuber H.C.;
RT "Human PAC clone RCIP704K03781 (p63 781K), sequenced in DHGP project
RT (Comparative Sequencing of a 1 Mb Region in Man (Chromosome 11p15), and
RT Mouse (Chromosome 7)).";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ277661; CAC14573.1;
FI NON_TER 8
SQ SEQUENCE 8 AA: 980 MW: F3AB133AA32C696 CRC64:

Query Match      18.2%: Score 2: DB 4: Length 8:
Best Local Similarity 100.0%: Pred. No. 8.3e+05:
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KE 4
DB 6 KE 7

RESULT 48
Q9NM5      PRELIMINARY:      PRT:      8 AA.
AC Q9NM5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Dihydrofolate reductase thymidylate synthase (Fragment).
GN F011
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eumetazoa; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH, COUGAR TC751G34, SEA OJIEK T82861, JRG BEVERLEY;
RA Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;
RT "Strain Typing of Toxoplasma gondii: Comparison of Antigen Coding and
RT Housekeeping Genes.";
RL J. Parasitol. 0:0-0(2000).
DR EMBL: AF249695; AAF79153.1;
DR EMBL: AF249692; AAF79150.1;
DR EMBL: AF249693; AAF79151.1;
DR EMBL: AF249694; AAF79152.1;
FI NON_TER 1
SQ SEQUENCE 8 AA: 1035 MW: 33CAAAA05B33644 CRC54:

Query Match      18.2%: Score 2: DB 5: Length 8:
Best Local Similarity 100.0%: Pred. No. 8.3e+05:
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KE 4
DB 3 KE 4

RESULT 49
Q9TRX8      PRELIMINARY:      PRT:      8 AA.
AC Q9TRX8;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Osteopontin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9911;
RN [1]
RP SEQUENCE.
RX MEDLINE=91282766; PubMed=1676261;
RA Prince C.W., Dickie D., Kramdieck C.L.;
RT "Osteopontin, a substrate for transglutaminase and factor XIII
RT activity.";
RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).
FI NON_TER 1
SQ SEQUENCE 8 AA: 920 MW: 05DAFAF76322D767 CRC64:

Query Match      18.2%: Score 2: DB 6: Length 8:
Best Local Similarity 100.0%: Pred. No. 8.3e+05:
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 KP 6
DB 4 KP 5

RESULT 50
C18854      PRELIMINARY:      PRT:      8 AA.
AC C18854;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE CD19 antigen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu P.-C., Shibuya H., Katz M.L., Johnson G.S.;
RT "A BsmFI PCR/RELP in the canine CD19 antigen gene.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF024717; AAB81967.1;
FI NON_TER 1
SQ SEQUENCE 8 AA: 812 MW: 6735A1ADDB1325A7 CRC64:

Query Match      18.2%: Score 2: DB 6: Length 8:
Best Local Similarity 100.0%: Pred. No. 8.3e+05:
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KE 4
DB 3 KE 4

Search completed: September 30, 2003, 10:18:00
Job time : 60.6667 secs

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GenCore version 5.1.6  
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OM proteins - protein search, using sw model

Run on: September 30, 2003, 10:07:05 : Search time 11.633 Seconds  
(without alignments)  
39.331 Million cell updates/sec

Title: US-09-787-443-17

Perfect score: 11

Sequence: 1 AKKEPKNPND 11

Scoring table: MEMO

Gapop 60.0 : Gapext 60.0

Searched: 328717 seqs, 42310558 residues

Word size : 0

Total number of hits satisfying chosen parameters: 78457

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/protdata/1/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/protdata/1/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/protdata/1/1aa/6A\_COMB.pep:\*

4: /cgn2\_6/protdata/1/1aa/6B\_COMB.pep:\*

5: /cgn2\_6/protdata/1/1aa/PCUS\_COMB.pep:\*

6: /cgn2\_6/protdata/1/1aa/back:iles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	45.5	12	3	US-08-464-841A : Sequence 1, Appl
2	4	36.4	8	2	US-08-459-568-85 Sequence 85, Appl
3	4	36.4	8	2	US-08-499-411-85 Sequence 85, Appl
4	4	36.4	9	2	US-08-934-224-24 Sequence 24, Appl
5	4	36.4	8	2	US-08-934-402-24 Sequence 24, Appl
6	4	36.4	8	2	US-09-257-611-24 Sequence 24, Appl
7	4	36.4	8	2	US-08-932-815-24 Sequence 24, Appl
8	4	36.4	8	2	US-08-413-859A-2 Sequence 2, Appl
9	4	36.4	8	3	US-08-515-859A-85 Sequence 85, Appl
10	4	36.4	8	3	US-09-231-797-24 Sequence 24, Appl
11	4	36.4	8	3	US-08-934-224-24 Sequence 24, Appl
12	4	36.4	8	3	US-08-933-843-24 Sequence 24, Appl
13	4	36.4	8	3	US-08-934-223-24 Sequence 24, Appl
14	4	36.4	8	3	US-09-413-492-24 Sequence 24, Appl
15	4	36.4	8	4	US-09-586-472-85 Sequence 85, Appl
16	4	36.4	8	4	US-08-197-484-19 Sequence 19, Appl
17	4	36.4	8	4	US-09-528-706-85 Sequence 85, Appl
18	4	36.4	8	5	PCI-US95-02121-19 Sequence 19, Appl
19	4	36.4	9	2	US-08-407-468-11 Sequence 11, Appl
20	4	36.4	9	2	US-08-318-859A-45 Sequence 45, Appl
21	4	36.4	9	2	US-08-986-234-68 Sequence 68, Appl
22	4	36.4	10	1	US-07-789-184-45 Sequence 45, Appl
23	4	36.4	10	1	US-07-789-184-50 Sequence 50, Appl
24	4	36.4	10	1	US-07-789-184-60 Sequence 60, Appl
25	4	36.4	10	1	US-07-789-184-65 Sequence 65, Appl
26	4	36.4	10	1	US-07-789-184-66 Sequence 66, Appl
27	4	36.4	10	1	US-07-789-184-67 Sequence 67, Appl

28	4	36.4	10	1	US-07-789-184-203 Sequence 203, App
29	4	36.4	10	1	US-08-475-263-45 Sequence 45, Appl
30	4	36.4	10	1	US-08-475-263-50 Sequence 50, Appl
31	4	36.4	10	1	US-08-475-263-60 Sequence 60, Appl
32	4	36.4	10	1	US-08-475-263-65 Sequence 65, Appl
33	4	36.4	10	1	US-08-475-263-66 Sequence 66, Appl
34	4	36.4	10	1	US-08-475-263-67 Sequence 67, Appl
35	4	36.4	10	1	US-08-475-263-203 Sequence 203, App
36	4	36.4	10	1	US-08-485-886-45 Sequence 45, Appl
37	4	36.4	10	1	US-08-485-886-50 Sequence 50, Appl
38	4	36.4	10	1	US-08-485-886-60 Sequence 60, Appl
39	4	36.4	10	1	US-08-485-886-65 Sequence 65, Appl
40	4	36.4	10	1	US-08-485-886-66 Sequence 66, Appl
41	4	36.4	10	1	US-08-485-886-67 Sequence 67, Appl
42	4	36.4	10	1	US-08-485-886-203 Sequence 203, App
43	4	36.4	10	2	US-08-477-362-45 Sequence 45, Appl
44	4	36.4	10	2	US-08-477-362-50 Sequence 50, Appl
45	4	36.4	10	2	US-08-477-362-60 Sequence 60, Appl
46	4	36.4	10	2	US-08-477-362-65 Sequence 65, Appl
47	4	36.4	10	2	US-08-477-362-66 Sequence 66, Appl
48	4	36.4	10	2	US-08-477-362-67 Sequence 67, Appl
49	4	36.4	10	2	US-08-477-362-203 Sequence 203, App
50	4	36.4	10	2	US-08-477-134-45 Sequence 45, Appl
51	4	36.4	10	2	US-08-477-134-50 Sequence 50, Appl
52	4	36.4	10	2	US-08-477-134-60 Sequence 60, Appl
53	4	36.4	10	2	US-08-477-134-65 Sequence 65, Appl
54	4	36.4	10	2	US-08-477-134-66 Sequence 66, Appl
55	4	36.4	10	2	US-08-477-134-67 Sequence 67, Appl
56	4	36.4	10	2	US-08-477-134-203 Sequence 203, App
57	4	36.4	10	3	US-08-473-489A-45 Sequence 45, Appl
58	4	36.4	10	3	US-08-473-489A-50 Sequence 50, Appl
59	4	36.4	10	3	US-08-473-489A-60 Sequence 60, Appl
60	4	36.4	10	3	US-08-473-489A-65 Sequence 65, Appl
61	4	36.4	10	3	US-08-473-489A-66 Sequence 66, Appl
62	4	36.4	10	3	US-08-473-489A-67 Sequence 67, Appl
63	4	36.4	10	3	US-08-473-489A-203 Sequence 203, App
64	4	36.4	10	3	US-08-485-695-45 Sequence 45, Appl
65	4	36.4	10	3	US-08-485-695-50 Sequence 50, Appl
66	4	36.4	10	3	US-08-485-695-60 Sequence 60, Appl
67	4	36.4	10	3	US-08-485-695-65 Sequence 65, Appl
68	4	36.4	10	3	US-08-485-695-66 Sequence 66, Appl
69	4	36.4	10	3	US-08-485-695-67 Sequence 67, Appl
70	4	36.4	10	3	US-08-485-695-203 Sequence 203, App
71	4	36.4	10	3	US-08-018-760-45 Sequence 45, Appl
72	4	36.4	10	3	US-08-018-760-50 Sequence 50, Appl
73	4	36.4	10	3	US-08-018-760-60 Sequence 60, Appl
74	4	36.4	10	3	US-08-018-760-65 Sequence 65, Appl
75	4	36.4	10	3	US-08-018-760-66 Sequence 66, Appl
76	4	36.4	10	3	US-08-018-760-67 Sequence 67, Appl
77	4	36.4	10	3	US-08-018-760-203 Sequence 203, App
78	4	36.4	10	4	US-08-837-199A-26 Sequence 26, Appl
79	4	36.4	11	1	US-08-111-939-7 Sequence 7, Appl
80	4	36.4	11	3	US-09-100-930A-10 Sequence 10, Appl
81	4	36.4	12	3	US-08-461-384B-7 Sequence 7, Appl
82	4	36.4	12	3	US-08-407-207A-4 Sequence 4, Appl
83	4	36.4	13	2	US-08-889-291-24 Sequence 24, Appl
84	4	36.4	13	3	US-09-098-244-24 Sequence 24, Appl
85	4	36.4	13	3	US-09-208-059-27 Sequence 27, Appl
86	4	36.4	13	3	US-08-842-306B-41 Sequence 41, Appl
87	4	36.4	13	3	US-08-842-306B-42 Sequence 42, Appl
88	4	36.4	13	3	US-08-838-973B-41 Sequence 41, Appl
89	4	36.4	13	3	US-08-838-973B-42 Sequence 42, Appl
90	4	36.4	13	4	US-09-375-314-24 Sequence 24, Appl
91	4	36.4	13	4	US-08-771-212A-37 Sequence 37, Appl
92	4	36.4	13	4	US-08-771-212A-38 Sequence 38, Appl
93	4	36.4	13	4	US-09-767-395-24 Sequence 24, Appl
94	4	36.4	15	1	US-08-080-073-19 Sequence 19, Appl
95	4	36.4	15	1	US-08-080-073-21 Sequence 21, Appl
96	4	36.4	15	1	US-08-080-073-27 Sequence 27, Appl
97	4	36.4	15	3	US-08-976-255-21 Sequence 21, Appl
98	4	36.4	15	4	US-09-009-953-216 Sequence 216, App
99	3	27.3	8	1	US-07-666-719-4 Sequence 4, Appl
100	3	27.3	8	1	US-08-014-426-13 Sequence 13, Appl

161	3	27.3	8	1	US-08-116-743-45	Sequence 46, Appl	174	3	27.3	8	5	PCT-US94-01319-13	Sequence 13, Appl
162	3	27.3	8	1	US-08-036-553B-15	Sequence 15, Appl	175	3	27.3	8	5	PCT-US94-05083C-15	Sequence 15, Appl
163	3	27.3	8	1	US-08-201-044A-27	Sequence 27, Appl	176	3	27.3	8	5	PCT-US95-06846A-15	Sequence 15, Appl
164	3	27.3	8	1	US-08-469-563-15	Sequence 15, Appl	177	3	27.3	8	5	PCT-US96-00310-7	Sequence 7, Appl
165	3	27.3	8	1	US-08-372-953-7	Sequence 7, Appl	178	3	27.3	8	5	PCT-US96-00310-10	Sequence 10, Appl
166	3	27.3	8	1	US-08-240-514-39	Sequence 49, Appl	179	3	27.3	8	6	5179037-11	Patent No. 5179037
167	3	27.3	8	1	US-08-249-381-2	Sequence 2, Appl	180	3	27.3	8	6	5258287-41	Patent No. 5258287
168	3	27.3	8	1	US-08-249-324A-15	Sequence 15, Appl	181	3	27.3	9	1	US-07-657-769B-9	Sequence 9, Appl
169	3	27.3	8	1	US-08-461-507-8	Sequence 8, Appl	182	3	27.3	9	1	US-07-657-769B-49	Sequence 49, Appl
170	3	27.3	8	1	US-08-043-548-20	Sequence 20, Appl	183	3	27.3	9	1	US-08-116-733-45	Sequence 45, Appl
171	3	27.3	8	1	US-08-456-343-20	Sequence 20, Appl	184	3	27.3	9	1	US-08-178-570-39	Sequence 39, Appl
172	3	27.3	8	1	US-08-469-529A-15	Sequence 15, Appl	185	3	27.3	9	1	US-07-807-529A-55	Sequence 55, Appl
173	3	27.3	8	1	US-08-622-302A-33	Sequence 33, Appl	186	3	27.3	9	1	US-07-789-184-30	Sequence 40, Appl
174	3	27.3	8	2	US-08-467-603-6	Sequence 6, Appl	187	3	27.3	9	1	US-07-789-184-41	Sequence 41, Appl
175	3	27.3	8	2	US-08-473-190-43	Sequence 43, Appl	188	3	27.3	9	1	US-07-789-184-56	Sequence 56, Appl
176	3	27.3	8	2	US-08-784-594A-18	Sequence 18, Appl	189	3	27.3	9	1	US-07-789-184-204	Sequence 204, Appl
177	3	27.3	8	2	US-08-535-298-10	Sequence 10, Appl	190	3	27.3	9	1	US-08-475-263-30	Sequence 30, Appl
178	3	27.3	8	2	US-08-637-759B-171	Sequence 171, Appl	191	3	27.3	9	1	US-08-475-263-41	Sequence 41, Appl
179	3	27.3	8	2	US-08-637-759B-496	Sequence 496, Appl	192	3	27.3	9	1	US-08-475-263-56	Sequence 56, Appl
180	3	27.3	8	2	US-08-469-663-15	Sequence 15, Appl	193	3	27.3	9	1	US-08-475-263-204	Sequence 204, Appl
181	3	27.3	8	2	US-08-19-148-6	Sequence 6, Appl	194	3	27.3	9	1	US-08-464-531-11	Sequence 11, Appl
182	3	27.3	8	2	US-08-466-793-6	Sequence 6, Appl	195	3	27.3	9	1	US-08-485-886-30	Sequence 30, Appl
183	3	27.3	8	2	US-08-934-222-134	Sequence 134, Appl	196	3	27.3	9	1	US-08-485-886-41	Sequence 41, Appl
184	3	27.3	8	2	US-08-421-861A-6	Sequence 6, Appl	197	3	27.3	9	1	US-08-485-886-56	Sequence 56, Appl
185	3	27.3	8	2	US-08-494-533-2	Sequence 2, Appl	198	3	27.3	9	1	US-08-485-886-204	Sequence 204, Appl
186	3	27.3	8	2	US-08-933-402-144	Sequence 144, Appl	199	3	27.3	9	2	US-08-477-362-30	Sequence 30, Appl
187	3	27.3	8	2	US-09-207-621-144	Sequence 144, Appl	200	3	27.3	9	2	US-08-477-362-41	Sequence 41, Appl
188	3	27.3	8	2	US-08-48-190A-46	Sequence 46, Appl	201	3	27.3	9	2	US-08-477-362-56	Sequence 56, Appl
189	3	27.3	8	2	US-08-532-818-134	Sequence 134, Appl	202	3	27.3	9	2	US-08-477-362-204	Sequence 204, Appl
190	3	27.3	8	2	US-08-792-933-7	Sequence 7, Appl	203	3	27.3	9	2	US-08-621-803-203	Sequence 203, Appl
191	3	27.3	8	2	US-09-819-013-4	Sequence 4, Appl	204	3	27.3	9	2	US-08-477-134-30	Sequence 30, Appl
192	3	27.3	8	3	US-08-450-215-46	Sequence 46, Appl	205	3	27.3	9	2	US-08-477-134-41	Sequence 41, Appl
193	3	27.3	8	3	US-09-352-742-11	Sequence 11, Appl	206	3	27.3	9	2	US-08-477-134-56	Sequence 56, Appl
194	3	27.3	8	3	US-08-471-355A-171	Sequence 171, Appl	207	3	27.3	9	2	US-08-477-134-204	Sequence 204, Appl
195	3	27.3	8	3	US-08-671-355A-496	Sequence 496, Appl	208	3	27.3	9	2	US-08-705-660-3	Sequence 3, Appl
196	3	27.3	8	3	US-09-287-145A-46	Sequence 46, Appl	209	3	27.3	9	2	US-08-621-259A-176	Sequence 176, Appl
197	3	27.3	8	3	US-09-231-792-134	Sequence 134, Appl	210	3	27.3	9	2	US-08-461-598-11	Sequence 11, Appl
198	3	27.3	8	3	US-09-129-075-15	Sequence 15, Appl	211	3	27.3	9	2	US-08-718-661-7	Sequence 7, Appl
199	3	27.3	8	3	US-08-934-224-134	Sequence 134, Appl	212	3	27.3	9	2	US-08-586-764-2	Sequence 2, Appl
200	3	27.3	8	3	US-08-933-643-134	Sequence 134, Appl	213	3	27.3	9	2	US-08-894-339-1	Sequence 1, Appl
201	3	27.3	8	3	US-09-943-223-134	Sequence 134, Appl	214	3	27.3	9	2	US-08-874-678-29	Sequence 29, Appl
202	3	27.3	8	3	US-08-470-343-15	Sequence 15, Appl	215	3	27.3	9	2	US-08-318-856A-7	Sequence 7, Appl
203	3	27.3	8	3	US-09-092-636-11	Sequence 11, Appl	216	3	27.3	9	2	US-08-318-856A-19	Sequence 19, Appl
204	3	27.3	8	3	US-09-166-798-2	Sequence 2, Appl	217	3	27.3	9	2	US-08-460-890A-65	Sequence 65, Appl
205	3	27.3	8	3	US-09-142-324-2	Sequence 42, Appl	218	3	27.3	9	2	US-08-369-643-39	Sequence 39, Appl
206	3	27.3	8	3	US-08-457-611-2	Sequence 1, Appl	219	3	27.3	9	2	US-08-473-489A-30	Sequence 30, Appl
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208	3	27.3	8	3	US-08-473-611-15	Sequence 15, Appl	221	3	27.3	9	2	US-08-473-489A-56	Sequence 56, Appl
209	3	27.3	8	3	US-08-473-611-21	Sequence 21, Appl	222	3	27.3	9	2	US-08-473-489A-204	Sequence 204, Appl
210	3	27.3	8	3	US-08-473-611-32	Sequence 32, Appl	223	3	27.3	9	2	US-08-989-045-3	Sequence 3, Appl
211	3	27.3	8	3	US-08-473-611-42	Sequence 42, Appl	224	3	27.3	9	2	US-08-471-546-1	Sequence 1, Appl
212	3	27.3	8	3	US-08-473-611-52	Sequence 52, Appl	225	3	27.3	9	2	US-08-167-641C-65	Sequence 65, Appl
213	3	27.3	8	3	US-08-473-611-62	Sequence 62, Appl	226	3	27.3	9	2	US-08-159-339A-209	Sequence 209, Appl
214	3	27.3	8	3	US-08-473-611-72	Sequence 72, Appl	227	3	27.3	9	2	US-08-159-339A-233	Sequence 233, Appl
215	3	27.3	8	3	US-08-473-611-82	Sequence 82, Appl	228	3	27.3	9	2	US-08-159-339A-981	Sequence 981, Appl
216	3	27.3	8	3	US-08-473-611-92	Sequence 92, Appl	229	3	27.3	9	2	US-08-471-586-6	Sequence 6, Appl
217	3	27.3	8	3	US-08-473-611-102	Sequence 102, Appl	230	3	27.3	9	2	US-08-472-040A-77	Sequence 77, Appl
218	3	27.3	8	3	US-08-473-611-112	Sequence 112, Appl	231	3	27.3	9	2	US-08-322-137-11	Sequence 11, Appl
219	3	27.3	8	3	US-08-473-611-122	Sequence 122, Appl	232	3	27.3	9	2	US-08-322-137-29	Sequence 29, Appl
220	3	27.3	8	3	US-08-473-611-132	Sequence 132, Appl	233	3	27.3	9	2	US-08-643-839-29	Sequence 29, Appl
221	3	27.3	8	3	US-08-473-611-142	Sequence 142, Appl	234	3	27.3	9	2	US-08-485-695-30	Sequence 30, Appl
222	3	27.3	8	3	US-08-473-611-152	Sequence 152, Appl	235	3	27.3	9	2	US-08-485-695-41	Sequence 41, Appl
223	3	27.3	8	3	US-08-473-611-162	Sequence 162, Appl	236	3	27.3	9	2	US-08-485-695-56	Sequence 56, Appl
224	3	27.3	8	3	US-08-473-611-172	Sequence 172, Appl	237	3	27.3	9	2	US-08-485-695-204	Sequence 204, Appl
225	3	27.3	8	3	US-08-473-611-182	Sequence 182, Appl	238	3	27.3	9	2	US-08-476-242-3	Sequence 3, Appl
226	3	27.3	8	3	US-08-473-611-192	Sequence 192, Appl	239	3	27.3	9	2	US-08-460-971A-55	Sequence 55, Appl
227	3	27.3	8	3	US-08-473-611-202	Sequence 202, Appl	240	3	27.3	9	2	US-09-068-753B-1	Sequence 1, Appl
228	3	27.3	8	3	US-08-473-611-212	Sequence 212, Appl	241	3	27.3	9	2	US-08-462-040-65	Sequence 65, Appl
229	3	27.3	8	3	US-08-473-611-222	Sequence 222, Appl	242	3	27.3	9	2	US-08-462-040-65	Sequence 30, Appl
230	3	27.3	8	3	US-08-473-611-232	Sequence 232, Appl	243	3	27.3	9	2	US-08-018-760-30	Sequence 41, Appl
231	3	27.3	8	3	US-08-473-611-242	Sequence 242, Appl	244	3	27.3	9	2	US-08-018-760-41	Sequence 56, Appl
232	3	27.3	8	3	US-08-473-611-252	Sequence 252, Appl	245	3	27.3	9	2	US-08-018-760-56	Sequence 204, Appl
233	3	27.3	8	3	US-08-473-611-262	Sequence 262, Appl	246	3	27.3	9	2	US-08-018-760-204	Sequence 1, Appl
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235	3	27.3	8	3	US-08-473-611-282	Sequence 282, Appl						US-09-100-930A-24	Sequence 24, Appl
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238	3	27.3	8	3	US-08-473-611-312	Sequence 312, Appl							
239	3	27.3	8	3	US-08-473-611-322	Sequence 322, Appl							
240	3	27.3	8	3	US-08-473-611-332	Sequence 332, Appl							
241	3	27.3	8	3	US-08-473-611-342	Sequence 342, Appl							
242	3	27.3	8	3	US-08-473-611-352	Sequence 352, Appl							
243	3	27.3	8	3	US-08-473-611-362	Sequence 362, Appl							
244	3	27.3	8	3	US-08-473-611-372	Sequence 372, Appl							
245	3	27.3	8	3	US-08-473-611-382	Sequence 382, Appl							
246	3	27.3	8	3	US-08-473-611-392	Sequence 392, Appl							

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249	3	27.3	9	3	US-09-217-352-20	Sequence 20, App	322	10	1	US-08-082-2690-3	Sequence 3, Appl
250	3	27.3	9	3	US-08-818-112-13	Sequence 13, App	323	10	1	US-08-466-344-24	Sequence 24, Appl
251	3	27.3	9	3	US-09-502-660-101	Sequence 104, App	324	10	1	US-08-485-886-4	Sequence 26, Appl
252	3	27.3	9	3	US-09-502-660-127	Sequence 127, App	325	10	1	US-08-485-886-4	Sequence 4, Appl
253	3	27.3	9	3	US-09-518-047-76	Sequence 79, Appl	326	10	1	US-08-485-886-29	Sequence 10, Appl
254	3	27.3	9	3	US-09-518-047-116	Sequence 116, App	327	10	1	US-08-485-886-36	Sequence 29, Appl
255	3	27.3	9	4	US-07-954-320A-6	Sequence 6, Appl	328	10	1	US-08-485-886-40	Sequence 36, Appl
256	3	27.3	9	4	US-09-44-283-46	Sequence 36, Appl	329	10	1	US-08-485-886-43	Sequence 40, Appl
257	3	27.3	9	4	US-09-064-824-41	Sequence 11, Appl	330	10	1	US-08-485-886-44	Sequence 43, Appl
258	3	27.3	9	4	US-04-818-111-128	Sequence 128, App	331	10	1	US-08-485-886-48	Sequence 44, Appl
259	3	27.3	9	4	US-09-446-116-4	Sequence 4, Appl	332	10	1	US-08-485-886-48	Sequence 48, Appl
260	3	27.3	9	4	US-09-056-516-134	Sequence 133, App	333	10	1	US-08-485-886-51	Sequence 49, Appl
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262	3	27.3	9	4	US-09-643-630-39	Sequence 60, App	335	10	1	US-08-485-886-55	Sequence 55, Appl
263	3	27.3	9	4	US-09-372-526-120	Sequence 128, App	336	10	1	US-08-485-886-58	Sequence 58, Appl
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265	3	27.3	9	4	US-09-260-629-16	Sequence 16, Appl	338	10	1	US-08-485-886-64	Sequence 64, Appl
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267	3	27.3	9	4	US-09-260-629-16	Sequence 16, Appl	340	10	1	US-08-485-886-112	Sequence 112, App
268	3	27.3	9	4	US-09-260-629-16	Sequence 16, Appl	341	10	1	US-08-485-886-112	Sequence 112, App
269	3	27.3	9	4	US-09-260-629-16	Sequence 16, Appl	342	10	1	US-08-485-886-138	Sequence 138, App
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271	3	27.3	9	5	PCT-US95/004749	Sequence 39, Appl	344	10	1	US-08-485-886-137	Sequence 137, App
272	3	27.3	9	5	PCT-US95/09262-176	Sequence 176, App	345	10	2	US-08-611-928-30	Sequence 30, Appl
273	3	27.3	10	6	5368712-5	Patent No. 5368712	346	10	2	US-08-477-362-10	Sequence 4, Appl
274	3	27.3	10	1	US-07-666-719-12	Sequence 10, Appl	347	10	2	US-08-477-362-10	Sequence 10, Appl
275	3	27.3	10	1	US-07-657-7698-4	Sequence 8, Appl	348	10	2	US-08-477-362-29	Sequence 29, Appl
276	3	27.3	10	1	US-07-657-7698-4	Sequence 48, Appl	349	10	2	US-08-477-362-36	Sequence 36, Appl
277	3	27.3	10	1	US-08-178-212-10	Sequence 30, App	350	10	2	US-08-477-362-40	Sequence 40, Appl
278	3	27.3	10	1	US-08-604-626-30	Sequence 40, App	351	10	2	US-08-477-362-44	Sequence 43, Appl
279	3	27.3	10	1	US-08-213-876A-18	Sequence 18, Appl	352	10	2	US-08-477-362-48	Sequence 44, Appl
280	3	27.3	10	1	US-08-097-832E-4	Sequence 4, Appl	353	10	2	US-08-477-362-49	Sequence 49, Appl
281	3	27.3	10	1	US-08-465-155-12	Sequence 121, App	354	10	2	US-08-477-362-51	Sequence 51, Appl
282	3	27.3	10	1	US-08-465-155-12	Sequence 121, App	355	10	2	US-08-477-362-55	Sequence 55, Appl
283	3	27.3	10	1	US-07-789-184-4	Sequence 4, Appl	356	10	2	US-08-477-362-58	Sequence 58, Appl
284	3	27.3	10	1	US-07-789-184-10	Sequence 10, Appl	357	10	2	US-08-477-362-58	Sequence 58, Appl
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287	3	27.3	10	1	US-07-789-184-40	Sequence 40, Appl	360	10	2	US-08-477-362-64	Sequence 64, Appl
288	3	27.3	10	1	US-07-789-184-43	Sequence 43, App	361	10	2	US-08-477-362-112	Sequence 112, App
289	3	27.3	10	1	US-07-789-184-44	Sequence 44, Appl	362	10	2	US-08-477-362-138	Sequence 138, App
290	3	27.3	10	1	US-07-789-184-47	Sequence 47, Appl	363	10	2	US-08-477-362-191	Sequence 191, App
291	3	27.3	10	1	US-07-789-184-49	Sequence 49, App	364	10	2	US-08-477-362-197	Sequence 197, App
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299	3	27.3	10	1	US-07-789-184-140	Sequence 140, App	372	10	2	US-08-477-134-49	Sequence 49, Appl
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302	3	27.3	10	1	US-08-475-253-10	Sequence 10, Appl	375	10	2	US-08-477-134-58	Sequence 58, Appl
303	3	27.3	10	1	US-08-475-253-29	Sequence 29, Appl	376	10	2	US-08-477-134-58	Sequence 58, Appl
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306	3	27.3	10	1	US-08-475-253-43	Sequence 43, Appl	379	10	2	US-08-477-134-112	Sequence 112, App
307	3	27.3	10	1	US-08-475-253-44	Sequence 44, Appl	380	10	2	US-08-477-134-138	Sequence 138, App
308	3	27.3	10	1	US-08-475-253-48	Sequence 48, Appl	381	10	2	US-08-477-134-191	Sequence 191, App
309	3	27.3	10	1	US-08-475-253-49	Sequence 49, App	382	10	2	US-08-477-134-197	Sequence 197, App
310	3	27.3	10	1	US-08-475-253-51	Sequence 51, App	383	10	2	US-08-556-597-118	Sequence 118, App
311	3	27.3	10	1	US-08-475-253-55	Sequence 55, Appl	384	10	2	US-08-483-506A-10	Sequence 10, Appl
312	3	27.3	10	1	US-08-475-253-58	Sequence 58, App	385	10	2	US-08-483-506A-11	Sequence 11, Appl
313	3	27.3	10	1	US-08-475-253-59	Sequence 59, Appl	386	10	2	US-08-563-148E-2	Sequence 2, Appl
314	3	27.3	10	1	US-08-475-253-63	Sequence 63, Appl	387	10	2	US-08-595-043A-73	Sequence 73, Appl
315	3	27.3	10	1	US-08-475-253-64	Sequence 64, Appl	388	10	2	US-08-359-850-5	Sequence 5, Appl
316	3	27.3	10	1	US-08-475-264-112	Sequence 112, App	389	10	2	US-08-318-856A-48	Sequence 48, Appl
317	3	27.3	10	1	US-08-475-264-138	Sequence 138, App	390	10	2	US-08-696-944-5	Sequence 5, Appl
318	3	27.3	10	1	US-08-475-264-191	Sequence 191, App	391	10	3	US-08-473-489A-4	Sequence 4, Appl
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403	?	27.3	10	3	US-08-474-489A-59	Sequence 59, App.
404	?	27.3	10	3	US-08-474-489A-63	Sequence 63, App.
405	?	27.3	10	3	US-08-474-489A-64	Sequence 64, App.
406	?	27.3	10	3	US-08-474-489A-112	Sequence 112, App.
407	?	27.3	10	3	US-08-474-489A-136	Sequence 136, App.
408	?	27.3	10	3	US-08-474-489A-190	Sequence 190, App.
409	?	27.3	10	3	US-08-474-489A-192	Sequence 192, App.
410	?	27.3	10	3	US-08-159-339A-474	Sequence 458, App.
411	?	27.3	10	3	US-08-159-339A-1037	Sequence 1037, App.
412	?	27.3	10	3	US-08-545-8600-7P	Sequence 78, App.
413	?	27.3	10	3	US-09-224-024-14	Sequence 14, App.
414	?	27.3	10	3	US-09-224-024-14	Sequence 14, App.
415	?	27.3	10	3	US-09-274-891-36	Sequence 40, App.
416	?	27.3	10	3	US-08-485-695-4	Sequence 40, App.
417	?	27.3	10	3	US-08-485-695-10	Sequence 10, App.
418	?	27.3	10	3	US-08-485-695-29	Sequence 29, App.
419	?	27.3	10	3	US-08-485-695-36	Sequence 36, App.
420	?	27.3	10	3	US-08-485-695-41	Sequence 41, App.
421	?	27.3	10	3	US-08-485-695-44	Sequence 44, App.
422	?	27.3	10	3	US-08-485-695-44	Sequence 44, App.
423	?	27.3	10	3	US-08-485-695-48	Sequence 48, App.
424	?	27.3	10	3	US-08-485-695-48	Sequence 48, App.
425	?	27.3	10	3	US-08-485-695-51	Sequence 51, App.
426	?	27.3	10	3	US-08-485-695-51	Sequence 51, App.
427	?	27.3	10	3	US-08-485-695-58	Sequence 58, App.
428	?	27.3	10	3	US-08-485-695-59	Sequence 59, App.
429	?	27.3	10	3	US-08-485-695-64	Sequence 64, App.
430	?	27.3	10	3	US-08-485-695-64	Sequence 64, App.
431	?	27.3	10	3	US-08-485-695-112	Sequence 112, App.
432	?	27.3	10	3	US-08-485-695-124	Sequence 124, App.
433	?	27.3	10	3	US-08-485-695-191	Sequence 191, App.
434	?	27.3	10	3	US-08-485-695-192	Sequence 192, App.
435	?	27.3	10	3	US-08-151-123-10	Sequence 10, App.
436	?	27.3	10	3	US-09-011-600-4	Sequence 4, App.
437	?	27.3	10	3	US-08-630-909A-23	Sequence 23, App.
438	?	27.3	10	3	US-08-074-760-5	Sequence 4, App.
439	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
440	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
441	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
442	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
443	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
444	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
445	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
446	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
447	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
448	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
449	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
450	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
451	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
452	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
453	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
454	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
455	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
456	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
457	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
458	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
459	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
460	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
461	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
462	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
463	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
464	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.
465	?	27.3	10	3	US-08-074-760-5	Sequence 5, App.

## ALIGNMENTS

RESULT 1  
US-08-454-841A-1  
Sequence 1, Application US/0844-841A  
Patent No. 613889  
GENERAL INFORMATION:  
APPLICANT: HARRIS, DENISE, CURRY, JOSE;  
APPLICANT: LAMARCA, KARLA;  
TITLE OF INVENTION: HARP FAMILY GROWTH FACTORS, PREPARATION  
METHODS THEREFOR AND USES THEREOF  
NUMBER OF SEQUENCES: 8  
DEPENDENT ADDRESS:  
ADDRESS: BIERMAN & MUSEGGAN  
STREET: 609 TREK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER RESEARCH FORM:  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC DOS/MS DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US-08/454-841A  
FILING DATE: 23 AUGUST 1995  
CLASSIFICATION: 532  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PC/FR94/00219  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSEGGAN  
REGISTRATION NUMBER: 10,684  
REFERENCE/DECKET NUMBER: 102,165

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 661-8000  
 TELEFAX: (212) 661-8002  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12  
 TYPE: Amino Acid  
 STRANDEDNESS: Unknown  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-464-84:A-1

Query Match 45.5% Score 5.08 Length 12  
 Best Local Similarity 100.0% Pred. No. 18  
 Matches 5: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEP 6  
 DB 5 KKEP 9

RESULT 2  
 US-08-459-568-85  
 Sequence 85, Application US/08459568  
 Patent No. 581104

GENERAL INFORMATION:  
 APPLICANT: Huang, Shi  
 TITLE OF INVENTION: Retinoblastoma Protein Interacting  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 NUMBER OF SEQUENCES: 93  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/459,568  
 FILING DATE: 02-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/399,411  
 FILING DATE: 06-MAR-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-459-568-85

Query Match 36.4% Score 4.08 Length 8  
 Best Local Similarity 100.0% Pred. No. 25  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11  
 DB 2 KPND 5

RESULT 3

US-08-399-411-85  
 Sequence 85, Application US/08399411  
 Patent No. 581108  
 GENERAL INFORMATION:  
 APPLICANT: Huang, Shi  
 TITLE OF INVENTION: Retinoblastoma Protein - Interacting  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 NUMBER OF SEQUENCES: 93  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Campbell and Flores  
 STREET: 4370 La Jolla Village Drive, Suite 700  
 CITY: San Diego  
 STATE: California  
 COUNTRY: USA  
 ZIP: 92122

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/399,411  
 FILING DATE: 06-MAR-1995  
 CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
 NAME: Campbell, Cathryn A.  
 REGISTRATION NUMBER: 31,815  
 REFERENCE/DOCKET NUMBER: P-LJ 1264  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 535-9001  
 TELEFAX: (619) 535-8949  
 INFORMATION FOR SEQ ID NO: 85:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-399-411-85

Query Match 36.4% Score 4.08 Length 8  
 Best Local Similarity 100.0% Pred. No. 25  
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11  
 DB 2 KPND 5

RESULT 4

US-08-934-222-24  
 Sequence 24, Application US/08934222  
 Patent No. 592896  
 GENERAL INFORMATION:  
 APPLICANT: EVANS, Herbert J.  
 APPLICANT: KINI, R. Manjunatha  
 TITLE OF INVENTION: Polypeptides That Include Conformation-  
 TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interac  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 3000 K Street NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20007

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/934,222  
 FILING DATE: 19-SEP-1997



PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/532,818  
 FILING DATE: 03-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/143,364  
 FILING DATE: 29-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/051,741  
 FILING DATE: 23-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Isacson, John P.  
 REGISTRATION NUMBER: 33,751  
 REFERENCE/DOCKET NUMBER: 040433/0148  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

US-08-944-222-24

Query Match 36.4% Score 4: DB 2: Length 8;  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KEKP 6  
 IIII  
 DB 4 KEKP 7

RESULT 5  
 US-08-944-402-24

Sequence 24, Application US/0894402

Patent No. 5948887

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

TITLE OF INVENTION: Site

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,402

FILING DATE: 19-SEPT-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isacson, John P.

REGISTRATION NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-933-402-24

Query Match 36.4% Score 4: DB 2: Length 8;  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KEKP 6  
 IIII  
 DB 4 KEKP 7

RESULT 6

US-09-207-621-24

Sequence 24, Application US/09207621

Patent No. 5952465

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha

TITLE OF INVENTION: Polypeptides That Include Conformation

TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: Suite 500, 3000 K Street NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/207,621

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/532,818

FILING DATE: 03-MAY-1996

APPLICATION NUMBER: PCT/US94/04294

FILING DATE: 21-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364

FILING DATE: 29-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/051,741

FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isacson, John P.

REGISTRATION NUMBER: 33,751

REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-09-207-621-24

Query Match 36.4% Score 4: DB 2: Length 8;  
 Best Local Similarity 100.0% Pred. No. 2.5e+05;  
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KEKP 6  
 IIII  
 DB 4 KEKP 7

RESULT 7

US-08-532-818-24

Sequence 24, Application US/08532818

Patent No. 5965698

GENERAL INFORMATION:

APPLICANT: EVANS, Herbert J.

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1 APPLICANT: KINI, R. Manjunatha
2 TITLE OF INVENTION: Polypeptides That Include Conformation-
3 TITLE OF INVENTION: Constraining Groups Which Flank A Protein Protein Interaction
4 TITLE OF INVENTION: Site
5 NUMBER OF SEQUENCES: 153
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Foley & Lardner
8 STREET: Suite 500, 3000 K Street NW
9 CITY: Washington
10 STATE: DC
11 COUNTRY: USA
12 ZIP: 20007
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: PatentIn Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/532,814
20 FILING DATE: 03-MAY-1996
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: PCT/US94/04294
23 FILING DATE: 21-APR-1994
24 APPLICATION NUMBER: U.S. 08/144,464
25 FILING DATE: 29-OCT-1993
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: U.S. 08/054,741
28 FILING DATE: 23-APR-1993
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Jackson, John P.
31 REGISTRATION NUMBER: 33,751
32 REFERENCE/DOCKET NUMBER: 64043/0148
33 INFORMATION FOR SEQ ID NO: 24:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 8 amino acids
36 TYPE: amino acid
37 TOPOLOGY: linear
38 US 08-532-818-24
39
40 Query Match 36.4% Score 4: 1P 2: Length 8;
41 Best Local Similarity 100.0% Pred. No. 2.5e+05;
42 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
43
44 QY 3 KEKP 6
45 DB 4 KEKP 7
46
47 RESULT 8
48 US-08-516-856A-2
49 Sequence 2: Application US/08/516856A
50 Patent No. 5972351
51 GENERAL INFORMATION:
52 APPLICANT: Adrian V.S. Hill, et al.
53 TITLE OF INVENTION: PLASMODIUM FALCIPARUM MIT CLASS 17
54 TITLE OF INVENTION: RESTRICTED CELL LINES DERIVED FROM PRE-ERYTHROCYTIC STAGE
55 TITLE OF INVENTION: ANTIGENS (AS AGEN-HEL)
56 NUMBER OF SEQUENCES: 86
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE: Wenderoth, Lind & Parnack, LLP
59 STREET: 2033 K Street, N.W., Suite 800
60 CITY: Washington
61 STATE: D.C.
62 COUNTRY: U.S.A.
63 ZIP: 20006
64 COMPUTER READABLE FORM:
65 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
66 COMPUTER: IBM PC compatible
67 OPERATING SYSTEM: PC-DOS/MS-DOS
68 SOFTWARE: WordPerfect 5.1+
69 CURRENT APPLICATION DATA:
70 APPLICATION NUMBER: US/08/516-856A

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1 FILING DATE: October 3, 1994
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: GB 92 08 068.8
4 FILING DATE: April 3, 1992
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: GB 92 17 704.7
7 FILING DATE: August 20, 1992
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: WO INT/GB93/00711
10 FILING DATE: April 5, 1993
11 ATTORNEY/AGENT INFORMATION:
12 NAME: Lee Cheng
13 REGISTRATION NUMBER: 40,949
14 REFERENCE/DOCKET NUMBER: 263-PP1R15770S
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (202) 721-8200
17 TELEFAX: (202) 721-8250
18 INFORMATION FOR SEQ ID NO: 2:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 8 amino acid residues
21 TYPE: amino acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: peptide
25 ORIGINAL SOURCE:
26 ORGANISM: Plasmodium falciparum
27 US-08-518-856A-2
28
29 Query Match 36.4% Score 4: DB 2: Length 8;
30 Best Local Similarity 100.0% Pred. No. 2.5e+05;
31 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
32
33 QY 8 KPND 11
34 DB 1 KPND 4
35
36 RESULT 9
37 US-08-516-859A-R5
38 Sequence 85: Application US/08516859A
39 Patent No. 6069231
40 GENERAL INFORMATION:
41 APPLICANT: Huang, Shi
42 TITLE OF INVENTION: Retinoblastoma Protein - Interacting
43 TITLE OF INVENTION: Zinc Finger Proteins
44 NUMBER OF SEQUENCES: 106
45 CORRESPONDENCE ADDRESS:
46 ADDRESSEE: Campbell & Flores LLP
47 STREET: 4370 La Jolla Village Drive, Suite 700
48 CITY: San Diego
49 STATE: California
50 COUNTRY: USA
51 ZIP: 92122
52 COMPUTER READABLE FORM:
53 MEDIUM TYPE: Floppy disk
54 COMPUTER: IBM PC compatible
55 OPERATING SYSTEM: PC-DOS/MS-DOS
56 SOFTWARE: PatentIn Release #1.0, Version #1.25
57 CURRENT APPLICATION DATA:
58 APPLICATION NUMBER: US/08/516,859A
59 FILING DATE: 18-AUG-1995
60 CLASSIFICATION: 514
61 PRIOR APPLICATION DATA:
62 APPLICATION NUMBER: US 08/399,411
63 FILING DATE: 06-MAR-1995
64 PRIOR APPLICATION DATA:
65 APPLICATION NUMBER: US 08/292,683
66 FILING DATE: 18-AUG-1994
67 ATTORNEY/AGENT INFORMATION:
68 NAME: Campbell, Cathryn A.
69 REGISTRATION NUMBER: 31,815
70 REFERENCE/DOCKET NUMBER: P-LJ 1776
71 TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (619) 535-9501  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 85  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US 08 934-224 R5

Query Match 36.4% Score 41 DB 6100044  
Best Local Similarity 100.0% Ident No. 2 Gaps 0  
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 8 KEK 11  
DB 2 KEK 5

RESULT 11  
US-09-231-797-24  
Sequence 24, Application US/09231797  
Patent No. 6100044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
Constraining Groups Which Flank A Protein  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 4000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09231797  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/512,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/143,464  
FILING DATE: 29-OCT-1994  
APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/SECRET NUMBER: 040433/0149  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09 934-224 24

Query Match 36.4% Score 41 DB 6100044  
Best Local Similarity 100.0% Ident No. 2 Gaps 0  
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 8 KEK 11  
DB 4 KEK 7

RESULT 11  
US-08-934-224-24  
Sequence 24, Application US/08934224  
Patent No. 6100044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
Constraining Groups Which Flank A Protein-Protein Interac  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 4000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,224  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/512,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,464  
FILING DATE: 29-OCT-1994  
APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/SECRET NUMBER: 040433/0149  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08 934-224 24

Query Match 36.4% Score 41 DB 6100044  
Best Local Similarity 100.0% Ident No. 2 Gaps 0  
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 8 KEK 5  
DB 4 KEK 7

RESULT 12  
US-08-934-224-24  
Sequence 24, Application US/08934224  
Patent No. 6100044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
Constraining Groups Which Flank A Protein-Protein Interac  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 4000 K Street NW  
CITY: Washington

STATE: DC  
 COUNTRY: USA  
 ZIP: 20007  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/533,613  
 FILING DATE: 19-SEPT-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/532,819  
 FILING DATE: 03-MAY-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/143,064  
 FILING DATE: 29-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/051,741  
 FILING DATE: 23-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Isaacson, John P.  
 REGISTRATION NUMBER: 33,751  
 REFERENCE/DOCKET NUMBER: 040433/0148  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-533-843-24

Query Match 36.48; Score 4; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEKP 6  
 DB 4 KEKP 7

## RESULT 14

US-08-944-223-24  
 Sequence 24, Application US/08/944,223  
 Patent No. 6147189

GENERAL INFORMATION:  
 APPLICANT: EVANS, Herbert J.  
 APPLICANT: KINI, R. Manjunatha  
 TITLE OF INVENTION: Polypeptides That Include A Protein In  
 TITLE OF INVENTION: Constraining Groups Which Flank A Protein-  
 TITLE OF INVENTION: Site  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 3000 K Street NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20007  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/534,223  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/532,819  
 FILING DATE: 03-MAY-1996  
 APPLICATION NUMBER: PC/US94/01294  
 FILING DATE: 21-APR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/143,064  
 FILING DATE: 29-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Isaacson, John P.  
 REGISTRATION NUMBER: 33,751  
 REFERENCE/DOCKET NUMBER: 040433/0148  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-944-223-24

Query Match 36.48; Score 4; DB 3; Length 8;

FILING DATE: 29-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/051,741  
 FILING DATE: 23-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Isaacson, John P.  
 REGISTRATION NUMBER: 33,751  
 REFERENCE/DOCKET NUMBER: 040433/0148  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-934-223-24

Query Match 36.48; Score 4; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEKP 6  
 DB 4 KEKP 7

## RESULT 14

US-09-413-492-24  
 Sequence 24, Application US/09413492  
 Patent No. 6258550

GENERAL INFORMATION:  
 APPLICANT: EVANS, Herbert J.  
 APPLICANT: KINI, R. Manjunatha  
 TITLE OF INVENTION: Polypeptides That Include Conformation-  
 TITLE OF INVENTION: Constraining Groups Which Flank A Protein-  
 TITLE OF INVENTION: Site  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 3000 K Street NW  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20007  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/413,492  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/532,819  
 FILING DATE: 03-MAY-1996  
 APPLICATION NUMBER: PC/US94/04294  
 FILING DATE: 21-APR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/143,364  
 FILING DATE: 29-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. 08/051,741  
 FILING DATE: 23-APR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Isaacson, John P.  
 REGISTRATION NUMBER: 33,751  
 REFERENCE/DOCKET NUMBER: 040433/0148  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-09-413-492-24

Query Match 36.48; Score 4; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KEXP 6

DB 4 KEXP 7

RESULT 15

US-09-586-472-85

; Sequence 85, Application: US/09586472

; Patent No. 6423335

; GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

Zinc Finger Proteins

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09586472

FILING DATE: 01-Jun-2000

CLASSIFICATION: unknown

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/586 700

FILING DATE: 17-Mar-2002

APPLICATION NUMBER: US 08/516 999

FILING DATE: 18-Aug-1995

APPLICATION NUMBER: US 08/099 411

FILING DATE: 06-Mar-1995

APPLICATION NUMBER: US 08/292 193

FILING DATE: 18-Aug-1994

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P 11 410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9401

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 85

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: linear

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 85

US-09-586-472-85

Query Match

Best Local Similarity 36.4%; Score 4; DB 4; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KPNL 11

DB 2 KPNL 5

RESULT 16

US 08 197-484-19

; Sequence 19, Application US/08197484

; Patent No. 5419311

; GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.

ADDRESSEE: CHESTNUT, Robert W.

APPLICANT: SEITZ, Alessandro D.

APPLICANT: GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: Stewart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105 1434

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FER-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/535,811

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/149,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (206) 423-6793

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-197 484-15

Query Match

Best Local Similarity 36.4%; Score 4; DB 4; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KPNL 11

DB 1 KPNL 4

RESULT 17

US-09 528-706-85

; Sequence 85, Application US/09528706

; Patent No. 6463985

; GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/528,706  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/516,859  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/292,683  
FILING DATE: 18-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 1776  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-528-706-85

Query Match 36.4% Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPND 11  
Db 2 KPND 5

RESULT 18  
PCT US95 02121-19  
SOURCE: Application PC/TUS9502121  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
TITLE OF INVENTION: CTL IMMUNITY  
NUMBER OF SEQUENCES: 154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02121  
FILING DATE: 16-FEB-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/197,494  
FILING DATE: 16-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/335,611  
FILING DATE: 26-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/874,491  
FILING DATE: 27-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/827,682  
FILING DATE: 29-JAN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/749,568  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:

COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/407,468  
FILING DATE: 20-MAR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/080,788  
FILING DATE: 28-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,340  
FILING DATE: 30-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Heines, M. Henry  
REGISTRATION NUMBER: 28,219  
REFERENCE/DOCKET NUMBER: 012418-002020US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product- "OTHER"  
OTHER INFORMATION: /note- "Xaa = Phe N-substituted with various R groups"

Query Match 36.4% Score 4; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KPND 11  
Db 1 KPND 4

RESULT 19  
US-08-407-468-11  
Sequence 11, Application US/08407468  
Patent No. 5866681  
GENERAL INFORMATION:  
APPLICANT: Scarborough, Robert M.  
TITLE OF INVENTION: Thrombin Receptor Antagonists  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/407,468  
FILING DATE: 20-MAR-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/080,788  
FILING DATE: 28-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,340  
FILING DATE: 30-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Heines, M. Henry  
REGISTRATION NUMBER: 28,219  
REFERENCE/DOCKET NUMBER: 012418-002020US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product- "OTHER"  
OTHER INFORMATION: /note- "Xaa = Phe N-substituted with various R groups"

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FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /product: "OTHER"
OTHER INFORMATION: /note: "Xaa - cyclohexylalanine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product: "OTHER"
OTHER INFORMATION: /note: "Xaa - cyclohexylalanine"
FEATURE:
NAME/KEY: Modified site
LOCATION: 9
OTHER INFORMATION: /product: "OTHER"
OTHER INFORMATION: /note: "Xaa - lysine"
US 08 437-468-11
Query Match 36.4% Score 4; DB 2; Length 9;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KPND 11
DB 5 KPND 8
RESULT 20
US 08-418-896A-45
: Sequence 45, Application US/08318896A
: Patent No. 5972351
: GENERAL INFORMATION:
: APPLICANT: Adrian V.S. Hill, et al.
: TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I,
: TITLE OF INVENTION: RESTRICTED CD8 EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
: NUMBER OF SEQUENCES: 86
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wenderoth, Lind & Ponder, L.L.P.
: STREET: 2033 K Street, N.W., Suite 800
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20006
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/418,866A
: FILING DATE: October 3, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 92 08 066 A
: FILING DATE: April 3, 1994
: APPLICATION NUMBER: GB 92 17 704 A
: FILING DATE: August 20, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/GB93/00311
: FILING DATE: April 5, 1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee Cheng
: REGISTRATION NUMBER: 40,949
: REFERENCE/DOCKET NUMBER: 263-PPI-157705
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 721-8200
: TELEFAX: (202) 721-8250
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acid residues
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /product: "OTHER"
OTHER INFORMATION: /note: "Xaa - cyclohexylalanine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product: "OTHER"
OTHER INFORMATION: /note: "Xaa - cyclohexylalanine"
FEATURE:
NAME/KEY: Modified site
LOCATION: 9
OTHER INFORMATION: /product: "OTHER"
OTHER INFORMATION: /note: "Xaa - lysine"
US 08 437-468-11
Query Match 36.4% Score 4; DB 2; Length 9;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KPND 11
DB 5 KPND 8
RESULT 21
US 08-986 234-66
: Sequence 68, Application US/08986234
: Patent No. 5981786
: GENERAL INFORMATION:
: APPLICANT: Wallen, et al.
: TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
: FILE REFERENCE: UNNE-00081
: CURRENT APPLICATION NUMBER: US/08/986,234
: CURRENT FILING DATE: 1997-12-05
: NUMBER OF SEQ ID NOS: 114
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 68
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus
US 08-986-234-68
Query Match 36.4% Score 4; DB 2; Length 9;
Best Local Similarity 100.0% Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KKEK 5
DB 3 KKEK 6
RESULT 22
US 07-789-184-45
: Sequence 45, Application US/07789184
: Patent No. 5688768
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/789,184
: FILING DATE: 19911107
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
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1 INFORMATION FOR SEQ ID NO: 45:

2 SEQUENCE CHARACTERISTICS:

3 LENGTH: 10 amino acids

4 TYPE: AMINO ACID

5 STRANDEDNESS: single

6 TOPOLOGY: linear

7 FEATURE:

8 NAME/KEY: Modified-site

9 LOCATION: 1

10 OTHER INFORMATION: /note- "This position is Mpr."

11 OTHER INFORMATION: S-Me Mpr or Mba."

12 FEATURE:

13 NAME/KEY: Modified-site

14 LOCATION: 3

15 OTHER INFORMATION: /note- "This position is Cha."

16 FEATURE:

17 NAME/KEY: Modified-site

18 LOCATION: 4

19 OTHER INFORMATION: /note- "This position is Cha."

20 FEATURE:

21 NAME/KEY: Modified-site

22 LOCATION: 10

23 OTHER INFORMATION: /note- "This position is K NH2."

24 US-07-789-184-45

Query Match

36.4%; Score 4; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11

DB 6 KPND 9

RESULT 23

US-07-789-184-50

Sequence 50, Application US/07789184

Patent No. 5688768

GENERAL INFORMATION:

APPLICANT: COUGHLIN, SHAUN R.

APPLICANT: SCARBOROUGH, ROBERT M.

TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

RELATED PHARMACEUTICALS

NUMBER OF SEQUENCES: 223

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07789184

FILING DATE: 19911107

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20502-20

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 34-0154

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

NAME/KEY: Modified site

LOCATION: 1

OTHER INFORMATION: /note- "This position is Mpr."

1 TOPOLOGY: linear

2 NAME/KEY: Modified-site

3 LOCATION: 1

4 OTHER INFORMATION: /note- "This position is Mpr,

5 OTHER INFORMATION: S-Me Mpr or Mba."

6 FEATURE:

7 NAME/KEY: Modified-site

8 LOCATION: 3

9 OTHER INFORMATION: /note- "This position is Cha."

10 FEATURE:

11 NAME/KEY: Modified-site

12 LOCATION: 4

13 OTHER INFORMATION: /note- "This position is Cha."

14 FEATURE:

15 NAME/KEY: Modified-site

16 LOCATION: 10

17 OTHER INFORMATION: /note- "This position is A-NH2."

18 US-07-789-184-50

Query Match

36.4%; Score 4; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11

DB 6 KPND 9

RESULT 24

US-07-789-184-60

Sequence 60, Application US/07789184

Patent No. 5688768

GENERAL INFORMATION:

APPLICANT: COUGHLIN, SHAUN R.

APPLICANT: SCARBOROUGH, ROBERT M.

TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND

RELATED PHARMACEUTICALS

NUMBER OF SEQUENCES: 223

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07789184

FILING DATE: 19911107

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22000-20502-20

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 34-0154

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

NAME/KEY: Modified site

LOCATION: 1

OTHER INFORMATION: /note- "This position is Mpr."



```

1 FEATURE:
2 NAME/KEY: Modified-site
3 LOCATION: 3
4 OTHER INFORMATION: /note- "This position is Cha."
5 FEATURE:
6 NAME/KEY: Modified-site
7 LOCATION: 4
8 OTHER INFORMATION: /note- "This position is Cha."
9 FEATURE:
10 NAME/KEY: Modified-site
11 LOCATION: 10
12 OTHER INFORMATION: /note "This position is A-NH2."
13 US-07 789-184-60
14
15 Query Match: 36.4%, Score 4, DP 1, Length 10;
16 Best Local Similarity: 100.0%, Pred. No. 1, Re-02;
17 Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;
18
19 CY 8 KIND 11
20 DB 6 KIND 9
21
22 RESULT 25
23 US-07 789-184 65
24 Sequence 65, Application US/07789184
25 Patent No. 5648766
26 GENERAL INFORMATION:
27 APPLICANT: COUGHLIN, SHAWN R.
28 APPLICANT: SCARBOROUGH, ROBERT M.
29 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
30 TITLE OF INVENTION: RELATED PHARMACEUTICALS
31 NUMBER OF SEQUENCES: 223
32 CORRESPONDENCE ADDRESS:
33 ADDRESSEE: MORRISON & FORSTER
34 STREET: 735 Page Mill Road
35 CITY: Palo Alto
36 STATE: California
37 COUNTRY: USA
38 ZIP: 94304-1018
39 COMPUTER READABLE FORM:
40 MEDIUM TYPE: Floppy disk
41 OPERATING SYSTEM: IBM PC compatible
42 SOFTWARE: Patent In Release #1.0, Version #1.25
43 CURRENT APPLICATION DATA:
44 APPLICATION NUMBER: US/07/789,184
45 FILING DATE: 19911107
46 CLASSIFICATION: 514
47 NAME: MURASHIGE, KATE H.
48 REGISTRATION NUMBER: 29,959
49 REFERENCE/DOCKET NUMBER: 22000-20502.20
50 TELEPHONE: (415) 813-5600
51 TELEFAX: (415) 494-0792
52 TELEX: 44-0154
53 INFORMATION FOR SEQ ID NO: 65:
54 SEQUENCE CHARACTERISTICS:
55 LENGTH: 10 amino acids
56 TYPE: AMINO ACID
57 STRANDEDNESS: single
58 TOPOLOGY: linear
59 FEATURE:
60 NAME/KEY: Modified-site
61 LOCATION: 1
62 OTHER INFORMATION: /note- "This position is Cha."
63 FEATURE:
64 NAME/KEY: Modified-site
65 LOCATION: 3
66 OTHER INFORMATION: /note "This position is Cha."
67 FEATURE:
68 NAME/KEY: Modified-site

```

```

1 FEATURE:
2 NAME/KEY: Modified-site
3 LOCATION: 4
4 OTHER INFORMATION: /note- "This position is Cha."
5 FEATURE:
6 NAME/KEY: Modified-site
7 LOCATION: 10
8 OTHER INFORMATION: /note "This position is A-NH2."
9 US-07 789-184-65
10
11 Query Match: 36.4%, Score 4, DP 1, Length 10;
12 Best Local Similarity: 100.0%, Pred. No. 1, Re-02;
13 Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0;
14
15 CY 8 KIND 11
16 DB 6 KIND 9
17
18 RESULT 26
19 US-07 789-184 66
20 Sequence 66, Application US/07789184
21 Patent No. 5688768
22 GENERAL INFORMATION:
23 APPLICANT: COUGHLIN, SHAWN R.
24 APPLICANT: SCARBOROUGH, ROBERT M.
25 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
26 TITLE OF INVENTION: RELATED PHARMACEUTICALS
27 NUMBER OF SEQUENCES: 223
28 CORRESPONDENCE ADDRESS:
29 ADDRESSEE: MORRISON & FORSTER
30 STREET: 735 Page Mill Road
31 CITY: Palo Alto
32 STATE: California
33 COUNTRY: USA
34 ZIP: 94304-1018
35 COMPUTER READABLE FORM:
36 MEDIUM TYPE: Floppy disk
37 OPERATING SYSTEM: IBM PC compatible
38 SOFTWARE: Patent In Release #1.0, Version #1.25
39 CURRENT APPLICATION DATA:
40 APPLICATION NUMBER: US/07/789,184
41 FILING DATE: 19911107
42 CLASSIFICATION: 514
43 NAME: MURASHIGE, KATE H.
44 REGISTRATION NUMBER: 29,959
45 REFERENCE/DOCKET NUMBER: 22000-20502.20
46 TELEPHONE: (415) 813-5600
47 TELEFAX: (415) 494-0792
48 TELEX: 44-0154
49 INFORMATION FOR SEQ ID NO: 66:
50 SEQUENCE CHARACTERISTICS:
51 LENGTH: 10 amino acids
52 TYPE: AMINO ACID
53 STRANDEDNESS: single
54 TOPOLOGY: linear
55 FEATURE:
56 NAME/KEY: Modified-site
57 LOCATION: 1
58 OTHER INFORMATION: /note- "This position is Mba."
59 FEATURE:
60 NAME/KEY: Modified-site
61 LOCATION: 4
62 OTHER INFORMATION: /note- "This position is Cha."
63 FEATURE:
64 NAME/KEY: Modified-site
65 LOCATION: 10
66 OTHER INFORMATION: /note "This position is K-NH2."

```

US-07-789-184-66

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

RESULT 27

US-07-789-184-67  
Sequence 67, Application US/07789184  
Patent No. 5688768  
GENERAL INFORMATION:  
APPLICANT: CUGHILIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07789-184  
FILING DATE: 19911107  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34 0154  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note- "This position is  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: Sncmpt.  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note- "This position is Cha."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /note- "This position is K-NH2."  
US-07-789-184-67

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 5 KPND 9

RESULT 28  
US-07-789-184-203  
Sequence 203, Application US/07789184  
Patent No. 5688768  
GENERAL INFORMATION:  
APPLICANT: CUGHILIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07789-184  
FILING DATE: 19911107  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34-0154  
INFORMATION FOR SEQ ID NO: 203:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note- "This position is (2-Mba)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 3  
OTHER INFORMATION: /note- "This position is (Cha)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note- "This position is (Cha)."  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 10  
OTHER INFORMATION: /note- "This position is K-NH2."  
US-07-789-184-203

Query Match 36.4%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
DB 6 KPND 9

```

RESULT 29
US-08-475-263-45
: Sequence 45, Application US/08475263
: Patent No. 5759994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/475,263
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note= "This position is Mpr."
: OTHER INFORMATION: S-Me Mpr. or Mba."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note= "This position is A-NH2."
: OTHER INFORMATION: /note= "This position is A-NH2."
US-08-475-263-45
Query Match 36.4%, Score 4: DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB 6 KPND 9

```

```

RESULT 30
US-08-475-263-50
: Sequence 50, Application US/08475264
: Patent No. 5759994
: GENERAL INFORMATION:

```

```

: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/475,263
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note= "This position is Mpr."
: OTHER INFORMATION: S-Me Mpr. or Mba."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note= "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note= "This position is A-NH2."
: OTHER INFORMATION: /note= "This position is A-NH2."
US-08-475-263-50
Query Match 36.4%, Score 4: DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB 6 KPND 9

```

```

RESULT 31
US-08-475-263-60
: Sequence 60, Application US/08475263
: Patent No. 5759994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/Docket NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "This position is Mpr."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note= "This position is A-NH2."
US-08 475 263-66

```

```

Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 KPND 11
DB 6 KPND 9

```

```

RESULT 32
US-08-475-263-65
Sequence 65, Application US/08475263
Patent No. 5759994
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA

```

```

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,263
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/Docket NUMBER: 22000-20502.03
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "This position is Mpr."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note= "This position is A-NH2."
US-08-475-263-65

```

```

Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 KPND 11
DB 6 KPND 9

```

```

RESULT 33
US-08-475-263-66
Sequence 66, Application US/08475263
Patent No. 5759994
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

```

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/475,263
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 66:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is Cha."
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
: US-08-475-263-66
:
: Query Match 36.4% Score 4; DB 1; Length 10;
: Best Local Similarity 100.0%; Pred. No. 1.7e+02;
: Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 8 KPNQ 11
: DB 6 KPNQ 9
:
: RESULT 34
: US-08-475-263-67
: Sequence 67, Application US/08/475,263
: Patent No. 575994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/475,263
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
:
: Query Match 36.4% Score 4; DB 1; Length 10;
: Best Local Similarity 100.0%; Pred. No. 1.7e+02;
: Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 8 KPNQ 11
: DB 6 KPNQ 9
:
: RESULT 35
: US-08-475-263-203
: Sequence 203, Application US/08/475,263
: Patent No. 575994
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/475,263
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.03
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763

```

```

TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "This position is (Mpr)."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "This position is (Cha)."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "This position is (Cha)."
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note= "This position is K-NH2."
US 08 475-263-203

```

```

Query Match: 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 KPN0 11
DB 6 KPN0 9

```

```

RESULT 36
US-08-485-886-45
Sequence 45, Application US/08485886
Patent No. 5798248
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.886
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5660
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "This position is Mpr,
OTHER INFORMATION: S Me Mpr or Mba."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note= "This position is Cha."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /note= "This position is Cha."
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note= "This position is K-NH2."
US-08-485-886-45

```

```

Query Match: 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 KPN0 11
DB 6 KPN0 9

```

```

RESULT 37
US-08-485-886-50
Sequence 50, Application US/08485886
Patent No. 5798248
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.886
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

```

```

1 STRANDEDNESS: single
2 TOPOLOGY: linear
3
4 FEATURE:
5   NAME/KEY: Modified-site
6   LOCATION: 1
7   OTHER INFORMATION: /note- "this position is Mpr."
8
9 FEATURE:
10  NAME/KEY: Modified-site
11  LOCATION: 3
12  OTHER INFORMATION: /note "this position is Cha."
13
14 FEATURE:
15  NAME/KEY: Modified-site
16  LOCATION: 4
17  OTHER INFORMATION: /note "this position is Cha."
18
19 FEATURE:
20  NAME/KEY: Modified-site
21  LOCATION: 10
22  OTHER INFORMATION: /note "this position is K-NH2."
23
24 US-08-485-886-60

```

```

Query Match          36.4% Score 4: 109 11 Length 10:
Best Local Similarity 100.0% Pred. No. 1.7e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

CY      8 KPNB 11
EB      6 KPNB 9

```

```

RESULT 18
US-08-485-886-60
Sequence 60, Application US/08485886
Patent No. 5798248
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAWN K.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FIERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,886
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

```

```

1 FEATURE:
2   NAME/KEY: Modified-site
3   LOCATION: 1
4   OTHER INFORMATION: /note- "This position is Mpr."
5
6 FEATURE:
7   NAME/KEY: Modified-site
8   LOCATION: 3
9   OTHER INFORMATION: /note "this position is Cha."
10
11 FEATURE:
12  NAME/KEY: Modified-site
13  LOCATION: 4
14  OTHER INFORMATION: /note "this position is Cha."
15
16 FEATURE:
17  NAME/KEY: Modified-site
18  LOCATION: 10
19  OTHER INFORMATION: /note- "this position is K-NH2."
20
21 US-08-485-886-60

```

```

Query Match          36.4% Score 4: 109 11 Length 10:
Best Local Similarity 100.0% Pred. No. 1.7e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

CY      8 KPNB 11
EB      6 KPNB 9

```

```

RESULT 19
US-08-485-886-65
Sequence 65, Application US/08485886
Patent No. 5798248
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAWN K.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FIERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,886
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 22000-20502.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

```

```

: OTHER INFORMATION: /note- "This position is Mpr."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is A NH2."
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-66

Query Match          36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB      6 KPND 9

RESULT 40
US-08-485-886-66
: Sequence 66, Application US/08485886
: Patent No. 5798248
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: FILING DATE: 07-NOV-1991
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 66:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is Mpr."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."

```

```

: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-66

Query Match          36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPND 11
DB      6 KPND 9

RESULT 41
US-08-485-886-67
: Sequence 67, Application US/08485886
: Patent No. 5798248
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is
: OTHER INFORMATION: Smpw."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."

```



```

: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-57
Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPN0 1;
    III
Db 6 KPN0 9

RESULT 42
US-08-485-886-203
: Sequence 203; Application US/08485886
: Patent No. 5798246
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: City: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,886
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 203:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is (X-MLA).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is (Cha).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4

```

```

: OTHER INFORMATION: /note- "This position is (Cha).".
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: /note- "This position is K-NH2."
US-08-485-886-203
Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPN0 1;
    III
Db 6 KPN0 9

RESULT 43
US-08-477-362-45
: Sequence 45; Application US/08477362
: Patent No. 5849507
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: City: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477.362
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DCKET NUMBER: 22000-20502.20
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 34-0154
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /note- "This position is Mpr,
: OTHER INFORMATION: S-Me Mpr or Mba."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 3
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: /note- "This position is Cha."
: FEATURE:

```

```

1 NAME/KEY: Modified-site
2 LOCATION: 10
3 OTHER INFORMATION: /note- "This position is K NH2."
4 US-08-477 362-45
5
6 Query Match 36.4% Score 4; DB 2; Length 10;
7 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
8 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9
10 QY 8 KPND 11
11 Db 6 KPND 9
12
13 RESULT 44
14 US-08-477-362-50
15 : Sequence 50, Application US/08477362
16 : Patent No. 5849507
17 : GENERAL INFORMATION:
18 : APPLICANT: COUGHLIN, SHAUN R.
19 : APPLICANT: SCARBOROUGH, ROBERT M.
20 : TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
21 : TITLE OF INVENTION: RELATED PHARMACEUTICALS
22 : NUMBER OF SEQUENCES: 223
23 : CORRESPONDENCE ADDRESS:
24 : ADDRESSEE: MORRISON & FOERSTER
25 : STREET: 755 Page Mill Road
26 : CITY: Palo Alto
27 : STATE: California
28 : COUNTRY: USA
29 : ZIP: 94304-1018
30 : COMPUTER READABLE FORM:
31 : MEDIUM TYPE: Floppy disk
32 : COMPUTER: IBM PC compatible
33 : OPERATING SYSTEM: PC-DOS/MS-DOS
34 : SOFTWARE: Patent In Release #1.0, Version #1.25
35 : CURRENT APPLICATION DATA:
36 : APPLICATION NUMBER: US/08/477,362
37 : FILING DATE: 07-JUN-1995
38 : CLASSIFICATION: 435
39 : PRIOR APPLICATION DATA:
40 : APPLICATION NUMBER: US 07/789,184
41 : FILING DATE: 07-NOV-1991
42 : ATTORNEY/AGENT INFORMATION:
43 : NAME: MURASHIGE, KATE H.
44 : REGISTRATION NUMBER: 29,959
45 : REFERENCE/DCKET NUMBER: 22000-20502.20
46 : TELECOMMUNICATION INFORMATION:
47 : TELEPHONE: (415) 813-5600
48 : TELEFAX: (415) 494-0792
49 : TELEX: 34-0154
50 : INFORMATION FOR SEQ ID NO: 50:
51 : SEQUENCE CHARACTERISTICS:
52 : LENGTH: 10 amino acids
53 : TYPE: amino acid
54 : STRANDEDNESS: single
55 : TOPOLOGY: linear
56 : FEATURE:
57 : NAME/KEY: Modified-site
58 : LOCATION: 1
59 : OTHER INFORMATION: /note- "This position is Mpr."
60 : OTHER INFORMATION: S-Me Mpr G: Mpr."
61 : FEATURE:
62 : NAME/KEY: Modified-site
63 : LOCATION: 3
64 : OTHER INFORMATION: /note- "This position is Cha."
65 : FEATURE:
66 : NAME/KEY: Modified-site
67 : LOCATION: 4
68 : OTHER INFORMATION: /note- "This position is Cha."
69 : FEATURE:
70 : NAME/KEY: Modified-site
71 : LOCATION: 10
72 : OTHER INFORMATION: /note- "This position is K-NH2."
73 : NAME/KEY: Modified-site
74 : LOCATION: 10

```

```

1 OTHER INFORMATION: /note- "This position is A-NH2."
2 US-08-477-362-50
3
4 Query Match 36.4% Score 4; DB 2; Length 10;
5 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
6 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
7
8 QY 8 KPND 11
9 Db 6 KPND 9
10
11 RESULT 45
12 US-08-477-362-60
13 : Sequence 60, Application US/08477362
14 : Patent No. 5849507
15 : GENERAL INFORMATION:
16 : APPLICANT: COUGHLIN, SHAUN R.
17 : APPLICANT: SCARBOROUGH, ROBERT M.
18 : TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
19 : TITLE OF INVENTION: RELATED PHARMACEUTICALS
20 : NUMBER OF SEQUENCES: 223
21 : CORRESPONDENCE ADDRESS:
22 : ADDRESSEE: MORRISON & FOERSTER
23 : STREET: 755 Page Mill Road
24 : CITY: Palo Alto
25 : STATE: California
26 : COUNTRY: USA
27 : ZIP: 94304-1018
28 : COMPUTER READABLE FORM:
29 : MEDIUM TYPE: Floppy disk
30 : COMPUTER: IBM PC compatible
31 : OPERATING SYSTEM: PC-DOS/MS-DOS
32 : SOFTWARE: Patent In Release #1.0, Version #1.25
33 : CURRENT APPLICATION DATA:
34 : APPLICATION NUMBER: US/08/477,362
35 : FILING DATE: 07-JUN-1995
36 : CLASSIFICATION: 435
37 : PRIOR APPLICATION DATA:
38 : APPLICATION NUMBER: US 07/789,184
39 : FILING DATE: 07-NOV-1991
40 : ATTORNEY/AGENT INFORMATION:
41 : NAME: MURASHIGE, KATE H.
42 : REGISTRATION NUMBER: 29,959
43 : REFERENCE/DCKET NUMBER: 22000-20502.20
44 : TELECOMMUNICATION INFORMATION:
45 : TELEPHONE: (415) 813-5600
46 : TELEFAX: (415) 494-0792
47 : TELEX: 34-0154
48 : INFORMATION FOR SEQ ID NO: 60:
49 : SEQUENCE CHARACTERISTICS:
50 : LENGTH: 10 amino acids
51 : TYPE: amino acid
52 : STRANDEDNESS: single
53 : TOPOLOGY: linear
54 : FEATURE:
55 : NAME/KEY: Modified-site
56 : LOCATION: 1
57 : OTHER INFORMATION: /note- "This position is Mpr."
58 : FEATURE:
59 : NAME/KEY: Modified-site
60 : LOCATION: 3
61 : OTHER INFORMATION: /note- "This position is Cha."
62 : FEATURE:
63 : NAME/KEY: Modified-site
64 : LOCATION: 4
65 : OTHER INFORMATION: /note- "This position is Cha."
66 : FEATURE:
67 : NAME/KEY: Modified-site
68 : LOCATION: 10
69 : OTHER INFORMATION: /note- "This position is K-NH2."
70 : NAME/KEY: Modified-site
71 : LOCATION: 10
72 : OTHER INFORMATION: /note- "This position is K-NH2."
73 : NAME/KEY: Modified-site
74 : LOCATION: 10

```

Query Match 36.4% Score 4; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
 111  
 DB 6 KPND 9

RESULT 46  
 US-08-477-362-65  
 : Sequence 65, Application US/08477362  
 : Patent No. 5849507  
 : GENERAL INFORMATION:  
 : APPLICANT: CUGHELIN, SHAUN R.  
 : APPLICANT: SCARBOROUGH, ROBERT M.  
 : TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR R AND  
 : TITLE OF INVENTION: RELATED PHARMACEUTICALS  
 : NUMBER OF SEQUENCES: 223  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: MORRISON & FERNSTER  
 : STREET: 755 Page Mill Road  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94304-1018  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.2  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/477,362  
 : FILING DATE: 07-JUN-1995  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/789,184  
 : FILING DATE: 07-NOV-1991  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MURASHIGE, KATE H.  
 : REGISTRATION NUMBER: 29,959  
 : REFERENCE/DOCKET NUMBER: 2209C-20502.20  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 813-5600  
 : TELEFAX: (415) 494-0792  
 : TELEX: 34-0154  
 : INFORMATION FOR SEQ ID NO: 65:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 10 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : FEATURE:  
 : NAME/KEY: Modified-site  
 : LOCATION: 1  
 : OTHER INFORMATION: /note- "This position is R11"  
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 : US-08-477-362-65

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 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 KPND 11  
 111  
 DB 6 KPND 9

RESULT 47  
 US-08-477-362-66  
 : Sequence 66, Application US/08477362  
 : Patent No. 5849507  
 : GENERAL INFORMATION:  
 : APPLICANT: CUGHELIN, SHAUN R.  
 : APPLICANT: SCARBOROUGH, ROBERT M.  
 : TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
 : TITLE OF INVENTION: RELATED PHARMACEUTICALS  
 : NUMBER OF SEQUENCES: 223  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: MORRISON & FERNSTER  
 : STREET: 755 Page Mill Road  
 : CITY: Palo Alto  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 94304-1018  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/477,362  
 : FILING DATE: 07-JUN-1995  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/789,184  
 : FILING DATE: 07-NOV-1991  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MURASHIGE, KATE H.  
 : REGISTRATION NUMBER: 29,959  
 : REFERENCE/DOCKET NUMBER: 2209C-20502.20  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 813-5600  
 : TELEFAX: (415) 494-0792  
 : TELEX: 34-0154  
 : INFORMATION FOR SEQ ID NO: 66:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 10 amino acids  
 : TYPE: amino acid  
 : STRANDEDNESS: single  
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 : OTHER INFORMATION: /note- "This position is Cha."  
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Query Match 36.4% Score 4; DB 2; Length 10;  
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 Matches 4; Conservative 0; Mismatches 0; Indels 0;

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 111  
 DB 6 KPND 9

2b 6 KPN0 9

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Sequence 203, Application US/08477362  
Patent No. 5649507  
GENERAL INFORMATION:  
APPLICANT: COUGHLIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
TITLE OF INVENTION: RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FIERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,362  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/789,184  
FILING DATE: 07-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22,600,236,243  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
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INFORMATION FOR SEQ ID NO: 67:  
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Matches 4; Conservative 0; Mismatches 0; Indels 0;

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10 6 KPN0 9

RESULT 4a  
US-08-477-362-203  
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Patent No. 5649507  
GENERAL INFORMATION:  
APPLICANT: COUGHLIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
TITLE OF INVENTION: RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FIERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,362  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/789,184  
FILING DATE: 07-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502, 20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34-0154  
INFORMATION FOR SEQ ID NO: 203:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
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US-08-477-362-203

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

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RESULT 5b  
US-08-477-134-45

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Sequence 45, Application US/98477144
Patent No. 5856448
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT TETRAMIN PEPTIDES AND
TITLE OF INVENTION: RELATED PHARMACEUTICALS
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304 1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release 1.1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,144
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,144
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 45,959
REFERENCE/DOCKET NUMBER: 22600-29502.20
ELECTRONIC COMMUNICATION INFORMATION:
TELEPHONE: (415) 813-3600
TELEFAX: (415) 494-0792
TELEX: 34 0154
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
FEATURE:
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LOCATION: 1
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US 08-477-14-45

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Matches 4; Conservative 0; Mismatches 0; Gaps 0

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QY 8 KPN0 11
DB 6 KPN0 9

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GenCore version 5.1.6  
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#### SUMMARIES

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4	4	36.4	8	15	US-10-133-210-18	Sequence 181, Appl
5	4	36.4	9	9	US-09-010-7-4-1	Sequence 1, Appl
6	4	36.4	9	10	US-09-984-056-10	Sequence 10, Appl
7	4	36.4	9	10	US-09-994-057-10	Sequence 10, Appl
8	4	36.4	9	12	US-10-077-109-13	Sequence 13, Appl
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US-10-084-813-992

235	9	15	US-10-084-813-993	Sequence 993, App	308	3	27.3	10	11	US-09-572-404B-1696	Sequence 1696, Ap
236	9	15	US-10-043-662.2	Sequence 29, Appl	309	3	27.3	10	11	US-09-572-404B-1947	Sequence 1947, Ap
237	9	15	US-10-105-901.29	Sequence 29, Appl	310	3	27.3	10	11	US-09-572-404B-1949	Sequence 1949, Ap
238	9	15	US-10-024-282-692	Sequence 862, App	311	3	27.3	10	11	US-09-572-404B-1962	Sequence 1962, Ap
239	9	15	US-10-002-603-66	Sequence 66, Appl	312	3	27.3	10	11	US-09-572-404B-2141	Sequence 2141, Ap
240	9	15	US-10-002-603-91	Sequence 91, Appl	313	3	27.3	10	11	US-09-572-404B-2171	Sequence 2171, Ap
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242	9	15	US-10-002-603-112	Sequence 112, App	315	3	27.3	10	11	US-09-572-404B-3060	Sequence 3060, Ap
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244	9	15	US-10-002-603-184	Sequence 184, App	317	3	27.3	10	11	US-09-572-404B-3192	Sequence 3192, Ap
245	9	15	US-10-002-603-207	Sequence 207, App	318	3	27.3	10	11	US-09-820-053A-37	Sequence 37, Appl
246	9	15	US-10-002-603-222	Sequence 222, App	319	3	27.3	10	11	US-09-820-053A-38	Sequence 38, Appl
247	9	15	US-10-002-603-252	Sequence 242, App	320	3	27.3	10	11	US-09-820-053A-39	Sequence 39, Appl
248	9	15	US-10-002-603-277	Sequence 277, App	321	3	27.3	10	11	US-09-820-053A-143	Sequence 143, Appl
249	9	15	US-10-062-548-129	Sequence 157, App	322	3	27.3	10	12	US-09-932-165-144	Sequence 54, Appl
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255	9	15	US-10-109-171-125	Sequence 135, App	328	3	27.3	10	12	US-09-932-165-936	Sequence 548, Appl
256	9	15	US-10-109-171-125	Sequence 136, App	329	3	27.3	10	12	US-09-932-165-1063	Sequence 936, Appl
257	9	15	US-08-344-823-252	Sequence 252, App	330	3	27.3	10	12	US-09-932-165-1091	Sequence 1063, Appl
258	10	8	US-08-327-949.27	Sequence 27, Appl	331	3	27.3	10	12	US-09-932-165-1097	Sequence 1091, Appl
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405	3	27.3	11	10	US-09-843-629-17	Sequence 17, Appl	478	3	27.3	12	12	US-10-190-082-498	Sequence 498, App
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427	3	27.3	11	11	US-09-731-894-96	Sequence 96, Appl	500	3	27.3	12	15	US-10-174-105A-139	Sequence 139, App
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438	3	27.3	12	8	US-08-927-984-51	Sequence 51, App							
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## ALIGNMENTS

## RESULT 1

US-10-116-391-1  
: Sequence 1, Application: US/10116391  
: Publication No. US20030087255A1  
: GENERAL INFORMATION:  
: APPLICANT: BARRIKAULT, DENIS  
: APPLICANT: AGUIR, JOSE  
: TITLE OF INVENTION: PEPTIDES WHICH STIMULATE THE IMMUNE RESPONSE AND TISSUE  
: FILE REFERENCE: 1081-C2  
: CURRENT APPLICATION NUMBER: US/10/116,391  
: PRIOR FILING DATE: 2002-04-04  
: PRIOR FILING DATE: 2003-10-06  
: PRIOR FILING DATE: 1999-10-12  
: NUMBER OF SEQ. ID NOS: 22  
: SOFTWARE: Patent In Ver. 2.1  
: SEQ. ID NO: 1  
: LENGTH: 14

1 TYPE: PRT  
 2 ORGANISM: Unknown Organism  
 3 FEATURE:  
 4 OTHER INFORMATION: Description of Unknown Organism. HARP peptide fragment  
 5 US 10-116-391-1

Query Match: 45.5%; Score 5; DB 15; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEKP 6  
 11111  
 DB 2 KKEKP 6

RESULT 2  
 US-10-079-167-2  
 : Sequence 2; Application US/10079167  
 : Publication No. US20030138454A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Hill, Adrian V.S.  
 : APPLICANT: McShane, Helen  
 : APPLICANT: Gilbert, Sarah C.  
 : APPLICANT: Reece, William  
 : APPLICANT: Schneider, Joerg  
 : TITLE OF INVENTION: Vaccination Method  
 : FILE REFERENCE: 2907.1006-001  
 : CURRENT APPLICATION NUMBER: US/10-079-167  
 : CURRENT FILING DATE: 2002-02-19  
 : PRIOR APPLICATION NUMBER: US 09/454,204  
 : PRIOR FILING DATE: 1999-12-09  
 : PRIOR APPLICATION NUMBER: PCT/US98/01681  
 : PRIOR FILING DATE: 1998-06-09  
 : PRIOR APPLICATION NUMBER: GB 97 11957.2  
 : PRIOR FILING DATE: 1997-05-09  
 : PRIOR APPLICATION NUMBER: PCT/US96/04116  
 : PRIOR FILING DATE: 2001-09-13  
 : PRIOR APPLICATION NUMBER: GB 00 23204.3  
 : PRIOR FILING DATE: 2001-09-21  
 : NUMBER OF SEQ ID NOS: 99  
 : SOFTWARE: FASTSEQ for Windows Version 4.0  
 : SEQ ID NO: 2  
 : LENGTH: 6  
 : TYPE: PRT  
 : ORGANISM: Unknown  
 : FEATURE:  
 : OTHER INFORMATION: CTL Epitope of the Major Histocompatibility Complex

Query Match: 36.4%; Score 1; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 US 10-079-167-2  
 QY 8 KPNQ 11  
 1111  
 DB 3 KPNQ 4  
 RESULT 3  
 US-10-128-711-19  
 : Sequence 19; Application US/10128711  
 : Publication No. US20030099634A1  
 : GENERAL INFORMATION:  
 : APPLICANT: VITIELLO, Maria A.  
 : CHESTNUT, Robert W.  
 : SETTE, Alessandro D.  
 : CELIS, Esteban  
 : GRAY, Howard  
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
 : CTL IMMUNITY  
 : NUMBER OF SEQUENCES: 153  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend and Townsend Knowledge and Law

1 STREET: Stewart Street Tower, One Market Plaza  
 2 CITY: San Francisco  
 3 STATE: California  
 4 COUNTRY: US  
 5 ZIP: 94105-1493  
 6 COMPUTER READABLE FORM:  
 7 MEDIUM TYPE: Floppy disk  
 8 COMPUTER: IBM PC Compatible  
 9 OPERATING SYSTEM: PC-DOS/MS-DOS  
 10 SOFTWARE: Patent In Release #1.0, Version #1.25  
 11 CURRENT APPLICATION DATA:  
 12 APPLICATION NUMBER: US/10/128-711  
 13 FILING DATE: 22-Apr-2002  
 14 CLASSIFICATION: <Unknown>  
 15 PRIOR APPLICATION DATA:  
 16 APPLICATION NUMBER: US/08/197,484  
 17 FILING DATE: 16-FEB-1994  
 18 APPLICATION NUMBER: US 07/935,811  
 19 FILING DATE: 26-AUG-1992  
 20 APPLICATION NUMBER: US 07/874,491  
 21 FILING DATE: 27-APR-1992  
 22 APPLICATION NUMBER: US 07/827,682  
 23 FILING DATE: 29 JAN-1992  
 24 APPLICATION NUMBER: US 07/749,568  
 25 FILING DATE: 26-AUG-1991  
 26 ATTORNEY/AGENT INFORMATION:  
 27 NAME: Parmelee, Steven W.  
 28 REGISTRATION NUMBER: 31,990  
 29 REFERENCE/DOCKET NUMBER: 14137-26-4  
 30 TELECOMMUNICATION INFORMATION:  
 31 TELEPHONE: (206) 467-9600  
 32 TELEFAX: (206) 623-6793  
 33 INFORMATION FOR SEQ ID NO: 19:  
 34 SEQUENCE CHARACTERISTICS:  
 35 LENGTH: 8 amino acids  
 36 TYPE: amino acid  
 37 STRANDEDNESS: unknown  
 38 TOPOLOGY: unknown  
 39 MOLECULE TYPE: peptide  
 40 SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 41 US-10-128-711-19

Query Match: 36.4%; Score 4; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KPNQ 11  
 1111  
 DB 1 KPNQ 4

RESULT 4  
 US-10-133-210-181  
 : Sequence 181; Application US/10133210  
 : Publication No. US20030103964A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Delisi, Charles  
 : APPLICANT: Herzofsky, Jay  
 : APPLICANT: Gulukota, Kamalakara  
 : APPLICANT: Vaccaro, Dennis  
 : APPLICANT: Wong, Zhiping  
 : APPLICANT: Zhang, Chao  
 : TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND  
 : FILE REFERENCE: BU-035AX  
 : CURRENT APPLICATION NUMBER: US/10/133,210  
 : CURRENT FILING DATE: 2002-04-26  
 : NUMBER OF SEQ ID NOS: 281  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 181  
 : LENGTH: 8  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-10-133-210-181

Query Match 36.4%, Score 4; DB 15; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 Db 2 KKEK 5

## RESULT 5

US-09-010-714-1  
 : Sequence 1, Application US/09010714  
 : Patent No. US20020012942A1  
 : GENERAL INFORMATION:  
 : APPLICANT: McCarthy, James B.  
 : APPLICANT: Furcht, Leo T.  
 : APPLICANT: Iida, Joti  
 : TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED  
 : TITLE OF INVENTION: ACTIVITY  
 : FILE REFERENCE: 600.3320S01  
 : CURRENT APPLICATION NUMBER: US/09/010-714  
 : CURRENT FILING DATE: 1998-01-22  
 : NUMBER OF SEQ ID NOS: 11  
 : SOFTWARE: PatentIn Ver. 2.0  
 : SEQ ID NO 1:  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-09-010-714-1

Query Match 36.4%, Score 4; DB 9; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 Db 1 KKEK 4

## RESULT 6

US-09-984-056-10  
 : Sequence 10, Application US/09984056  
 : Patent No. US20020120106A1  
 : GENERAL INFORMATION:  
 : APPLICANT: HOGGCH, ELENORE S.  
 : TITLE OF INVENTION: ANTHRAX AND SMALL POX PREVENTION AND METHODS OF USE  
 : FILE REFERENCE: 09425-46903  
 : CURRENT APPLICATION NUMBER: US/09/984-056  
 : CURRENT FILING DATE: 2001-10-26  
 : PRIOR APPLICATION NUMBER: 60/303,396  
 : PRIOR FILING DATE: 2001-07-09  
 : PRIOR APPLICATION NUMBER: 60/278,761  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 09/146,755  
 : PRIOR FILING DATE: 1998-09-04  
 : PRIOR APPLICATION NUMBER: 09/617,144  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 08/198,139  
 : PRIOR FILING DATE: 1994-02-17  
 : NUMBER OF SEQ ID NOS: 103  
 : SOFTWARE: PatentIn 2.1  
 : SEQ ID NO 10  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Staphylococcus aureus  
 US-09-984-056-10

Query Match 36.4%, Score 4; DB 10; Length 9;

Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 Db 1 KKEK 4

## RESULT 7

US-09-984-057-10  
 : Sequence 10, Application US/09984057  
 : Patent No. US20020151677A1  
 : GENERAL INFORMATION:  
 : APPLICANT: HOGGCH, ELENORE S.  
 : TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING  
 : TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES  
 : FILE REFERENCE: 09425-46902  
 : CURRENT APPLICATION NUMBER: US/09/984,057  
 : CURRENT FILING DATE: 2001-10-26  
 : PRIOR APPLICATION NUMBER: 60/303,396  
 : PRIOR FILING DATE: 2001-07-09  
 : PRIOR APPLICATION NUMBER: 60/278,761  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 09/146,755  
 : PRIOR FILING DATE: 1998-09-04  
 : PRIOR APPLICATION NUMBER: 09/817,144  
 : PRIOR FILING DATE: 2001-03-27  
 : PRIOR APPLICATION NUMBER: 08/198,139  
 : PRIOR FILING DATE: 1994-02-17  
 : NUMBER OF SEQ ID NOS: 90  
 : SOFTWARE: PatentIn 2.1  
 : SEQ ID NO 10  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Staphylococcus aureus  
 US-09-984-057-10

Query Match 36.4%, Score 4; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
 Db 1 KKEK 4

## RESULT 8

US-10-077-106-13  
 : Sequence 13, Application US/10077106  
 : Publication No. US20030166531A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Cgillins, Mary  
 : APPLICANT: Madrenas, Joaquin  
 : APPLICANT: Cairneo, Beatriz  
 : APPLICANT: Kuchroo, Vijay  
 : TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE  
 : TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND  
 : FILE REFERENCE: GNN-027  
 : CURRENT APPLICATION NUMBER: US/10/077,106  
 : CURRENT FILING DATE: 2002-02-15  
 : PRIOR APPLICATION NUMBER: 60/269,757  
 : PRIOR FILING DATE: 2001-02-16  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 13  
 : LENGTH: 9  
 : TYPE: PRT  
 : ORGANISM: Homo sapiens  
 US-10-077-106-13

Query Match 36.4%, Score 4; DB 12; Length 9;

```

best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 9
US-10-077-106-15
: Sequence 15, Application US/100/7106
: Publication No. US20030166541A;
: GENERAL INFORMATION:
: APPLICANT: Collins, Mary
: APPLICANT: Madrenas, Joaquin
: APPLICANT: Carreno, Beatriz
: APPLICANT: Kuchroo, Vijay
: TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
: TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
: FILE REFERENCE: GNN-027
: CURRENT APPLICATION NUMBER: US/10/077,106
: PRIOR FILING DATE: 2002-02-15
: PRIOR FILING DATE: 2001-02-16
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-077-106-15

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 10
US-10-211-207-13
: Sequence 14, Application US/10211207
: Publication No. US2003004113A1
: GENERAL INFORMATION:
: APPLICANT: Collins, Mary
: APPLICANT: Madrenas, Joaquin
: APPLICANT: Carreno, Beatriz
: APPLICANT: Kuchroo, Vijay
: TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
: TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
: FILE REFERENCE: GNN-027
: CURRENT APPLICATION NUMBER: US/10/211,207
: CURRENT FILING DATE: 2002-08-02
: PRIOR FILING DATE: 2002-08-02
: PRIOR FILING DATE: 2002-02-15
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-211-207-13

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 11
US-10-211-207-15
: Sequence 15, Application US/10211207
: Publication No. US2003004113A1
: GENERAL INFORMATION:
: APPLICANT: Collins, Mary
: APPLICANT: Madrenas, Joaquin
: APPLICANT: Carreno, Beatriz
: APPLICANT: Kuchroo, Vijay
: TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
: TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
: FILE REFERENCE: GNN-027
: CURRENT APPLICATION NUMBER: US/10/211,207
: CURRENT FILING DATE: 2002-08-02
: PRIOR FILING DATE: 2002-08-02
: PRIOR FILING DATE: 2002-02-15
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-211-207-15

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 6 KKEK 9

RESULT 12
US-10-133-210-58
: Sequence 58, Application US/10133210
: Publication No. US20030103964A1
: GENERAL INFORMATION:
: APPLICANT: Delisi, Charles
: APPLICANT: Berzofsky, Jay
: APPLICANT: Gulukota, Kamalakr
: APPLICANT: Vaccaro, Dennis
: APPLICANT: Weng, Zhiping
: APPLICANT: Zhang, Chao
: TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
: FILE REFERENCE: BU-035AX
: CURRENT APPLICATION NUMBER: US/10/133,210
: CURRENT FILING DATE: 2002-04-26
: NUMBER OF SEQ ID NOS: 281
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 58
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-58

Query Match 36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
   III
Db 4 KKEK 7

RESULT 13

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US-10-211-088-27:
: Sequence 271, Application US/1021-088
: Publication No. US20030104479A1
: GENERAL INFORMATION:
: APPLICANT: Bright, Gary R.
: APPLICANT: Prekumar, D. David
: APPLICANT: Chen, Yih-Tai
: TITLE OF INVENTION: Fast in Proteins And Assays For Molecular B
: FILE REFERENCE: 01-1022-US
: CURRENT APPLICATION NUMBER: US/10-211-088
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/395,395
: PRIOR FILING DATE: 2001-08-01
: PRIOR APPLICATION NUMBER: 60/341,589
: PRIOR FILING DATE: 2001-12-13
: NUMBER OF SEQ ID NOS: 366
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 271
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Artificial sequence
: OTHER INFORMATION: Nuclear localization signal
US-10-211-088 271

Query Match          36.4%: Score 4; DB 1b; Length 9;
Best Local Similarity 100.0%: Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
DB 1111
: KKEK 4

RESULT 14
US-09-010-714-4
: Sequence 4, Application US/09010714
: Patent No. US20020012942A1
: GENERAL INFORMATION:
: APPLICANT: McCarthy, James B.
: APPLICANT: Furcht, Leo T.
: APPLICANT: Lida, Joel
: TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 1 INTEGRIN SIGNAL RELATED
: TITLE OF INVENTION: ACTIVITY
: FILE REFERENCE: 600,332US01
: CURRENT APPLICATION NUMBER: US/09-010-714
: CURRENT FILING DATE: 1998-01-22
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 4
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
US-09-010-714-4

Query Match          36.4%: Score 4; DB 9; Length 10;
Best Local Similarity 100.0%: Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
DB 1111
: KKEK 4

RESULT 15
US-09-984-056-91
: Sequence 91, Application US/09984056
: Patent No. US20020120106A1
: GENERAL INFORMATION:
: APPLICANT: BOGUCH, SAMUEL
: APPLICANT: BOGUCH, ELENOR S.
: TITLE OF INVENTION: ANTHRAX AND SMALL POX RESISTING AND METHODS OF USE
: FILE REFERENCE: 09425-46903

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: CURRENT APPLICATION NUMBER: US/09/984,056
: CURRENT FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: 60/303,396
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: 60/278,761
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/146,745
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 09/817,144
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 08/198,149
: PRIOR FILING DATE: 1994-02-17
: NUMBER OF SEQ ID NOS: 103
: SOFTWARE: PatentIn 2.1
: SEQ ID NO 91
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Bacillus anthracis
US-09-984-056-91

```

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Query Match          36.4%: Score 4; DB 10; Length 10;
Best Local Similarity 100.0%: Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 KKEK 5
DB 1111
: KKEK 6

```

```

RESULT 16
US-09-876-904A-572
: Sequence 572, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: FILE REFERENCE: TB-2002-00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 572
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
: FEATURE:
: OTHER INFORMATION: Yeast CBF5p.
US-09-876-904A-572

```

```

Query Match          36.4%: Score 4; DB 11; Length 10;
Best Local Similarity 100.0%: Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 KKEK 5
DB 1111
: KKEK 4

```

```

RESULT 17
US-09-572-404B 1774
: Sequence 1774, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572,404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203

```

```

: SOFTWARE: ProPatent version 1.0
: SEQ ID NO: 1774
: LENGTH: 10
: TYPE: PRI
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: Sequence located in MAPle at 453-454 and may interact with Sequen
: OTHER INFORMATION: in this patent.
US-09-572-404B 1774

Query Match      36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4; 1e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKEK 6
DB 1 KKEK 4

RESULT 18
US-10-155-693-26
: Sequence 26, Application US/10155693
: Publication No. US20030175876A1
: GENERAL INFORMATION:
: APPLICANT: FOX, GARY M.
: APPLICANT: KING, SHUOLAN
: APPLICANT: WEN, DUANZHI
: TITLE OF INVENTION: GLIAL CELL LINE DERIVED NEUR TROPHIC FACTOR RECEPTOR
: FILE REFERENCE: A-401C
: CURRENT APPLICATION NUMBER: US/10/155-693
: CURRENT FILING DATE: 2002-05-24
: PRIOR APPLICATION NUMBER: US/06/547,199
: PRIOR FILING DATE: 1997-04-14
: PRIOR APPLICATION NUMBER: US 60/615,907
: PRIOR FILING DATE: 1996-04-22
: PRIOR APPLICATION NUMBER: US 60/717,421
: PRIOR FILING DATE: 1996-05-09
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 26
: LENGTH: 10
: TYPE: PRI
: ORGANISM: HUMAN
US-10-155-693-26

Query Match      36.4% Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4; 1e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKEK 5
DB 1 KKEK 9

RESULT 19
US-10-239-313A-459
: Sequence 459, Application US/1023933A
: Publication No. US20030175285A1
: GENERAL INFORMATION:
: APPLICANT: KLINGNER - HAMOUR, Christine
: APPLICANT: CORVAIA, Nathalie
: APPLICANT: BECK, Alain
: APPLICANT: GOETSCH, Liliane
: TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
: TITLE OF INVENTION: N-TERMINAL A GLUTAMIN ACID-PP A GLUTAMINE IN THE FORM
: TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE SAVING ACID
: FILE REFERENCE: 343 727 - US
: CURRENT APPLICATION NUMBER: US/10/239-313A
: CURRENT FILING DATE: 2002-09-19
: PRIOR APPLICATION NUMBER: FR 00/56711
: PRIOR FILING DATE: 2000-03-23
: PRIOR APPLICATION NUMBER: PCT 01/30772
: PRIOR FILING DATE: 2001-03-22

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```

: NUMBER OF SEQ ID NOS: 697
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 458
: LENGTH: 10
: TYPE: PRI
: ORGANISM: Human Immunodeficiency virus
US-10-239-313A-458

Query Match      46.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4; 1e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
DB 4 KKEK 7

RESULT 20
US-10-133-210-31
: Sequence 31, Application US/10133210
: Publication No. US20030103964A1
: GENERAL INFORMATION:
: APPLICANT: Delisi, Charles
: APPLICANT: Berzofsky, Jay
: APPLICANT: Gulakota, Kamalakar
: APPLICANT: Vaccaro, Dennis
: APPLICANT: Weng, Zhiping
: APPLICANT: Zhang, Chao
: TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
: TITLE OF INVENTION: COMPOSITIONS THEREOF
: FILE REFERENCE: RU-035AX
: CURRENT APPLICATION NUMBER: US/10/133-210
: CURRENT FILING DATE: 2002-04-26
: NUMBER OF SEQ ID NOS: 281
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 31
: LENGTH: 10
: TYPE: PRI
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-31

Query Match      46.4% Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 4; 1e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5
DB 4 KKEK 7

RESULT 21
US-10-133-210-92
: Sequence 92, Application US/10133210
: Publication No. US20030103964A1
: GENERAL INFORMATION:
: APPLICANT: Delisi, Charles
: APPLICANT: Berzofsky, Jay
: APPLICANT: Gulakota, Kamalakar
: APPLICANT: Vaccaro, Dennis
: APPLICANT: Weng, Zhiping
: APPLICANT: Zhang, Chao
: TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
: TITLE OF INVENTION: COMPOSITIONS THEREOF
: FILE REFERENCE: RU 035AX
: CURRENT APPLICATION NUMBER: US/10/133-210
: CURRENT FILING DATE: 2002-04-26
: NUMBER OF SEQ ID NOS: 281
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 92
: LENGTH: 10
: TYPE: PRI

```

1 ORGANISM: Artificial Sequence  
 2 FEATURE:  
 3 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 4 US 10 72 602B 503

Query Match 36.4% Score 4 DB 10 Length 10  
 Best Local Similarity 100.0% Pred. No. 4.1e+02

Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KKEK 5

DB 7 KKEK 10

RESULT 24

US 10 072 602B 503

1 Sequence 503, Application US/10/72602B

2 Publication No. US2003019670A1

3 GENERAL INFORMATION:

4 APPLICANT: University of Utah Research Foundation

5 APPLICANT: Cognetix, Inc.

6 APPLICANT: Olivera, Baldomero M.

7 APPLICANT: McIntosh, C. Michael

8 APPLICANT: Watkins, Marion

9 APPLICANT: Garrett, James E.

10 APPLICANT: Gray, Lourdes C.

11 APPLICANT: Grilley, Michelle

12 APPLICANT: Schoenfeld, Robert M.

13 APPLICANT: Walker, Craig

14 APPLICANT: Shetty, Reshma

15 APPLICANT: Jones, Robert M.

16 TITLE OF INVENTION: Cone Scall Peptides

17 FILE REFERENCE: 2314 249

18 CURRENT APPLICATION NUMBER: US/10/072602B

19 CURRENT FILING DATE: 2002-02-11

20 PRIOR APPLICATION NUMBER: US 60/267,408

21 PRIOR FILING DATE: 2001-02-09

22 NUMBER OF SEQ ID NOS: 638

23 SOFTWARE: Patent in version 3.0

24 SEQ ID NO 503

25 LENGTH: 10

26 TYPE: PRT

27 ORGANISM: Agents characteristics

28 US-10-072 602B 503

Query Match 36.4% Score 4 DB 10 Length 10  
 Best Local Similarity 100.0% Pred. No. 4.1e+02

Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 ENKE 7

DB 6 ENKE 7

RESULT 24

US 10 072 602B 503

1 Sequence 503, Application US/08787443

2 Patent No. US200405564A1

3 GENERAL INFORMATION:

4 APPLICANT: Van Eyk, Jennifer E.

5 APPLICANT: Max, Alan S.

6 APPLICANT: Cole, Graham P.

7 TITLE OF INVENTION: Methods of Modulating Mast Cell Activation

8 FILE REFERENCE: 1997-021-0308

9 CURRENT APPLICATION NUMBER: US/09/876,904A

10 CURRENT FILING DATE: 2001-06-14

11 PRIOR APPLICATION NUMBER: 60/055,476

12 PRIOR FILING DATE: 1997-06-23

13 PRIOR APPLICATION NUMBER: 60/059,505

14 PRIOR FILING DATE: 1998-06-16

15 NUMBER OF SEQ ID NOS: 26

16 SOFTWARE: Patent in Ver. 2.1

17 SEQ ID NO 10

1 LENGTH: 11

2 TYPE: PRT

3 ORGANISM: Unknown

4 FEATURE:

5 NAME/KEY: PEPTIDE

6 LOCATION: (1)...(11)

7 OTHER INFORMATION: Residues 424 to 443 of chicken gizzard caldesmon

8 NAME/KEY: PEPTIDE

9 LOCATION: (11)

10 OTHER INFORMATION: Targeted Ser phospho-amino acid

11 US-09-876-904A-247

Query Match 46.4% Score 4 DB 9 Length 11  
 Best Local Similarity 100.0% Pred. No. 4.5e+02

Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 AKKE 4

DB 7 AKKE 10

RESULT 24

US-09-876-904A-247

1 Sequence 237, Application US/09876904A

2 Publication No. US2003007274A1

3 GENERAL INFORMATION:

4 APPLICANT: HOGLIKAS, TENI

5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

6 AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

7 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOOME COMPLEXES

8 FILE REFERENCE: TB-2002-00

9 CURRENT APPLICATION NUMBER: US/09/876,904A

10 CURRENT FILING DATE: 2001-06-08

11 PRIOR APPLICATION NUMBER: US 60/210,925

12 PRIOR FILING DATE: 2000-09-09

13 NUMBER OF SEQ ID NOS: 629

14 SOFTWARE: Patent in Ver. 2.1

15 SEQ ID NO 237

16 LENGTH: 11

17 TYPE: PRT

18 ORGANISM: Unknown Sequence

19 FEATURE:

20 OTHER INFORMATION: Description of Unknown Organism: Hydrophilic protein

21 US-09-876-904A-237

Query Match 46.4% Score 4 DB 11 Length 11  
 Best Local Similarity 100.0% Pred. No. 4.5e+02

Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 KKEK 5

DB 7 KKEK 10

RESULT 25

US-09-876-904A-254

1 Sequence 354, Application US/09876904A

2 Publication No. US2003007274A1

3 GENERAL INFORMATION:

4 APPLICANT: HOGLIKAS, TENI

5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

6 AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

7 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOOME COMPLEXES

8 FILE REFERENCE: TB-2002-00

9 CURRENT APPLICATION NUMBER: US/09/876,904A

10 CURRENT FILING DATE: 2001-06-08

11 PRIOR APPLICATION NUMBER: US 60/210,925

12 PRIOR FILING DATE: 2000-09-09

13 NUMBER OF SEQ ID NOS: 629

14 SOFTWARE: Patent in Ver. 2.1

15 SEQ ID NO 254

16 LENGTH: 11

17 TYPE: PRT

ORGANISM: Homo sapiens  
OTHER INFORMATION: Human ATF-3 (in basic region that binds DNA)  
US-09-876-904A-354

Query Match 36.4% Score 4; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKEK 5  
DB 7 KKEK 10

## RESULT 26

US-09-767-395-24

Sequence 24, Application US/09767395

Patent No. US20020004215A1

GENERAL INFORMATION:

APPLICANT: Osbourn, Jane K

Debyshire, Elaine J

McCaferly, John G

Vaughan, Tristan J

Johnson, Kevin S

TITLE OF INVENTION: Labelling and selection of molecules

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, G'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 243 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Vers.00, #1.25 (EPC)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/767,395

FILING DATE: 23-Jan-2001

C:ASSIGNATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/058,244

FILING DATE: <Unknown>

APPLICATION NUMBER: PCT/US97/01455

FILING DATE: 08-JUL-1997

APPLICATION NUMBER: GB 9714292.4

FILING DATE: 08-JUL-1997

APPLICATION NUMBER: GB 972484.4

FILING DATE: 29-NOV-1996

APPLICATION NUMBER: GB 9712618.5

FILING DATE: 18-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: David W. Clough

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 28111/44800

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-767-395-24

Query Match 36.4% Score 4; DB 9; Length 13;

Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NKPN 10  
DB 4 NKPN 4

## RESULT 27

US-09-873-676-27

Sequence 27, Application US/09873676

Patent No. US20020077289A1

GENERAL INFORMATION:

APPLICANT: MacDonald, Nicholas J.

APPLICANT: Sim, Kim L.

TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of U

FILE REFERENCE: 05213-0378 (43170-259333)

CURRENT APPLICATION NUMBER: US/09/873,676

CURRENT FILING DATE: 2001-06-04

PRIOR APPLICATION NUMBER: US 60/209,065

PRIOR FILING DATE: 2000-06-02

PRIOR APPLICATION NUMBER: US 60/289,387

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 123

SOFTWARE: PatentIn version 3.1

SEQ ID NO 27

LENGTH: 13

TYPE: PMT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthetic binding peptide

US-09-873-676-27

Query Match 36.4% Score 4; DB 9; Length 13;

Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKEP 6  
DB 3 KKEP 5

## RESULT 28

US-09-359-325A-18

Sequence 18, Application US/09359325A

Patent No. US20020107226A1

GENERAL INFORMATION:

APPLICANT: Berlin, Vivian

Levin, David

Ohya, Yoshikazu

TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING

ANTI-FUNGAL AGENTS, AND USES RELATED THERETO

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordpad

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/359,325A

FILING DATE: 22-Jul-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/631,319

FILING DATE: 11-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-074.08

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:



```

1  LENGTH: 13 amino acids
2  TYPE: amino acid
3  STRANDEDNESS: <unknown>
4  TOPOLOGY: linear
5  MOLECULE TYPE: protein
6  SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-459-425A-18

Query Match
Best Local Similarity 36.4%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 29
US-09-459-425A-19
1  Sequence 29, Application US/09359425A
2  Patent No. US20020107226A1
3  GENERAL INFORMATION:
4  APPLICANT: Berlin, Vivian
5  Levin, David
6  Ohya, Yoshikazu
7  TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING
8  ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
9  NUMBER OF SEQUENCES: 31
10  CORRESPONDENCE ADDRESS:
11  ADDRESSEE: FOLEY, HOAG & ERICK LLP
12  STREET: One Post Office Square
13  CITY: Boston
14  STATE: MA
15  COUNTRY: USA
16  ZIP: 02109-2170
17  COMPUTER READABLE FORM:
18  MEDIUM TYPE: Floppy disk
19  COMPUTER: IBM PC compatible
20  OPERATING SYSTEM: PC-DOS/MS-DOS
21  SOFTWARE: WordPad
22  CURRENT APPLICATION DATA:
23  APPLICATION NUMBER: US/09/459,425A
24  FILING DATE: 22-Jul-1999
25  PRIOR APPLICATION NUMBER:
26  APPLICATION NUMBER: US 08/641,419
27  FILING DATE: 11-Apr-1996
28  ATTORNEY/AGENT INFORMATION:
29  NAME: Vincent, Matthew L.
30  REGISTRATION NUMBER: 36,799
31  REFERENCE/DOC# NUMBER: MIV 074.06
32  TELECOMMUNICATION INFORMATION:
33  TELEPHONE: 617-832-1300
34  TELEFAX: 617-832-7000
35  INFORMATION FOR SEQ ID NO: 19:
36  SEQUENCE CHARACTERISTICS:
37  LENGTH: 13 amino acids
38  TYPE: amino acid
39  STRANDEDNESS: <unknown>
40  TOPOLOGY: linear
41  MOLECULE TYPE: protein
42  SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-459-425A-19

Query Match
Best Local Similarity 36.4%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 30
US-09-459-425A-19
1  Sequence 30, Application US/0945249
2  Patent No. US20020168748A1
3  GENERAL INFORMATION:
4  APPLICANT: BERLIN, VIVIAN
5  APPLICANT: DAMAGNEZ, VERONIQUE
6  APPLICANT: SMITH, SUSAN E.
7  TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
8  AND USES RELATED THERETO
9  FILE REFERENCE: MIV-074.06
10  CURRENT APPLICATION NUMBER: US/09/945,249
11  PRIOR APPLICATION NUMBER: 09/041,990
12  PRIOR FILING DATE: 2001-08-31
13  PRIOR FILING DATE: 1996-12-20
14  PRIOR APPLICATION NUMBER: 08/631,319
15  PRIOR FILING DATE: 1996-04-11
16  NUMBER OF SEQ ID NOS: 89
17  SOFTWARE: PatentIn Ver. 2.1
18  SEQ ID NO 24
19  LENGTH: 13
20  TYPE: PR1
21  ORGANISM: Homo sapiens
22  US-09-945-249-29

Query Match
Best Local Similarity 100.0%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 31
US-09-945-249-29
1  Sequence 29, Application US/0945249
2  Patent No. US20020168748A1
3  GENERAL INFORMATION:
4  APPLICANT: BERLIN, VIVIAN
5  APPLICANT: DAMAGNEZ, VERONIQUE
6  APPLICANT: SMITH, SUSAN E.
7  TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
8  AND USES RELATED THERETO
9  FILE REFERENCE: MIV-074.06
10  CURRENT APPLICATION NUMBER: US/09/945,249
11  CURRENT FILING DATE: 2001-08-31
12  PRIOR APPLICATION NUMBER: 09/041,990
13  PRIOR FILING DATE: 2001-01-13
14  PRIOR APPLICATION NUMBER: 08/771,212
15  PRIOR FILING DATE: 1996-12-20
16  PRIOR APPLICATION NUMBER: 08/631,319
17  PRIOR FILING DATE: 1996-04-11
18  NUMBER OF SEQ ID NOS: 89
19  SOFTWARE: PatentIn Ver. 2.1
20  SEQ ID NO 29
21  LENGTH: 13
22  TYPE: PR1
23  ORGANISM: Homo sapiens
24  US-09-945-249-29

Query Match
Best Local Similarity 100.0%; Score 4; DB 10; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNKP 9
DB 8 PNKP 11

RESULT 32
US-09-820-051A-98
```

? Sequence 88, Application US/09820053A  
? Publication No. US20030083243A1  
? GENERAL INFORMATION:  
? APPLICANT: Owen, Donald R.  
? TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES  
? FILE REFERENCE: HELX027  
? CURRENT APPLICATION NUMBER: US/99/820,53A  
? NUMBER OF SEQ ID NOS: 28  
? SOFTWARE: PatentIn Ver. 2.1  
? SEQ ID NO 88  
? LENGTH: 13  
? TYPE: PRT  
? ORGANISM: ARTIFICIAL SEQUENCE  
? FEATURE:  
? OTHER INFORMATION: SYNTHETIC SEQUENCE  
? NAME/KEY: MOD\_RES  
? LOCATION: (13)  
? OTHER INFORMATION: AMIDATION  
US-09-820-053A-88

Query Match 36.4%, Score 4, DB 10, Length 13,  
Best Local Similarity 100.0%, Pred. No. 5.1e+02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0:

QY 1 AKKE 4  
DB 9 AKKE 12

## RESULT 35

US-10-211-088-232  
? Sequence 232, Application US/10211088  
? Publication No. US20030104479A1  
? GENERAL INFORMATION:  
? APPLICANT: Bright, Gary R.  
? APPLICANT: Premkumar, D. David  
? APPLICANT: Chen, Yih-Tai  
? TITLE OF INVENTION: NO. US20030104479A1, Fusion Proteins And Assays For Molecular Biology  
? FILE REFERENCE: 01-1022-US  
? CURRENT APPLICATION NUMBER: US/10/211,088  
? PRIOR FILING DATE: 2002-10-15  
? PRIOR APPLICATION NUMBER: 60/409,395  
? PRIOR FILING DATE: 2001-08-01  
? PRIOR APPLICATION NUMBER: 60/441,529  
? PRIOR FILING DATE: 2003-12-13  
? NUMBER OF SEQ ID NOS: 366  
? SOFTWARE: PatentIn version 3.1  
? SEQ ID NO 232  
? LENGTH: 35  
? TYPE: PRT  
? ORGANISM: Artificial sequence  
? FEATURE:  
? OTHER INFORMATION: Nuclear localization signal.  
US-10-211-088-232

Query Match 36.4%, Score 4, DB 10, Length 13,  
Best Local Similarity 100.0%, Pred. No. 5.1e+02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0:

QY 2 KKEK 5  
DB 3 KKEK 6

## RESULT 34

US-10-109-171-88  
? Sequence 88, Application US/10109171  
? Publication No. US20030109452A1  
? GENERAL INFORMATION:  
? APPLICANT: Owen, Donald R.  
? TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE  
? FILE REFERENCE: HELX028

? CURRENT APPLICATION NUMBER: US/10/109,171  
? CURRENT FILING DATE: 2002-03-28  
? NUMBER OF SEQ ID NOS: 165  
? SOFTWARE: PatentIn Ver. 2.1  
? SEQ ID NO 88  
? LENGTH: 13  
? TYPE: PRT  
? ORGANISM: ARTIFICIAL SEQUENCE  
? FEATURE:  
? OTHER INFORMATION: SYNTHETIC SEQUENCE  
? NAME/KEY: MOD\_RES  
? LOCATION: (13)  
? OTHER INFORMATION: AMIDATION  
US-10-109-171-88

Query Match 36.4%, Score 4, DB 15, Length 13,  
Best Local Similarity 100.0%, Pred. No. 5.1e+02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0:

QY 2 AKKE 4  
DB 9 AKKE 12

## RESULT 35

US-09-010-714-2  
? Sequence 2, Application US/09010714  
? Patent No. US20020912942A1  
? GENERAL INFORMATION:  
? APPLICANT: McCarthy, James H.  
? APPLICANT: Furcht, Leo T.  
? APPLICANT: Iida, Joji  
? TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED  
? FILE REFERENCE: 560,332US01  
? CURRENT APPLICATION NUMBER: US/09/010,714  
? CURRENT FILING DATE: 1998-01-22  
? NUMBER OF SEQ ID NOS: 11  
? SOFTWARE: PatentIn Ver. 2.0  
? SEQ ID NO 2  
? LENGTH: 14  
? TYPE: PRT  
? ORGANISM: Homo sapiens  
US-09-010-714-2

Query Match 36.4%, Score 4, DB 9, Length 14,  
Best Local Similarity 100.0%, Pred. No. 5.4e+02,  
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0:

QY 2 KKEK 5  
DB 4 KKEK 7

## RESULT 36

US-09-966-782A-43  
? Sequence 43, Application US/09966782A  
? Publication No. US20030022183A1  
? GENERAL INFORMATION:  
? APPLICANT: Battaglin, P.  
? APPLICANT: Feder, J. N.  
? APPLICANT: Mintier, G.  
? APPLICANT: Ramanathan, C. S.  
? APPLICANT: Westphal, R.  
? APPLICANT: Hawken, D. R.  
? APPLICANT: Cacace, A.  
? APPLICANT: Barber, L.  
? APPLICANT: Kornacker, M. G.  
? TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBM7,  
? FILE REFERENCE: 00044NP  
? CURRENT APPLICATION NUMBER: US/09/966,782A  
? CURRENT FILING DATE: 2001-09-26

1 PRIOR APPLICATION NUMBER: 60/245,241  
 2 PRIOR FILING DATE: 2000-09-27  
 3 PRIOR APPLICATION NUMBER: 60/268,590  
 4 PRIOR FILING DATE: 2001-02-14  
 5 PRIOR APPLICATION NUMBER: 60/115,427  
 6 PRIOR FILING DATE: 2001-08-28  
 7 NUMBER OF SEQ ID NOS: 64  
 8 SOFTWARE: PatentIn Ver. 2.1  
 9 SEQ ID NO 43  
 10 LENGTH: 15  
 11 TYPE: PRF  
 12 ORGANISM: Artificial Sequence  
 13 FEATURE:  
 14 OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 15 OTHER INFORMATION: Polypeptide  
 16 US-09 945-249-43

Query Match 36.4% Score 4; DB 10; Length 15;

Best Local Similarity 100.0% Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 6

DB 10 KKK 13

#### RESULT 47

US-09-945-249-80

1 Sequence 80, Application US/09945249

2 Patent No. US20020168748A1

3 GENERAL INFORMATION:

4 APPLICANT: BERLIN, VIVIAN

5 APPLICANT: DAMAGNEZ, VERONIQUE

6 APPLICANT: SMITH, SUSAN E.

7 TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS.

8 FILE REFERENCE: MIV-074.06

9 CURRENT APPLICATION NUMBER: US/09/945,249

10 PRIOR FILING DATE: 2001-08-31

11 PRIOR APPLICATION NUMBER: 09/041,990

12 PRIOR FILING DATE: 2001-01-15

13 PRIOR APPLICATION NUMBER: 08/771,212

14 PRIOR FILING DATE: 1996-12-20

15 PRIOR APPLICATION NUMBER: 08/641,819

16 PRIOR FILING DATE: 1996-04-11

17 NUMBER OF SEQ ID NOS: 89

18 SOFTWARE: PatentIn Ver. 2.1

19 SEQ ID NO 80

20 LENGTH: 15

21 TYPE: PRF

22 ORGANISM: Artificial Sequence

23 FEATURE:

24 OTHER INFORMATION: Description of Artificial Sequence: peptide that

25 OTHER INFORMATION: corresponds to the C-termini of Phase of Glucase

26 OTHER INFORMATION: substrates

27 US-09 945-249-80

Query Match

Best Local Similarity 100.0% Pred. No. 5.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKK 5

DB 5 KKK 8

#### RESULT 48

US-09 945-249-80

1 Sequence 81, Application US/09945249

2 Patent No. US20020168748A1

3 GENERAL INFORMATION:

4 APPLICANT: BERLIN, VIVIAN

5 APPLICANT: DAMAGNEZ, VERONIQUE

6 APPLICANT: SMITH, SUSAN E.

7 APPLICANT: DAMAGNEZ, VERONIQUE

8 APPLICANT: SMITH, SUSAN E.

9 APPLICANT: DAMAGNEZ, VERONIQUE

10 APPLICANT: SMITH, SUSAN E.

11 APPLICANT: DAMAGNEZ, VERONIQUE

12 APPLICANT: SMITH, SUSAN E.

13 APPLICANT: DAMAGNEZ, VERONIQUE

14 APPLICANT: SMITH, SUSAN E.

15 APPLICANT: DAMAGNEZ, VERONIQUE

16 APPLICANT: SMITH, SUSAN E.

17 APPLICANT: DAMAGNEZ, VERONIQUE

18 APPLICANT: SMITH, SUSAN E.

19 APPLICANT: DAMAGNEZ, VERONIQUE

20 APPLICANT: SMITH, SUSAN E.

21 APPLICANT: DAMAGNEZ, VERONIQUE

22 APPLICANT: SMITH, SUSAN E.

23 APPLICANT: DAMAGNEZ, VERONIQUE

24 APPLICANT: SMITH, SUSAN E.

25 APPLICANT: DAMAGNEZ, VERONIQUE

26 APPLICANT: SMITH, SUSAN E.

27 APPLICANT: DAMAGNEZ, VERONIQUE

28 APPLICANT: SMITH, SUSAN E.

29 APPLICANT: DAMAGNEZ, VERONIQUE

30 APPLICANT: SMITH, SUSAN E.

31 APPLICANT: DAMAGNEZ, VERONIQUE

32 APPLICANT: SMITH, SUSAN E.

33 APPLICANT: DAMAGNEZ, VERONIQUE

34 APPLICANT: SMITH, SUSAN E.

35 APPLICANT: DAMAGNEZ, VERONIQUE

36 APPLICANT: SMITH, SUSAN E.

37 APPLICANT: DAMAGNEZ, VERONIQUE

38 APPLICANT: SMITH, SUSAN E.

39 APPLICANT: DAMAGNEZ, VERONIQUE

40 APPLICANT: SMITH, SUSAN E.

41 APPLICANT: DAMAGNEZ, VERONIQUE

42 APPLICANT: SMITH, SUSAN E.

43 APPLICANT: DAMAGNEZ, VERONIQUE

44 APPLICANT: SMITH, SUSAN E.

45 APPLICANT: DAMAGNEZ, VERONIQUE

46 APPLICANT: SMITH, SUSAN E.

47 APPLICANT: DAMAGNEZ, VERONIQUE

48 APPLICANT: SMITH, SUSAN E.

49 APPLICANT: DAMAGNEZ, VERONIQUE

50 APPLICANT: SMITH, SUSAN E.

51 APPLICANT: DAMAGNEZ, VERONIQUE

52 APPLICANT: SMITH, SUSAN E.

53 APPLICANT: DAMAGNEZ, VERONIQUE

54 APPLICANT: SMITH, SUSAN E.

55 APPLICANT: DAMAGNEZ, VERONIQUE

56 APPLICANT: SMITH, SUSAN E.

57 APPLICANT: DAMAGNEZ, VERONIQUE

58 APPLICANT: SMITH, SUSAN E.

59 APPLICANT: DAMAGNEZ, VERONIQUE

60 APPLICANT: SMITH, SUSAN E.

61 APPLICANT: DAMAGNEZ, VERONIQUE

62 APPLICANT: SMITH, SUSAN E.

63 APPLICANT: DAMAGNEZ, VERONIQUE

64 APPLICANT: SMITH, SUSAN E.

65 APPLICANT: DAMAGNEZ, VERONIQUE

66 APPLICANT: SMITH, SUSAN E.

67 APPLICANT: DAMAGNEZ, VERONIQUE

68 APPLICANT: SMITH, SUSAN E.

69 APPLICANT: DAMAGNEZ, VERONIQUE

70 APPLICANT: SMITH, SUSAN E.

71 APPLICANT: DAMAGNEZ, VERONIQUE

72 APPLICANT: SMITH, SUSAN E.

73 APPLICANT: DAMAGNEZ, VERONIQUE

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75 APPLICANT: DAMAGNEZ, VERONIQUE

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77 APPLICANT: DAMAGNEZ, VERONIQUE

78 APPLICANT: SMITH, SUSAN E.

79 APPLICANT: DAMAGNEZ, VERONIQUE

80 APPLICANT: SMITH, SUSAN E.

81 APPLICANT: DAMAGNEZ, VERONIQUE

82 APPLICANT: SMITH, SUSAN E.

83 APPLICANT: DAMAGNEZ, VERONIQUE

84 APPLICANT: SMITH, SUSAN E.

85 APPLICANT: DAMAGNEZ, VERONIQUE

86 APPLICANT: SMITH, SUSAN E.

87 APPLICANT: DAMAGNEZ, VERONIQUE

88 APPLICANT: SMITH, SUSAN E.

89 APPLICANT: DAMAGNEZ, VERONIQUE

90 APPLICANT: SMITH, SUSAN E.

91 APPLICANT: DAMAGNEZ, VERONIQUE

92 APPLICANT: SMITH, SUSAN E.

93 APPLICANT: DAMAGNEZ, VERONIQUE

94 APPLICANT: SMITH, SUSAN E.

95 APPLICANT: DAMAGNEZ, VERONIQUE

96 APPLICANT: SMITH, SUSAN E.

97 APPLICANT: DAMAGNEZ, VERONIQUE

98 APPLICANT: SMITH, SUSAN E.

99 APPLICANT: DAMAGNEZ, VERONIQUE

100 APPLICANT: SMITH, SUSAN E.

101 APPLICANT: DAMAGNEZ, VERONIQUE

102 APPLICANT: SMITH, SUSAN E.

103 APPLICANT: DAMAGNEZ, VERONIQUE

104 APPLICANT: SMITH, SUSAN E.

105 APPLICANT: DAMAGNEZ, VERONIQUE

106 APPLICANT: SMITH, SUSAN E.

107 APPLICANT: DAMAGNEZ, VERONIQUE

108 APPLICANT: SMITH, SUSAN E.

109 APPLICANT: DAMAGNEZ, VERONIQUE

110 APPLICANT: SMITH, SUSAN E.

111 APPLICANT: DAMAGNEZ, VERONIQUE

112 APPLICANT: SMITH, SUSAN E.

113 APPLICANT: DAMAGNEZ, VERONIQUE

114 APPLICANT: SMITH, SUSAN E.

115 APPLICANT: DAMAGNEZ, VERONIQUE

116 APPLICANT: SMITH, SUSAN E.

117 APPLICANT: DAMAGNEZ, VERONIQUE

118 APPLICANT: SMITH, SUSAN E.

119 APPLICANT: DAMAGNEZ, VERONIQUE

120 APPLICANT: SMITH, SUSAN E.

121 APPLICANT: DAMAGNEZ, VERONIQUE

122 APPLICANT: SMITH, SUSAN E.

123 APPLICANT: DAMAGNEZ, VERONIQUE

124 APPLICANT: SMITH, SUSAN E.

125 APPLICANT: DAMAGNEZ, VERONIQUE

126 APPLICANT: SMITH, SUSAN E.

127 APPLICANT: DAMAGNEZ, VERONIQUE

128 APPLICANT: SMITH, SUSAN E.

129 APPLICANT: DAMAGNEZ, VERONIQUE

130 APPLICANT: SMITH, SUSAN E.

131 APPLICANT: DAMAGNEZ, VERONIQUE

132 APPLICANT: SMITH, SUSAN E.

133 APPLICANT: DAMAGNEZ, VERONIQUE

134 APPLICANT: SMITH, SUSAN E.

135 APPLICANT: DAMAGNEZ, VERONIQUE

136 APPLICANT: SMITH, SUSAN E.

137 APPLICANT: DAMAGNEZ, VERONIQUE

138 APPLICANT: SMITH, SUSAN E.

139 APPLICANT: DAMAGNEZ, VERONIQUE

140 APPLICANT: SMITH, SUSAN E.

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142 APPLICANT: SMITH, SUSAN E.

143 APPLICANT: DAMAGNEZ, VERONIQUE

144 APPLICANT: SMITH, SUSAN E.

145 APPLICANT: DAMAGNEZ, VERONIQUE

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147 APPLICANT: DAMAGNEZ, VERONIQUE

148 APPLICANT: SMITH, SUSAN E.

149 APPLICANT: DAMAGNEZ, VERONIQUE

150 APPLICANT: SMITH, SUSAN E.

151 APPLICANT: DAMAGNEZ, VERONIQUE

152 APPLICANT: SMITH, SUSAN E.

153 APPLICANT: DAMAGNEZ, VERONIQUE

154 APPLICANT: SMITH, SUSAN E.

155 APPLICANT: DAMAGNEZ, VERONIQUE

156 APPLICANT: SMITH, SUSAN E.

157 APPLICANT: DAMAGNEZ, VERONIQUE

158 APPLICANT: SMITH, SUSAN E.

159 APPLICANT: DAMAGNEZ, VERONIQUE

160 APPLICANT: SMITH, SUSAN E.

161 APPLICANT: DAMAGNEZ, VERONIQUE

162 APPLICANT: SMITH, SUSAN E.

163 APPLICANT: DAMAGNEZ, VERONIQUE

164 APPLICANT: SMITH, SUSAN E.

165 APPLICANT: DAMAGNEZ, VERONIQUE

166 APPLICANT: SMITH, SUSAN E.

167 APPLICANT: DAMAGNEZ, VERONIQUE

168 APPLICANT: SMITH, SUSAN E.

169 APPLICANT: DAMAGNEZ, VERONIQUE

170 APPLICANT: SMITH, SUSAN E.

171 APPLICANT: DAMAGNEZ, VERONIQUE

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173 APPLICANT: DAMAGNEZ, VERONIQUE

174 APPLICANT: SMITH, SUSAN E.

175 APPLICANT: DAMAGNEZ, VERONIQUE

176 APPLICANT: SMITH, SUSAN E.

177 APPLICANT: DAMAGNEZ, VERONIQUE

178 APPLICANT: SMITH, SUSAN E.

179 APPLICANT: DAMAGNEZ, VERONIQUE

180 APPLICANT: SMITH, SUSAN E.

181 APPLICANT: DAMAGNEZ, VERONIQUE

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183 APPLICANT: DAMAGNEZ, VERONIQUE

184 APPLICANT: SMITH, SUSAN E.

185 APPLICANT: DAMAGNEZ, VERONIQUE

186 APPLICANT: SMITH, SUSAN E.

187 APPLICANT: DAMAGNEZ, VERONIQUE

188 APPLICANT: SMITH, SUSAN E.

189 APPLICANT: DAMAGNEZ, VERONIQUE

190 APPLICANT: SMITH, SUSAN E.

191 APPLICANT: DAMAGNEZ, VERONIQUE

192 APPLICANT: SMITH, SUSAN E.

ADDRESSEE: Clark & Ebling LLP  
 STREET: 176 Federal Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/641,610  
 FILING DATE: 01-APR-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,275  
 REFERENCE/DOCKET NUMBER: 06142/347001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-428-0200  
 TELEFAX: 617-428-7045  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 US 08-641,610-13

Query Match 27.4% Score 3: DB 8: Length 8:  
 Best Local Similarity 100.0% Pred. No. 5e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 AKK 3  
 III  
 DB 3 AKK 5

RESULT 41  
 US-05 981-824-32  
 : Sequence 12, Application US/08981824  
 : Publication No. US20020114816A1  
 : GENERAL INFORMATION:  
 : APPLICANT: ENDEL, Josef  
 : APPLICANT: STAHL, Peter  
 : APPLICANT: ALBERT, Winfried  
 : APPLICANT: SCHNEBEL, Dolores  
 : APPLICANT: BOITARD, Christian  
 : APPLICANT: VAN ENDELT, Peter  
 : APPLICANT: JUNG, Gunther-Gerhard  
 : TITLE OF INVENTION: AUTOREACTIVE PEPTIDES FROM HUMAN GLUCAMIC ACID  
 : FILE REFERENCE: 564-7029  
 : CURRENT APPLICATION NUMBER: US/08/981,824  
 : CURRENT FILING DATE: 1998-09-18  
 : EARLIER APPLICATION NUMBER: PCT/EP96/09004  
 : EARLIER FILING DATE: 1996-07-15  
 : EARLIER APPLICATION NUMBER: DE/195 25 744.7  
 : EARLIER FILING DATE: 1995-07-14  
 : NUMBER OF SEQ ID NOS: 47  
 : SOFTWARE: PatentIn Ver. 2.1  
 : SEQ ID NO 42  
 : LENGTH: 8  
 : TYPE: PKI  
 : ORGANISM: Homo sapiens  
 US 08-981 824-32

Query Match 27.4% Score 3: DB 8: Length 8:  
 Best Local Similarity 100.0% Pred. No. 5e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KEK 5  
 III  
 DB 5 KEK 7

RESULT 42  
 US-09-374-671-6  
 : Sequence 6, Application US/09374671  
 : Patent No. US20020012963A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Morquensiero, Jay P.  
 : APPLICANT: Kalciozzy, Andriey  
 : APPLICANT: Bizidaukas, Christine B.  
 : APPLICANT: Brauer, Andrew W.  
 : TITLE OF INVENTION: Allergenic Proteins and Peptides from Dog  
 : NUMBER OF SEQUENCES: 104  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 : STREET: 28 State Street  
 : CITY: Boston  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII-text  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/374,671  
 : FILING DATE:  
 : CLASSIFICATION:  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/491,861  
 : FILING DATE:  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Mandigaorian, Amy E.  
 : REGISTRATION NUMBER: 16,207  
 : REFERENCE/DOCKET NUMBER: IM1-026CP(IPC-048CP)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 227-7400  
 : TELEFAX: (617) 742-4214  
 : INFORMATION FOR SEQ ID NO: 6:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 8 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: Peptide  
 : FRAGMENT TYPE: Internal  
 : US-09-374-671-6

Query Match 27.4% Score 3: DB 9: Length 8:  
 Best Local Similarity 100.0% Pred. No. 5e+05;  
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 EXP 6  
 III  
 DB 6 EXP 8

RESULT 43  
 US-09-358-423-11  
 : Sequence 11, Application US/09358423  
 : Patent No. US20020951790A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Allan W. Clippes  
 : APPLICANT: Robert L. Clancy  
 : APPLICANT: Louis McShane  
 : APPLICANT: Christopher J. Smith  
 : APPLICANT: David R. Tyrcan  
 : APPLICANT: Row Ho

? TITLE OF INVENTION: H. PYLORI ANTIGENS  
 ? FILE REFERENCE: 064727.0106  
 ? CURRENT APPLICATION NUMBER: US/09/458,423  
 ? PRIOR FILING DATE: 1999-07-22  
 ? PRIOR APPLICATION NUMBER: GB 9701487.2  
 ? PRIOR FILING DATE: 1997-01-24  
 ? PRIOR APPLICATION NUMBER: GB 9710629.8  
 ? PRIOR FILING DATE: 1997-05-22  
 ? PRIOR APPLICATION NUMBER: PCT/GB98/00220  
 ? PRIOR FILING DATE: 1998-01-26  
 ? NUMBER OF SEQ ID NOS: 41  
 ? SOFTWARE: FASTSEQ for Windows Version 3.0  
 ? SEQ ID NO 1:  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: H. pylori  
 US 09-358 423-11

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKE 5  
 DB 111  
 5 KKE 5

RESULT 44  
 US-09-458 423-12  
 ? Sequence 12, Application US/09/58424  
 ? Patent No. US20020051750A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Allan W. Cripps  
 ? APPLICANT: Robert L. Clancy  
 ? APPLICANT: Lois McShane  
 ? APPLICANT: Christopher J. Smith  
 ? APPLICANT: David R. Tyreman  
 ? APPLICANT: How Ho  
 ? TITLE OF INVENTION: H. PYLORI ANTIGENS  
 ? FILE REFERENCE: 064727.0106  
 ? CURRENT APPLICATION NUMBER: US/09/458,423  
 ? PRIOR FILING DATE: 1999-07-22  
 ? PRIOR APPLICATION NUMBER: GB 9701487.2  
 ? PRIOR FILING DATE: 1997-01-24  
 ? PRIOR APPLICATION NUMBER: GB 9710629.8  
 ? PRIOR FILING DATE: 1997-05-22  
 ? PRIOR APPLICATION NUMBER: PCT/GB98/00220  
 ? PRIOR FILING DATE: 1998-01-26  
 ? NUMBER OF SEQ ID NOS: 41  
 ? SOFTWARE: FASTSEQ for Windows Version 3.0  
 ? SEQ ID NO 12  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: H. pylori  
 US-09-458 423-12

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKE 5  
 DB 111  
 3 KKE 5

RESULT 45  
 US 09-804-733A 19  
 ? Sequence 19, Application US/09/804733A  
 ? Patent No. US20020059656A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Monsanto Company  
 ? TITLE OF INVENTION: RECOMBINANT PROTEINS CONTAINING REPEATING UNITS  
 ? FILE REFERENCE: MTC6614.2

? CURRENT APPLICATION NUMBER: US/09/804,733A  
 ? CURRENT FILING DATE: 2001-03-13  
 ? PRIOR APPLICATION NUMBER: US 60/188,990  
 ? PRIOR FILING DATE: 2000-03-13  
 ? NUMBER OF SEQ ID NOS: 29  
 ? SOFTWARE: Patent in version 3.0  
 ? SEQ ID NO 19  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial Sequence  
 ? FEATURE:  
 ? NAME/KEY: VARIANT  
 ? LOCATION: (1)-(6)  
 ? OTHER INFORMATION: fusion protein  
 US 09-804-733A 19

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KPN 7  
 DB 111  
 5 KPN 7

RESULT 46  
 US-09-813-653 5  
 ? Sequence 5, Application US/09/813653  
 ? Patent No. US20020064770A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Nestor, John  
 ? APPLICANT: Wilson, Carol  
 ? APPLICANT: See, Raymond  
 ? APPLICANT: Tan, Hehir, Christina  
 ? TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compou  
 ? FILE REFERENCE: CNS 005  
 ? CURRENT APPLICATION NUMBER: US/09/813,653  
 ? CURRENT FILING DATE: 2001-03-20  
 ? PRIOR APPLICATION NUMBER: US 60/190,946  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: US 60/190,996  
 ? PRIOR FILING DATE: 2000-03-21  
 ? PRIOR APPLICATION NUMBER: US 60/191,299  
 ? NUMBER OF SEQ ID NOS: 44  
 ? SOFTWARE: Patent in version 3.0  
 ? SEQ ID NO 5  
 ? LENGTH: 8  
 ? TYPE: PRT  
 ? ORGANISM: Artificial sequence  
 ? FEATURE:  
 ? OTHER INFORMATION: preferred peptide for pdz binding domain  
 US-09-813-653-5

Query Match 27.3% Score 3; DB 9; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 KKE 4  
 DB 111  
 3 KKE 5

RESULT 47  
 US-09-813-448-2  
 ? Sequence 2, Application US/09/813448  
 ? Patent No. US20020142346A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Nestor, John  
 ? APPLICANT: Wilson, Carol  
 ? TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou  
 ? FILE REFERENCE: CNS-006  
 ? CURRENT APPLICATION NUMBER: US/09/813,448

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: CURRENT FILING DATE: 2001-03-20
: PRIOR APPLICATION NUMBER: US 60/190,946
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/150,996
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/141,293
: PRIOR FILING DATE: 2000-03-21
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: preferred amino acids for PL2 binding domain
US-09-813 448-2

```

```

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 KKE 4
   |||
Db 3 KKE 5

```

```

RESULT 48
US-09-956 955A-7
: Sequence 7, Application US/09466955A
: Patent No. US2002015563A1
: GENERAL INFORMATION:
: APPLICANT: Perez Villar, Juan J.
: APPLICANT: Chang, Han
: APPLICANT: Yang, Wen-Pin
: APPLICANT: Wu, Yuli
: APPLICANT: Whitney, Gena S.
: APPLICANT: Kanner, Steven B.
: TITLE OF INVENTION: Identification and cloning of a full length Human
: TITLE OF INVENTION: Cink-related gene, MIST (Mast cell immunoreceptor)
: TITLE OF INVENTION: Signal transducer
: FILE REFERENCE: 3053-4113051
: CURRENT APPLICATION NUMBER: US/09/966,955A
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 60/237060
: PRIOR FILING DATE: 2000-09-29
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 8
: TYPE: PRT
: ORGANISM: HUMAN
: FEATURE:
: OTHER INFORMATION: PHOSPHOPETIDE DERIVED FROM THE SEQUENCE OF HUMAN
: OTHER INFORMATION: SEP-75
: NAME/KEY: MOD_RES
: LOCATION: (3)
: OTHER INFORMATION: PHOSPHORYLATION: TYR IN POSITION 43 IS
: OTHER INFORMATION: PHOSPHORYLATED.
US-09-956 955A-7

```

```

Query Match 27.3% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 9 PND 11
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Db 6 PND 8

```

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RESULT 49
US-09-726-470A-67
: Sequence 67, Application US/09726470A

```

```

: Publication No. US200300346628A1
: GENERAL INFORMATION:
: APPLICANT: Zheleva, Daniela I
: APPLICANT: Fischer, Peter M
: APPLICANT: McInnes, Campbell
: APPLICANT: Andrews, Martin JI
: APPLICANT: Chao, Wenq C
: APPLICANT: Atkinson, Gail E
: TITLE OF INVENTION: p21 Peptides
: FILE REFERENCE: C01-014
: CURRENT APPLICATION NUMBER: US/09/726,470A
: CURRENT FILING DATE: 2000-11-29
: PRIOR APPLICATION NUMBER: GB 9928333.6
: PRIOR FILING DATE: 1999-11-30
: NUMBER OF SEQ ID NOS: 275
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 67
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: p21 derived
: OTHER INFORMATION: peptide
: OTHER INFORMATION: Synthesised with free amino terminus and as the
: OTHER INFORMATION: C-terminal carboxamide
US-09-726-470A-67

```

```

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 AKK 3
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Db 2 AKK 4

```

```

RESULT 50

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```

US-09-876-904A-57
: Sequence 57, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSCENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 57
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Chicken Ets1
: OTHER INFORMATION: core NLS peptide
US-09-876-904A-57

```

```

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 7 NKP 9
   |||
Db 5 NKP 7

```

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Search completed: September 30, 2003, 10:33:04
Job time : 22.5 secs

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Gender version 5.1.6  
Copyright (c) 1994 - 2003 CompuLink Ltd.

OM proteins - protein search, using sw model

Run on: September 30, 2003, 16:07:34; sorted, into 42,083 segments  
 (with 1000 segments)  
 42,083 Mapped segments: 42,083 segments/1000

Title: US-09-787-443-19

11 : 33.00'S 133.10'E

Sequence: 1 AEGGKKKKMRA 11

Score: num; attq: attq; attg: attg

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1994	60.0	60.0
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2019	60.0	60.0
2020	60.0	60.0

Searched: 1107863 seqs. 158724874 residues

word size : 1

Total: number of hits satisfying chosen criteria: 100

## Minimum Invariant Property

Maximum DB seq	length: 8
Maximum DB seq	length: 15

post-processing: listing first 500 samples: 1.1s

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8:	/SIDSI/qcgdata/qgeneseq/qgeneseq	emb1/AA1987.EAI
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10:	/SIDSI/qcgdata/qgeneseq/qgeneseq	emb1/AA1989.EAI
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24:	/SIDSI/qcgdata/qgeneseq/qgeneseq	emb1/AA2003.EAI

Prod. No. is the number of results produced by the test; have a score greater than or equal to the score in the result being printed, and is derived by analysis of the total score distribution.

## SUMMARY: E. S.

Res. #	No.	Query			DB	ID	Description
		Score	Match	Length			
1	11	100.0	11	21	AA886527	NCAM tgi binding p	
2	11	100.0	11	23	ABG69347	Human neural cell	
3	7	63.6	13	23	ABH74438	DNA repair protein	
4	7	64.6	13	23	ABH74375	Nucleolar protein p9	
5	6	54.5	8	15	AAH25117	(2'-phosphoryl)ethyl	
6	6	54.5	8	15	AAH25138	Polyoxymethylene	
7	6	54.5	9	15	AAH25137	Polyoxymethylene	
8	6	54.5	9	15	AAH25138	Polyoxymethylene	
9	6	54.5	10	15	AAH25139	Receptor kinase	



83	5	45.5	10	23	ABG79941	MB1 class 1 molecu	156	5	45.5	15	21	AAV51283	K4B-Ras protein de
84	5	45.5	10	23	ABG79973	MB1 class 1 molecu	157	5	45.5	15	21	AAV82557	K4B-Ras protein de
85	5	45.5	10	23	ABG79984	MB1 class 1 molecu	158	5	45.5	15	21	AAV58865	Membrane binding e
86	5	45.5	10	23	ABG79982	9 Lysine peptide	159	5	45.5	15	21	AAV68697	Ras peptide used t
87	5	45.5	10	24	ABG99719	Human immunodefici	160	5	45.5	15	21	AAV59299	Ras peptide derive
88	5	45.5	10	24	ABG99771	Human immunodefici	161	5	45.5	15	21	AAV69630	K4B-Ras-derived pe
89	5	45.5	10	24	ABG99794	Human immunodefici	162	5	45.5	15	21	AAV58603	Ras peptide used i
90	5	45.5	10	24	ABG99768	Human immunodefici	163	5	45.5	15	21	AAV58606	Ras peptide used i
91	5	45.5	10	24	ABG99793	Human immunodefici	164	5	45.5	15	21	AAV58637	K4B-Ras protein Ra
92	5	45.5	10	24	ABG99792	Human immunodefici	165	5	45.5	15	22	AAV85421	Ras peptide. Synt
93	5	45.5	11	22	ABP14506	HIV A03 super moti	166	5	45.5	15	22	AAE11766	Human K4B-Ras prot
94	5	45.5	11	22	ABP14507	HIV A03 super moti	167	5	45.5	15	22	AAU08707	Human Ras peptide
95	5	45.5	11	22	ABP14508	HIV A03 super moti	168	5	45.5	15	22	AAE08746	K4B-Ras protein de
96	5	45.5	11	22	ABP17204	HIV B27 super moti	169	5	45.5	15	22	AAE07265	Human K4B-Ras prot
97	5	45.5	11	22	ABP17205	HIV B27 super moti	170	5	45.5	15	22	AAE36809	Amino acid sequenc
98	5	45.5	11	22	ABP17206	HIV B27 super moti	171	5	45.5	15	22	AAE36842	Amino acid sequenc
99	5	45.5	11	22	ABP22406	HIV A03 motif gag	172	5	45.5	15	22	AAE36845	Ras derived peptid
100	5	45.5	11	22	ABP20558	HIV A03 motif gag	173	5	45.5	15	22	AAE83322	K4B-Ras protein de
101	5	45.5	11	22	ABP20732	HIV A03 motif gag	174	5	45.5	15	22	AAE74936	K4B-Ras protein de
102	5	45.5	11	22	ABP22767	HIV A11 motif gag	175	5	45.5	15	22	AAE72373	Ras peptide used i
103	5	45.5	11	22	ABP22878	HIV A11 motif gag	176	5	45.5	15	22	AAE60573	K4B-Ras geranylger
104	5	45.5	11	23	ABP24598	Transcription fact	177	5	45.5	15	22	AAE68574	Ras peptide. Und
105	5	45.5	11	23	ABP24599	Transcription fact	178	5	45.5	15	22	AAE59853	Ras peptide. Und
106	5	45.5	12	19	AAE54406	Nuclear localisati	179	5	45.5	15	22	AAE59853	K4B-Ras protein de
107	5	45.5	12	21	AAV79945	Beta-amyloid hyper	180	5	45.5	15	22	AAE59853	K4B-Ras protein de
108	5	45.5	12	21	AAV79945	Mortalin (p115)	181	5	45.5	15	22	AAE59853	K4B-Ras protein de
109	5	45.5	12	22	AAE22065	Nuclear localisati	182	5	45.5	15	23	ABE84480	Human K4B0-Ras pro
110	5	45.5	12	23	AAE17649	Fluorescent timer	183	5	45.5	15	23	AAE24538	Ras peptide used i
111	5	45.5	12	23	AAE17649	Fluorescent timer	184	5	45.5	15	23	AAU97073	Ras peptide #3. S
112	5	45.5	12	24	AAE54467	Nucleotide SEQ 10	185	5	45.5	15	23	ABE78779	Human Miller-Dieke
113	5	45.5	13	17	AAE12914	Nucleotide SEQ 10	186	5	45.5	15	23	AAU93302	Granulocyte-colony
114	5	45.5	13	23	AAE99772	Anti death protect	187	5	45.5	15	24	AAU76808	Human Ras peptide
115	5	45.5	13	24	ABE99772	Amino acid sequenc	188	5	45.5	15	23	AAE15866	Human Ras peptide
116	5	45.5	14	19	AAE40682	Peptide membrane b	189	5	45.5	15	23	AAU09694	Ras peptide derive
117	5	45.5	14	21	AAE01793	Protein sensitive	190	5	45.5	15	23	ABP96407	HIV-1 gag epitope
118	5	45.5	14	21	AAE58412	HIV8 ORF 65-deriva	191	5	45.5	15	24	AAE33873	K4B-Ras peptide
119	5	45.5	14	22	AAE47348	Ras peptide. Synt	192	5	45.5	15	24	AAU26605	Amino acid pendant
120	5	45.5	14	23	ABE57301	Protein kinase 11c	193	4	36.4	8	7	AAE61397	Prenyl-protein tra
121	5	45.5	14	23	ABE81741	Anti-infective memb	194	4	36.4	8	18	AAW32275	M. catarrhalis out
122	5	45.5	14	23	AAE85741	Neutrophil-linked	195	4	36.4	8	18	AAW48862	Delivery peptide u
123	5	45.5	14	24	ABE99775	Peptide used as pe	196	4	36.4	8	18	AAW38782	Delivery peptide u
124	5	45.5	14	24	ABE56446	Protein 2 assay peptid	197	4	36.4	8	18	AAW38819	Delivery peptide u
125	5	45.5	14	24	ABE99446	Peptide substrate	198	4	36.4	8	18	AAW59810	Chimeric adenoviru
126	5	45.5	14	24	ABE55029	Protein kinase	199	4	36.4	8	18	AAW18640	Peptide resulting
127	5	45.5	15	10	AAE590193	Anti-infective peptid	200	4	36.4	8	19	AAV21080	Human p53 cellular
128	5	45.5	15	16	AAE66733	Neutrophil lympho	201	4	36.4	8	19	AAV20160	Human neurofilamen
129	5	45.5	15	19	AAE40682	Peptide membrane l	202	4	36.4	8	19	AAW79168	Conserved sequence
130	5	45.5	15	20	AAE31112	K4B-Ras peptide	203	4	36.4	8	20	AAV42244	Multivalent ligand
131	5	45.5	15	20	AAV42244	Peptide substrate 8	204	4	36.4	8	20	AAV43412	Multivalent ligand
132	5	45.5	15	20	AAV42244	Ras peptide deriva	205	4	36.4	8	20	AAV43412	Flase substrate Ca
133	5	45.5	15	20	AAV42244	K4B-Ras peptide	206	4	36.4	8	21	AAE21219	RTR tetramer. Syn
134	5	45.5	15	20	AAV42244	K4B-Ras peptide	207	4	36.4	8	21	AAE21220	ASA tetramer. Syn
135	5	45.5	15	20	AAV42244	K4B-Ras peptide	208	4	36.4	8	21	AAE21222	RTR tetramer conta
136	5	45.5	15	20	AAV42244	K4B-Ras peptide	209	4	36.4	8	21	AAE36033	Human beta3 subuni
137	5	45.5	15	20	AAV42244	K4B-Ras peptide	210	4	36.4	8	21	AAE08150	Peptide modulating
138	5	45.5	15	20	AAV42244	Peptide fragment 4	211	4	36.4	8	21	AAE08152	Peptide modulating
139	5	45.5	15	20	AAV42244	Ras peptide deriva	212	4	36.4	8	21	AAE08152	Conus kappa-A cono
140	5	45.5	15	20	AAV42244	Peptide derived 11	213	4	36.4	8	21	AAV90544	HLA-B8-binding HIV
141	5	45.5	15	20	AAV42244	Peptide derived 11	214	4	36.4	8	21	AAV66384	HLA-B8-binding HIV
142	5	45.5	15	20	AAE99776	Ras peptide SEQ 10	215	4	36.4	8	22	ABP13143	HIV A02 super moti
143	5	45.5	15	20	AAE99776	Ras peptide SEQ 10	216	4	36.4	8	22	ABP14441	HIV A03 super moti
144	5	45.5	15	20	AAE99776	Ras peptide SEQ 10	217	4	36.4	8	22	ABP14644	HIV A03 super moti
145	5	45.5	15	20	AAE99776	Ras peptide SEQ 10	218	4	36.4	8	22	ABP16988	HIV B27 super moti
146	5	45.5	15	21	AAE01793	Ras peptide. Synt	219	4	36.4	8	22	ABP19387	HIV B62 super moti
147	5	45.5	15	21	AAE27077	K4B-Ras-derived Ra	220	4	36.4	8	22	ABP20815	HIV A03 motif gag
148	5	45.5	15	21	AAE27077	K4B-Ras-derived Ra	221	4	36.4	8	22	ABP21678	HIV A03 motif pol
149	5	45.5	15	21	AAE27077	K4B-Ras-derived Ra	222	4	36.4	8	22	ABP22925	HIV A11 motif gag
150	5	45.5	15	21	AAE27077	K4B-Ras-derived Ra	223	4	36.4	8	22	ABP23557	HIV A11 motif pol
151	5	45.5	15	21	AAE14599	Ras peptide. Mamm	224	4	36.4	8	22	AAU08714	Preferred peptide
152	5	45.5	15	21	AAE14599	Human K4B-Ras deri	225	4	36.4	8	22	AAE97316	HMG-1/2 box domain
153	5	45.5	15	21	AAE14599	Human K4B-Ras deri	226	4	36.4	8	22	AAE00704	Internal peptide o
154	5	45.5	15	21	AAE14599	Human Ras trinitroyl	227	4	36.4	8	22	AAE70276	Peptide #20. Und
155	5	45.5	15	21	AAE14599	K4B-Ras peptide 10	228	4	36.4	8	22	AAE31765	Amino acid sequenc

229	4	36.4	8	23	AA528473	NLS based peptide	302	4	36.4	9	24	ABR02934	Human cancer-relat
230	4	36.4	8	23	AB59581	Adaptor domain pep	303	4	36.4	9	24	ABR02963	Human cancer-relat
231	4	36.4	8	23	AB52588	CXC chemokine rece	304	4	36.4	9	24	ABR03099	Human cancer-relat
232	4	36.4	8	23	AA078918	Lupinus latens nuc	305	4	36.4	9	24	ABR03159	Human cancer-relat
233	4	36.4	8	23	AA01390	Cysteine-X-Cysteine	306	4	36.4	9	24	ABR06474	Human cancer-relat
234	4	36.4	8	23	AB005967	Monoclonal antibod	307	4	36.4	9	24	ABR06475	Human cancer-relat
235	4	36.4	8	23	AA076375	Neureptin-like in	308	4	36.4	9	24	ABR06477	Human cancer-relat
236	4	36.4	8	23	AA052777	PL2 domain-binding	309	4	36.4	9	24	ABR06496	Human cancer-relat
237	4	36.4	8	23	AB074249	Simple nuclear fac	310	4	36.4	9	24	ABR06689	Human cancer-relat
238	4	36.4	8	23	AB074249	Transcription fact	311	4	36.4	9	24	ABR06691	Human cancer-relat
239	4	36.4	8	23	AB074241	Transcription fact	312	4	36.4	9	24	ABR06694	Human cancer-relat
240	4	36.4	8	23	AB074231	Transcription fact	313	4	36.4	9	24	ABR06707	Human cancer-relat
241	4	36.4	8	24	AB008788	Lys-C digested Mor	314	4	36.4	9	24	ABR06719	Human cancer-relat
242	4	36.4	9	14	AA023038	Gro-gamma cytokine	315	4	36.4	10	13	AAE30815	Bacteriophage fd r
243	4	36.4	9	15	AA057514	Peptide (14) inhib	316	4	36.4	10	14	AAE323049	Leukocyte-binding
244	4	36.4	9	15	AA057516	Peptide (16) inhib	317	4	36.4	10	14	AAE32527	Peptide inhibitor
245	4	36.4	9	15	AA057517	Peptide (17) inhib	318	4	36.4	10	15	AAE36336	Antigenic fragment
246	4	36.4	9	15	AA057518	Peptide (18) inhib	319	4	36.4	10	15	AAE36274	SV40 nuclear membr
247	4	36.4	9	15	AA057519	Peptide (19) inhib	320	4	36.4	10	15	AAE36280	Peptide fragment (
248	4	36.4	9	15	AA057520	Peptide (20) inhib	321	4	36.4	10	15	AAE36280	Bradykinin recepto
249	4	36.4	9	15	AA057521	Peptide (21) inhib	322	4	36.4	10	15	AAE36280	Peptide neutralisi
250	4	36.4	9	15	AA057522	Peptide (22) inhib	323	4	36.4	10	15	AAE36280	Peptide neutralisi
251	4	36.4	9	15	AA057523	Peptide (23) inhib	324	4	36.4	10	16	AAE36280	Peptide neutralisi
252	4	36.4	9	15	AA057524	Peptide (24) inhib	325	4	36.4	10	16	AAE36280	Peptide neutralisi
253	4	36.4	9	15	AA057525	Peptide (25) inhib	326	4	36.4	10	16	AAE36280	Peptide neutralisi
254	4	36.4	9	15	AA057526	Peptide (26) inhib	327	4	36.4	10	16	AAE36280	Peptide neutralisi
255	4	36.4	9	15	AA057527	Peptide (27) inhib	328	4	36.4	10	16	AAE36280	Peptide neutralisi
256	4	36.4	9	15	AA057528	Peptide (28) inhib	329	4	36.4	10	16	AAE36280	Peptide neutralisi
257	4	36.4	9	15	AA057529	Peptide (29) inhib	330	4	36.4	10	16	AAE36280	Peptide neutralisi
258	4	36.4	9	15	AA057530	Peptide (30) inhib	331	4	36.4	10	16	AAE36280	Peptide neutralisi
259	4	36.4	9	15	AA057531	Peptide (31) inhib	332	4	36.4	10	16	AAE36280	Peptide neutralisi
260	4	36.4	9	18	AA038864	Delivery peptide 2	333	4	36.4	10	18	AAE36280	Peptide neutralisi
261	4	36.4	9	18	AA038864	Delivery peptide 3	334	4	36.4	10	18	AAE36280	Peptide neutralisi
262	4	36.4	9	18	AA038864	Delivery peptide 4	335	4	36.4	10	18	AAE36280	Peptide neutralisi
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265	4	36.4	9	18	AA038864	Delivery peptide 7	338	4	36.4	10	18	AAE36280	Peptide neutralisi
266	4	36.4	9	18	AA038864	Delivery peptide 8	339	4	36.4	10	18	AAE36280	Peptide neutralisi
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269	4	36.4	9	18	AA038864	Delivery peptide 11	342	4	36.4	10	18	AAE36280	Peptide neutralisi
270	4	36.4	9	18	AA038864	Delivery peptide 12	343	4	36.4	10	18	AAE36280	Peptide neutralisi
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273	4	36.4	9	18	AA038864	Delivery peptide 15	346	4	36.4	10	18	AAE36280	Peptide neutralisi
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285	4	36.4	9	18	AA038864	Delivery peptide 27	358	4	36.4	10	18	AAE36280	Peptide neutralisi
286	4	36.4	9	18	AA038864	Delivery peptide 28	359	4	36.4	10	18	AAE36280	Peptide neutralisi
287	4	36.4	9	18	AA038864	Delivery peptide 29	360	4	36.4	10	18	AAE36280	Peptide neutralisi
288	4	36.4	9	18	AA038864	Delivery peptide 30	361	4	36.4	10	18	AAE36280	Peptide neutralisi
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291	4	36.4	9	18	AA038864	Delivery peptide 33	364	4	36.4	10	18	AAE36280	Peptide neutralisi
292	4	36.4	9	18	AA038864	Delivery peptide 34	365	4	36.4	10	18	AAE36280	Peptide neutralisi
293	4	36.4	9	18	AA038864	Delivery peptide 35	366	4	36.4	10	18	AAE36280	Peptide neutralisi
294	4	36.4	9	18	AA038864	Delivery peptide 36	367	4	36.4	10	18	AAE36280	Peptide neutralisi
295	4	36.4	9	18	AA038864	Delivery peptide 37	368	4	36.4	10	18	AAE36280	Peptide neutralisi
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298	4	36.4	9	18	AA038864	Delivery peptide 40	371	4	36.4	10	18	AAE36280	Peptide neutralisi
299	4	36.4	9	18	AA038864	Delivery peptide 41	372	4	36.4	10	18	AAE36280	Peptide neutralisi
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301	4	36.4	9	18	AA038864	Delivery peptide 43	374	4	36.4	10	18	AAE36280	Peptide neutralisi

375	4	36.4	10	22	AAR70239	Polyionic peptide	448	4	36.4	12	15	AAR45681	Rabbit TFPI hepari
376	4	36.4	10	23	ABU57494	HIV cytotoxic lymph	449	4	36.4	12	15	AAR47667	Nerve growth facto
377	4	36.4	10	23	ABG75953	MHC class I molecu	450	4	36.4	12	15	AAR57401	Peptide for treati
378	4	36.4	10	23	ABP53304	Gene delivery rela	451	4	36.4	12	17	AAR96743	Hepatitis A virus
379	4	36.4	10	23	ABR00485	Peptide #1 used in	452	4	36.4	12	17	AAR94332	Anti-thrombogenic
380	4	36.4	10	23	AAU76375	Nociceptin-like im	453	4	36.4	12	17	AAR86961	Nuclear localisati
381	4	36.4	10	23	AAU76077	Nociceptin-like im	454	4	36.4	12	18	AAW27473	Human TSP homologu
382	4	36.4	10	23	AAU76114	Nociceptin-like pe	455	4	36.4	12	18	AAW27477	Human TSP homologu
383	4	36.4	10	23	ABU74326	Bipartite/split nu	456	4	36.4	12	18	AAW27471	Human TSP homologu
384	4	36.4	10	23	ABU74720	Transcription fact	457	4	36.4	12	18	AAW38866	Delivery peptide u
385	4	36.4	10	24	ASU66952	Human immunodefici	458	4	36.4	12	18	AAW38823	Delivery peptide u
386	4	36.4	10	24	ASU69795	Human immunodefici	459	4	36.4	12	18	AAW38786	Delivery peptide u
387	4	36.4	10	24	ASU69929	Human immunodefici	460	4	36.4	12	18	AAW19793	Compressing peptid
388	4	36.4	10	24	ABU65935	Human immunodefici	461	4	36.4	12	18	AAW25568	Synthetic heptati
389	4	36.4	10	24	ASU70142	Human immunodefici	462	4	36.4	12	18	AAW24439	Nucleic acid (NA)
390	4	36.4	10	24	ASU70191	Human cancer-relat	463	4	36.4	12	19	AAW4629	Amino acid sequenc
391	4	36.4	10	24	ABR03022	Human cancer-relat	464	4	36.4	12	19	AAW4630	Human acid sequenc
392	4	36.4	10	24	ABR02861	Human cancer-relat	465	4	36.4	12	19	AAW55555	Multiply branched
393	4	36.4	10	24	ABR03032	Human cancer-relat	466	4	36.4	12	19	AAW51570	Peptide prodrug co
394	4	36.4	10	24	ABR03042	Human cancer-relat	467	4	36.4	12	19	AAW55891	Human vascular per
395	4	36.4	10	24	ABR03053	Human cancer-relat	468	4	36.4	12	19	AAW55890	Human vascular per
396	4	36.4	10	24	ABR04233	Human cancer-relat	469	4	36.4	12	19	AAW53385	Vascular endotheli
397	4	36.4	10	24	ABR04255	Human cancer-relat	470	4	36.4	12	19	AAW53386	Vascular endotheli
398	4	36.4	10	24	ABR05370	Human cancer-relat	471	4	36.4	12	20	AAW31628	HIV-1 matrix prote
399	4	36.4	10	24	ABR05571	Human cancer-relat	472	4	36.4	12	20	AAW86737	Anticoagulant pept
400	4	36.4	10	24	ABR05574	Human cancer-relat	473	4	36.4	12	20	AAW86738	Anticoagulant pept
401	4	36.4	10	24	ABR05598	Human cancer-relat	474	4	36.4	12	20	AAW86739	Anticoagulant pept
402	4	36.4	10	24	ABR05627	Human cancer-relat	475	4	36.4	12	20	AAW95384	Antimicrobial pept
403	4	36.4	10	24	ABR05769	Human cancer-relat	476	4	36.4	12	21	AAW35821	T7 phage coat prot
404	4	36.4	10	24	ABR05780	Human cancer-relat	477	4	36.4	12	21	AAW57615	Human vascular end
405	4	36.4	10	24	ABR05782	Human cancer-relat	478	4	36.4	12	21	AAW57616	Human vascular end
406	4	36.4	10	24	ABR05785	Human cancer-relat	479	4	36.4	12	21	AAW58057	Vascular endotheli
407	4	36.4	10	24	ABR05792	Human cancer-relat	480	4	36.4	12	21	AAW58058	Vascular endotheli
408	4	36.4	10	24	ABR05821	Human cancer-relat	481	4	36.4	12	22	ABW51257	Human secreted pro
409	4	36.4	11	13	AAW36180	PHL-2-T32 N termin	482	4	36.4	12	22	AAW98676	Human peptide #195
410	4	36.4	11	15	AAW55163	Fragment of retino	483	4	36.4	12	22	AAW98676	Human peptide #195
411	4	36.4	11	16	AAW2301	Anti-HIV MBPc.3.	484	4	36.4	12	22	AAW98676	Human peptide #195
412	4	36.4	11	17	AAW2301	Human retinoic aci	485	4	36.4	12	22	AAW98676	Human peptide #195
413	4	36.4	11	18	AAW38865	Delivery peptide u	486	4	36.4	12	22	AAW98676	Human VEGF/VPF pep
414	4	36.4	11	18	AAW38865	Delivery peptide u	487	4	36.4	12	22	AAW98676	Human VEGF/VPF pep
415	4	36.4	11	18	AAW38765	Delivery peptide u	488	4	36.4	12	22	AAW98676	VEGF VPF antagonis
416	4	36.4	11	18	AAW16616	Phosphoinositide-3	489	4	36.4	12	23	AAW22420	Adaptor domain pep
417	4	36.4	11	18	AAW22674	M2 derivative of	490	4	36.4	12	23	ABW75882	Protease cleavage
418	4	36.4	11	18	AAW24436	Nucleic acid (NA)	491	4	36.4	12	23	ABW75882	Cyclodextrin glyco
419	4	36.4	11	20	AAW77457	Lipophilic binding	492	4	36.4	12	23	AAU76069	Nociceptin-like pe
420	4	36.4	11	20	AAW55735	Anticoagulant pept	493	4	36.4	12	23	AAU76070	Nociceptin-like pe
421	4	36.4	11	21	AAW55735	Anticoagulant pept	494	4	36.4	12	23	AAU76071	Nociceptin-like pe
422	4	36.4	11	21	AAW55735	Anticoagulant pept	495	4	36.4	12	23	AAU76099	Nociceptin-like pe
423	4	36.4	11	21	AAW55735	Anticoagulant pept	496	4	36.4	12	23	AAU76100	Nociceptin-like pe
424	4	36.4	11	21	AAW55735	Anticoagulant pept	497	4	36.4	12	23	AAU76102	Nociceptin-like pe
425	4	36.4	11	21	AAW55735	Anticoagulant pept	498	4	36.4	12	23	AAU76103	Nociceptin-like pe
426	4	36.4	11	21	AAW55735	Anticoagulant pept	499	4	36.4	12	23	AAU76104	Nociceptin-like pe
427	4	36.4	11	22	ABP13604	HIV AC2 super moti	500	4	36.4	12	23	AAU76105	Nociceptin-like pe
428	4	36.4	11	22	ABP13605	HIV AC2 super moti							Nociceptin-like pe
429	4	36.4	11	22	ABP13605	HIV AC2 super moti							Nociceptin-like pe
430	4	36.4	11	22	ABP13605	HIV AC2 super moti							Nociceptin-like pe
431	4	36.4	11	22	AAW42176	Human polypeptide							Nociceptin-like pe
432	4	36.4	11	22	AAW42176	Human polypeptide							Nociceptin-like pe
433	4	36.4	11	22	AAW42176	Human polypeptide							Nociceptin-like pe
434	4	36.4	11	22	AAW42176	Human polypeptide							Nociceptin-like pe
435	4	36.4	11	23	ABG75612	Ask tyrosine kinas							Nociceptin-like pe
436	4	36.4	11	23	ABG75612	Ask tyrosine kinas							Nociceptin-like pe
437	4	36.4	11	23	AAU94672	Molecular marker i							Nociceptin-like pe
438	4	36.4	11	23	AAU76079	Nociceptin-like pe							Nociceptin-like pe
439	4	36.4	11	23	ABH74427	Nociceptin-like pe							Nociceptin-like pe
440	4	36.4	11	23	ABH74427	Nociceptin-like pe							Nociceptin-like pe
441	4	36.4	11	24	AAO27060	Transcription fact							Nociceptin-like pe
442	4	36.4	11	24	AAO27060	Fibrinogen E fragm							Nociceptin-like pe
443	4	36.4	12	8	AAW27103	Fibrinogen E fragm							Nociceptin-like pe
444	4	36.4	12	8	AAW27103	Peptide which inh							Nociceptin-like pe
445	4	36.4	12	8	AAW27103	Peptide which inh							Nociceptin-like pe
446	4	36.4	12	12	AAW10937	Residues 205-216 o							Nociceptin-like pe
447	4	36.4	12	13	AAW24217	Fragment of tenase							Nociceptin-like pe
448	4	36.4	12	13	AAW24220	Fragment of tenase							Nociceptin-like pe

## ALIGNMENTS

RESULT :

AAW8547

ID AAW8547 standard; peptide: 11 AA.

XX AAW8547:

XX AAW8547:

DT 07-AUG-2000 (first entry)

DE NCAM IqI binding peptide #19.

XX NCAM:

KW NCAM: neural cell adhesion molecule; IqI: immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

```

XX OS Synthetic.
XX AC WO200018801-A2.
XX PN 06-APR 2000.
XX PD 21-SEP-1994; 99WD-DK00500.
XX PF 29-SEP-1994; 98DK-0007232.
XX PR 29-APR 1995; 99DK-0000542.
XX XX (BENK/) KONN L C B.
XX PA (BENK/) BOCK E.
XX PA (HCLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (OLSE/) OLSEN P H.
XX PA (JENS/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORU/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (HERE/) BEREZIN V.
XX XX
XX PI Konn LCB, Bock E, Holm A, Olsen M, Zsengraef S, Jensen PB;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V.
XX XX
XX PR WPI: 2000-293111/25.
XX DR
XX XX
XX XX Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and diseases e.g. Alzheimer's
XX PT and Parkinson's diseases.
XX XX
XX PS Example 4: Page 25; 119pp; English.
XX XX
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting of five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminus. The present sequence represents a peptide which binds to the
XX CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
XX CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting
XX CC the proliferation of NCAM presenting cells. The compound may be used in
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.
XX CC The compound may in particular be used to treat diseases of the central
XX CC and peripheral nervous systems such as post-operative nerve damage,
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
XX CC dementia, sclerosis, nerve degeneration associated with diabetes,
XX CC mellitus, disorders affecting the circulation, block of neuro-muscular
XX CC transmission and schizophrenia. Conditions affecting the muscles may also
XX CC be treated with the compound, such as conditions associated with impaired
XX CC function of neuromuscular connections (e.g. genetic or traumatic stroke or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to
XX CC learn, and to stimulate the memory of a subject.
XX XX
XX SQ Sequence 11 AA:
XX XX
XX XX Query Match 100.0%; Score 11; DB 21; Length 11;
XX XX Best Local Similarity 100.0%; Pred. No. 7e-05;
XX XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 AEGGKKKKMRA 11
XX DB 1 AEGGKKKKMRA 11
XX XX
XX XX REFSLT 2
XX XX ABG69347

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ID ARG69347 standard; Peptide: 11 AA.
XX AC ARG69347;
XX XX
XX DT 21-OCT-2002 (first entry)
XX XX
XX DE Human neural cell adhesion molecule (NCAM) peptide #19.
XX XX
XX KW Human: neural cell adhesion molecule; NCAM; heart muscle cell survival;
XX KW acute myocardial infarction; central nervous system disorder; stroke;
XX KW peripheral nervous system disorder; postoperative nerve damage;
XX KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
XX KW postischaemic damage; multiinfarct dementia; multiple sclerosis;
XX KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
XX KW Alzheimer's disease; Parkinson's disease; Huntington's disease.
XX KW atrophic muscle disorder; gonad degeneration; nephrosis.
XX OS Homo sapiens.
XX XX
XX PN WO200247719-A2.
XX XX
XX PD 20-JUN-2002.
XX XX
XX PF 12-DEC-2001; 2001WG-DK00822.
XX XX
XX PR 12-DEC-2000; 2000DK-0001863.
XX XX
XX PA (ENKA-) ENKAM PHARM AS.
XX XX
XX PI Hock E, Berezin V, Kohler LB;
XX DR WPI: 2002-583473/62.
XX XX
XX XX Use of a compound comprising a peptide of neural cell adhesion
XX PT molecule, in the preparation of medicament for preventing death of
XX PT cells presenting NCAM or NCAM ligand and treating central nervous
XX PT system diseases.
XX PS Disclosure; Page 16; 57pp; English.
XX XX
XX XX The invention relates to use of a compound (I) comprising a peptide
XX CC which comprises at least 5 contiguous amino acid residues of a sequence
XX CC of the neural cell adhesion molecule (NCAM), its fragment, variant or its
XX CC mimic, for the preparation of a medicament for preventing death of cells
XX CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
XX CC of a medicament for preventing death of cells presenting the NCAM or an
XX CC NCAM ligand. The medicament is for the stimulation of the survival of
XX CC heart muscle cells, such as survival after acute myocardial infarction.
XX CC The medicament is for the treatment of diseases or conditions of the
XX CC central and peripheral nervous system, such as postoperative nerve
XX CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
XX CC impaired myelination of nerve fibres, postischaemic damage, e.g.
XX CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
XX CC degeneration associated with diabetes mellitus, neuro-muscular
XX CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease
XX CC and Huntington's disease. The medicament is for the treatment of diseases
XX CC or conditions of the muscles including conditions with impaired function
XX CC of neuro-muscular connections, such as genetic or traumatic atrophic
XX CC muscle disorders, and for the treatment of diseases of conditions of
XX CC various organs, such as degenerative conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).
XX CC ABG69329-ABG69352 represent human NCAM peptides of the invention.
XX XX
XX SQ Sequence 11 AA:
XX XX
XX XX Query Match 100.0%; Score 11; DB 23; Length 11;
XX XX Best Local Similarity 100.0%; Pred. No. 7e-05;
XX XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 1 AEGGKKKKMRA 11
XX DB 1 AEGGKKKKMRA 11
XX XX
XX XX REFSLT 2
XX XX ABG69347

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XX 24-MAR-1993 (first entry)  
 XX (2-thioacetyl)glycylglycylglycylpentyl-L-lysine  
 DE Protein conjugate; carrier portion; diagnostic therapeutic;  
 XX blood clearance rate; diffusion; carrier; tumor.  
 KW  
 XX Synthetic.  
 CS  
 XX Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= 2-Thioacetyl- only  
 FT Binding site 4..8  
 FT /note= "Antimycinin Fab" attachment required"  
 XX QS5162505-A.  
 XX 10-NOV-1992.  
 XX 19-SEP-1989; 89US-0409150.  
 XX 19-SEP-1989; 89US-0409150.  
 XX (GENZ ) GENPACOR.  
 XX Boston RH, Dean RT, Lister-James G.  
 XX WPI: 1992-358123/48.  
 XX New positively charged protein conjugate used as carrier for  
 FT diagnostic or therapeutic radiolabeling  
 XX Disclosure: Column 14, 11pp; English.  
 XX The sequence given is a portion of a protein conjugate which contains  
 CC a pharmaceutical protein (Fab') linked to at least one positively  
 CC charged agent. This peptide represents the carrier portion of the  
 CC conjugate. The whole conjugate may be used as a diagnostic or  
 CC therapeutic agent. By attaching positively charged agents to the  
 CC conjugates the blood clearance rate is decreased in vivo, thereby  
 CC increasing blood concn. without reducing diffusion of the conjugates.  
 CC Each positively charged agent can be used as a carrier of one or more  
 CC therapeutic or diagnostic agent. The conjugates may be used in  
 CC vivo tumor imaging or treatment.  
 XX Sequence 8 AA:  
 SQ  
 Query Match 54.5%; Score 6; DH 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 8  
 DB 11111  
 2 GKKKK 7  
 RESULT 6  
 AAR60836  
 XX AAR60836 standard; peptide: 8 AA.  
 XX AAR60838;  
 XX 25-MAR-2003 (updated)  
 DT 05-JUN-1995 (first entry)  
 XX Polyoxyime hexa-GXL baseplate.  
 XX Polyoxyime; homopolyoxyime; heteropolyoxyime; peptide presentation;  
 KW cell imaging; complementary orthogonal specifically active molecule.  
 KW COSM: baseplate; immunogen.  
 XX Synthetic.  
 CS

XX Key Location/Qualifiers  
 FH Modified-site  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified site 4  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 5  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 6  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 7  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 FT Modified-site 8  
 FT /label= OTHER  
 FT /note= "glyoxyl-lysine"  
 XX W09425071-A1.  
 XX 10-NOV-1994.  
 XX 05-MAY-1994; 94WO-1B00093.  
 XX 05-MAY-1994; 94US-0057594.  
 PR 31-AUG-1993; 93US-0105504.  
 PR 31-AUG-1993; 93US-0114877.  
 XX (OFFC//) OFFORD R E.  
 PA (ROSE//) ROSE K.  
 XX Offord RE, Rose K;  
 PI WPI: 1994-357918/44.  
 XX Homo- and hetero polyoxyime compounds and their preparation - used  
 PT for peptide presentation to antibodies and in cell imaging etc.  
 XX Disclosure: Page 49-50; 85pp; English.  
 XX Peptides given in AAR60837-62 are used as baseplates and COSMs for the  
 CC preparation of polyoxyimes having varying spacing, charge,  
 CC lipophilicity, valency, conformational restraints, solubility and  
 CC other physical and biological properties. A hexa-GXL baseplate  
 CC structure is given in AAR60838.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 8 AA:  
 SQ  
 Query Match 54.5%; Score 6; DH 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 8  
 DB 11111  
 2 GKKKK 7  
 RESULT 7  
 AAR60837  
 ID AAR60837 standard; peptide: 9 AA.  
 XX AAR60837;  
 XX 25-MAR-2003 (updated)  
 DT 05-JUN-1995 (first entry)  
 XX Polyoxyime hexa-AcA baseplate.  
 XX Polyoxyime; homopolyoxyime; heteropolyoxyime; peptide presentation;  
 KW

KW cell imaging; complementary orthoformal specifically active molecule;  
 KW COSM: baseplate; immunogen;  
 XX Synthetic.

OS Key Location/Qualifiers  
 FH Modified-site 1 /label OTHER  
 FT Modified-site 4 /note "aminooxyacetyl glycine"  
 FT Modified-site 5 /label OTHER  
 FT Modified-site 6 /note "aminooxyacetyl lysine"  
 FT Modified-site 7 /label OTHER  
 FT Modified-site 8 /note "aminooxyacetyl lysine"  
 FT Modified-site 9 /label OTHER  
 FT Modified-site 10 /note "aminooxyacetyl lysine"

XX W09425071-A1  
 XX 10 NOV-1994  
 XX 05-MAY-1994 94WO-1806093  
 XX 05-MAY-1994 93US-0057594  
 XX 31-AUG-1994 94US-0105904  
 XX 31-AUG-1994 93US-0114877

XX (OFFD/) OFFORD R E.  
 XX (ROSE/) ROSE K.

XX Offord RE, ROSE K;  
 XX WPI: 1994-3579;8/44.

XX Hemo- and hetero-polyoxime compounds and their preparation - used  
 XX for peptide presentation to antibodies and in cell imaging etc.

PS Disclosure: Page 49; 85pp; English.

XX Peptides given in AAR60843-62 are used as baseplates and COSMs for the  
 XX preparation of polyoximes having varying spacing, charge,  
 XX lipophilicity, valency, conformational restraints, solubility and  
 XX other physical and biological properties. A penta-GXL baseplate  
 XX structure is given in AAR60847.  
 XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 54.5%; Score 6; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCKKKK 8  
 DE 2 GCKKKK 7

RESULT 8  
 AAR60840  
 ID AAR60840 standard; peptide: 9 AA.  
 XX AAR60840;  
 XX

XX 25-MAR-2003 (updated)  
 XX 05-JUN-1995 (first entry)

XX Polyoxime penta-GXL baseplate.  
 DE  
 XX  
 KW Polyoxime; homopolyoxime; heteropolyoxime; peptide presentation;  
 KW cell imaging; complementary orthoformal specifically active molecule;  
 KW COSM: baseplate; immunogen;  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH Modified-site 1 /label OTHER  
 FT Modified-site 4 /note "aminooxyacetyl glycine"  
 FT Modified-site 5 /label OTHER  
 FT Modified-site 6 /note "aminooxyacetyl lysine"  
 FT Modified-site 7 /label OTHER  
 FT Modified-site 8 /note "aminooxyacetyl lysine"  
 FT Modified-site 9 /label OTHER  
 FT Modified-site 10 /note "aminooxyacetyl lysine"

XX W09425071-A1  
 XX 10 NOV-1994  
 XX 05-MAY-1994 94WO-1806093  
 XX 05-MAY-1994 94US-0057594  
 XX 31-AUG-1994 94US-0105904  
 XX 31-AUG-1994 93US-0114877

XX (OFFD/) OFFORD R E.  
 XX (ROSE/) ROSE K.  
 XX Offord RE, ROSE K;  
 XX WPI: 1994-3579;8/44.

XX Hemo- and hetero-polyoxime compounds and their preparation - used  
 XX for peptide presentation to antibodies and in cell imaging etc.  
 PS Disclosure: Page 52; 85pp; English.

XX Peptides given in AAR60843-62 are used as baseplates and COSMs for the  
 XX preparation of polyoximes having varying spacing, charge,  
 XX lipophilicity, valency, conformational restraints, solubility and  
 XX other physical and biological properties. A penta-GXL baseplate  
 XX structure is given in AAR60840.  
 XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 54.5%; Score 6; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCKKKK 8  
 DE 2 GCKKKK 7

RESULT 9  
 AAR60849  
 ID AAR60849 standard; peptide: 10 AA.  
 XX

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AC AAR60841;
XX
XX 25-MAR-2003 (updated)
DT 05-JUN-1995 (first entry)
XX
XX Hexa-GXL-baseplate precursor.
DE
XX Polyoxyime; homopolyoxime; heteropolyoxime; peptide presentation;
KW cell imaging; complementary orthogonal specifically active molecule;
KW COSM; baseplate; immunogen.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 5 /label= OTHER
FT /note= "serine-lysine"
FT Modified-site 6 /label= OTHER
FT /note= "serine-lysine"
FT Modified-site 7 /label= OTHER
FT /note= "serine-lysine"
FT Modified-site 8 /label= OTHER
FT /note= "serine-lysine"
FT Modified-site 9 /label= OTHER
FT /note= "serine-lysine"
XX W09425071-AL.
PN
XX 10-NOV-1994.
PD
XX 05-MAY-1994; 94WO-1B00093.
XX
XX 05-MAY-1993; 93US-0057594.
PR 31-AUG-1993; 93US-0105904.
PR 31-AUG-1993; 93US-0114877.
XX
XX (OFFD/) OFFORD R E.
PA (ROSE/) ROSE K.
XX
XX Offord RE. Rose K;
PI
XX WPI: 1994-357918/44.
DR
XX Homo- and hetero-polyoxime compounds and their preparation - used
PT for peptide presentation to antibodies and in cell imaging etc.
XX
XX Disclosure: Page 50-51; 85pp; English.
XX
XX Peptides given in AAR60833-62 are used as baseplates and COSMs for the
CC preparation of polyoximes having varying spacing, charge,
CC lipophilicity, valency, conformational restraints, solubility and
CC other physical and biological properties. Peptide AAR60839 was used
CC in the preparation of hexa-GXL-baseplate (AAR60841).
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 AA:
XX
Query Match 54.5%; Score 6; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GKKKK 8
Qb 3 GKKKK 8
RESULT 10
AAR60841
1: AAR60841 standard; peptide: 11 AA

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XX AAR60841;
AC
XX 25-MAR-2003 (updated)
DT 05-JUN-1995 (first entry)
XX
XX Polyoxyime octa-GXL baseplate.
DE
XX Polyoxyime; homopolyoxime; heteropolyoxime; peptide presentation;
KW cell imaging; complementary orthogonal specifically active molecule;
KW COSM; baseplate; immunogen.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /label= OTHER
FT /note= "glyoxyl-glycine"
FT Modified-site 4 /label= OTHER
FT /note= "glyoxyl-lysine"
FT Modified-site 5 /label= OTHER
FT /note= "glyoxyl-lysine"
FT Modified-site 6 /label= OTHER
FT /note= "glyoxyl-lysine"
FT Modified-site 7 /label= OTHER
FT /note= "glyoxyl-lysine"
FT Modified-site 8 /label= OTHER
FT /note= "glyoxyl-lysine"
FT Modified-site 9 /label= OTHER
FT /note= "glyoxyl-lysine"
FT Modified-site 10 /label= OTHER
FT /note= "glyoxyl-lysine"
XX W09425071-AL.
PN
XX 10-NOV-1994.
PD
XX 05-MAY-1994; 94WO-1B00093.
XX
XX 05-MAY-1993; 93US-0057594.
PR 31-AUG-1993; 93US-0105904.
PR 31-AUG-1993; 93US-0114877.
XX
XX (OFFD/) OFFORD R E.
PA (ROSE/) ROSE K.
XX
XX Offord RE. Rose K;
PI
XX WPI: 1994-357918/44.
DR
XX Homo- and hetero-polyoxime compounds and their preparation - used
PT for peptide presentation to antibodies and in cell imaging etc.
XX
XX Disclosure: Page 53; 85pp; English.
XX
XX Peptides given in AAR60833-62 are used as baseplates and COSMs for the
CC preparation of polyoximes having varying spacing, charge,
CC lipophilicity, valency, conformational restraints, solubility and
CC other physical and biological properties. An octa-GXL baseplate
CC structure is given in AAR60841.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 11 AA:
XX
Query Match 54.5%; Score 6; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9;

```



Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 DB 11111  
 2 GKKKK 7

RESULT 11  
 ABB74856  
 ID ABB74856 standard; Peptide: 15 AA.  
 AC  
 AC ABB74856;  
 DT 15-NOV-1992 (first entry)  
 DE Lactoferrin introduced peptide (2).  
 DE Nuclear protein nuclear localisation signal peptide SpG ID No:620.  
 XX  
 XX Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;  
 KW liposome; micelle; karyophilic; cytostatic; anti-tumour; solid tumour;  
 KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;  
 KW breast carcinoma; prostate carcinoma.  
 XX  
 CS Bos taurus.  
 UN WU2031948: A2.  
 PN 14 DEC 2003.  
 XX  
 XX 08-JUN-2001: 2001WO-US18657.  
 PF 09-JUN-2000: 2000US-210925P.  
 PR (BOL/) BOLLIKAS T.  
 PA bollikas T.  
 PS bollikas T.  
 XX  
 XX WPI: 2002-164245/21.  
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with  
 PI nuclear localization signal/fusogenic peptide conjugates into targeted  
 PT liposome complexes -  
 PS Claim 14: Page 85; 107pp: English.  
 XX The present invention describes a method for producing micelles with  
 CC entrapped therapeutic agents. The method comprises: (1) combining  
 CC negatively charged agent with a cationic lipid in a ratio where 40-90 %  
 CC of the negatively charged atoms are neutralised by positive charges on  
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %  
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-  
 CC karyophilic peptide conjugates in a 0.0-1.0 ratio, therefore producing  
 CC micelles with entrapped therapeutic agents. Also described is a method  
 CC for delivering a therapeutic agent in vivo, comprising the administration  
 CC of the micelle. ABB74256 to ABB74856 represent specifically claimed  
 CC nuclear localisation signal (NLS) peptides for use in the method as the  
 CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic  
 CC and anti-tumour activities. The peptide-lipid-polynucleotide complexes  
 CC produced are useful for inhibiting the progression of neoplastic  
 CC diseases. The invention relates to the field of gene therapy and is  
 CC directed toward methods for producing peptide-lipid-polynucleotide  
 CC complexes suitable for delivery of polynucleotides. The encapsulated  
 CC molecules display therapeutic efficacy in eradicating solid tumours  
 CC including but not limited to breast carcinoma or prostate carcinoma.  
 CC ABB74245 to ABB74255 are used in the exemplification of the present  
 CC invention.  
 XX  
 XX Sequence 15 AA:  
 Query Match 54.5%; Score 6; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 11111  
 6 GKKKK 11

RESULT 12  
 AAR23932  
 ID AAR23932 standard; Protein: 8 AA.  
 XX  
 AC AAR23932;  
 DT 25-MAR-2003 (updated)  
 DT 15-NOV-1992 (first entry)  
 DE Lactoferrin introduced peptide (2).  
 XX  
 XX Human lactoferrin; LF; transformation; ss.  
 XX  
 CS Synthetic.  
 UN JP04108390-A.  
 PN C9-APR-1992.  
 PD  
 XX 29-AUG-1990: 90JP-0227619.  
 PF 29-AUG-1990: 90JP-0227619.  
 PR (SNOW) SNOW BRAND MILK PROD CO LTD.  
 PA WPI: 1992-171655/21.  
 XX Introduction of foreign genes into animal cells - using a  
 PT complex comprising the gene with lactoferrin.  
 PS Disclosure; Page 5; 10pp: Japanese.  
 XX The sequences given in AAR23931 - AAR23938 are synthetic peptides which  
 CC were introduced into human lactoferrin (LF) by introducing the DNA  
 CC encoding the peptide into the human LF gene and then incubating the  
 CC mixture. The introduction of the peptide caused increased  
 CC transformation rates compared to unmodified LF and this method could  
 CC be used to introduce an exogenous gene into an animal cell with no  
 CC stress.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX Sequence 8 AA:  
 Query Match 45.5%; Score 5; DB 13; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 DB 1 GKKKK 5

RESULT 13  
 AAR70582  
 ID AAR70582 standard; Peptide: 8 AA.  
 XX  
 AC AAR70582;  
 DT 14-FEB-1996 (first entry)  
 DE HIV(H35)-1, human immunodeficiency virus epitope.  
 XX  
 XX HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;  
 KW binding peptide; induce killer cell; prevention; treatment; AIDS;  
 KW autoimmune disease syndrome; vaccine.  
 XX Human immunodeficiency virus.  
 CS  
 XX WQ951125: A1

XX 27-APR-1995.  
 XX 19-OCT-1994; 94WO-0P01756.  
 XX 19-OCT-1993; 93JP-0261302.  
 XX (AJEN ) AJINOMOTO CO INC.  
 XX (AJEN ) AJINOMOTO KK.  
 XX Miwa K. Takiquehi M.  
 XX WPI: 1995-170188/22.  
 XX HLA-binding peptide fragments from HIV proteins induce killer  
 PT cells which target HIV-infected cells and can be incorporated into  
 PT anti-HIV vaccines  
 XX  
 PS Example 1; Page 10; 61pp; Japanese.  
 XX AAR70582 is a peptide fragment derived from an HIV (Human  
 CC Immunodeficiency Virus) protein and is capable of binding to a human  
 CC lymphocyte antigen. The peptide can induce killer cells which target  
 CC HIV-infected cells. It is also useful in the prevention and treatment of  
 CC HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may  
 CC incorporate a vector (such as vaccinia or bac) containing DNA encoding the  
 CC peptides.  
 XX  
 XX Sequence 8 AA;  
 Query Match 45.5%; Score 5; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB 3 GKKKK 7  
 RESULT 14  
 AAW#0767  
 ID AAW#0767 standard; peptide: 8 AA.  
 AC AAW#0767;  
 DE 04 DEC-1998 (first entry)  
 DE Bioactive fragment acting as biospecificity enhancer.  
 XX Factor XIIIa substrate domain; transglutaminase substrate domain;  
 XX bioactive factor; protein network; replacement devices; wound healing;  
 XX cell growth promotion; tissue regeneration; tissue regeneration;  
 XX angiogenesis; tissue engineering; neovascular bed; surgical adhesive;  
 XX cell transplantation; sealant; fibrin.  
 XX Unidentified.  
 XX Key Location/Qualifiers  
 XX Modified-site 1  
 XX /note- "dansylated leucine"  
 XX WC9844686-A1.  
 XX 08-OCT-1998.  
 XX 02-APR-1998; 98WO-US06517.  
 XX 03-APR-1997; 97US-0042143.  
 XX (CALY ) CALIFORNIA INST OF TECHNOLOGY  
 XX Hubbell J. Schense JC;  
 XX

DR WPI: 1998-542404/46.  
 XX A new modified fibrin containing a bioactive factor - useful to  
 PT promote cell growth, wound healing, and tissue regeneration  
 XX Claim 32; Page 6; 42pp; English.  
 XX This represents a bioactive fragment that can be used as a biosupportive  
 CC material in the composition of the invention. The composition comprises a  
 CC peptide with transglutaminase substrate domain (factor XIIIa substrate  
 CC domain) and a bioactive factor, covalently bound to a protein network,  
 CC particularly a fibrin network. The composition can be used in implantable  
 CC devices, for promotion of cell growth, wound healing and tissue  
 CC regeneration. They can be particularly used for nerve regeneration and  
 CC angiogenesis, in tissue engineering, for example to create neovascular  
 CC beds for cell transplantation, and as a surgical adhesive or sealant.  
 XX  
 XX Sequence 8 AA;  
 Query Match 45.5%; Score 5; DB 19; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GKKKK 8  
 DB 3 GKKKK 7  
 RESULT 25  
 AAY10184  
 ID AAY10184 standard; peptide: 8 AA.  
 AC AAY10184;  
 XX 12-MAY-1999 (first entry)  
 XX T cell epitope/MHC ligand SEQ ID NO:114.  
 XX Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 XX immunisation; tumour; infectious disease; immunotherapy; cancer;  
 XX malignant melanoma; viral disease; hepatitis; AIDS.  
 XX Synthetic.  
 XX Human immunodeficiency virus type 1.  
 XX WC9902183-A2.  
 XX 21-JAN 1999.  
 XX 10-JUL-1998; 98WO-US14289.  
 XX 10-DEC-1997; 97US-0988340.  
 XX 10-JUL-1997; 97CA-2209815.  
 XX (CTL1-) CTL IMMUNOTHERAPIES CORP.  
 XX Kuendig TM, Simard JCL;  
 XX WPI: 1999-120514/10.  
 XX Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 PT sustained CTL response, used to treat, e.g. AIDS  
 XX Disclosure: Page 27; 199pp; English.  
 XX The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,

an embryonic antigen, an oncogene antigen, a mutated tumor suppressor gene antigen, or a viral antigen. They can be used for the treatment of disease such as cancer, e.g. malignant melanoma or infectious disease, e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent cell stimulation that takes place in the milieu of the lymphoid organ, and it sustains stimulation that is necessary to keep CTL active, cytotoxic and reinvolved through the body. AAY10071 to AAY1069 represent examples of peptide antigens given in the present invention.

XX Sequence 8 AA;

Query Match 45.58; Score 5; DB 20; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9 Accch;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
L I I I I  
Eh 1 GKKKK 5

RESULT 16  
AAY84922

ID AAY84922 standard; peptide: # AA.

AA AAY84922;

XX 05-OCT-2000 (first entry)

XX HIV-1 gag p17 b8 restricted CTL epitope

XX Immunogen: particulate composition; immune response assessment; target, skin site; skin immune response; HIV-1; human immunodeficiency virus antibody; cell mediated immunity; antigen exposure; allergy.

XX human immunodeficiency virus type 1

XX WO200014547 A1.

XX 16 MAR-2000.

XX 01-SEP-1999; 99WO-G802915.

XX 04 SEP 1998; 98US-C099241.

XX 15 JUN 1999; 99US-C149345.

XX (F-900) POWERSHEFT RES LTD.

XX Sarpatte RF, Roberts LR, Fuller M.

XX WPI: 2000 257072/22.

XX Assessing an immune response against a selected agent in an individual comprises accelerating a particulate composition containing an immunogenic compound from a selected agent, into the target skin site of the individual.

XX Disclosure: Page 23; 41pp; English.

XX The invention relates to a method of using a particulate compound from a selected agent in the manufacture of a particulate composition for assessing an immune response against the selected agent in an individual. The method comprises: (a) accelerating the particulate composition into a target skin site on the body of the individual; (b) assessing the target site to determine the presence of a response to a localized skin immune reaction, where the presence of the immune reaction is indicative of an immune response against the selected agent. Peptides AAY84916 Y83925 represent examples of peptides that could be used in the method is used to detect human immunodeficiency virus type 1 (HIV-1). The method is useful for assessing immune response against HIV-1 and other mediated immunity, antigen exposure, or a target agent from an individual.

XX

SQ Sequence 8 AA;

Query Match 45.58; Score 5; DB 21; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9 Accch;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
L I I I I  
Eh 1 GKKKK 5

RESULT 17

ABP16668

ID ABP16668 standard; peptide: 8 AA.

XX ABP16668;

XX 15-JUN-2002 (first entry)

XX HIV B07 super motif gag peptide #1.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX WO200124810 A1.

XX 12 APR 2001.

XX 05-OCT-2000; 2000WO-052766.

XX 05 OCT-1999; 99US-0412863.

XX (EPIM ) EPIKONE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX Baker DM, Cellis E, Kubo RT, Grey HM;

XX WPI: 2001 354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

XX Claim 52; Page 209; 44pp; English.

XX The present invention describes a composition (1) comprising a prepared human immunodeficiency virus 1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABU25347 to ABP25497). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group based vaccine may be selected from conserved regions of viral or tumour associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence 8 AA.

XX Query Match 45.58; Score 5; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
DB 3 GKKKK 7

## RESULT 18

ABP18869  
ID ABP18869 standard; Peptide: 8 AA.

XX  
AC ABP18869;

DT 15 JUL-2002 (first entry)

DE HIV 362 super motif gag peptide #272.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;

KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX human immunodeficiency virus type 1.

OS WC200124810 A1.

PN 12-APR-2001.

PD 05-OCT-2000; 2000WO-US27766.

PE 05-OCT-1999; 99US-0412863.

PR (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cellis E, Kubo RT, Grey HM;

DB WPI: 2001 354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

XX peptide groups, useful for vaccinating against HIV-1

XX Claim 32: Page 255; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
XX sequence selected from 51 defined amino acid sequences (ABL25347 to  
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
XX may be used for immunising subjects against HIV-1 infections. The use of  
XX group-based vaccines has several advantages over traditional vaccines,  
XX particularly when compared to the use of whole antigens in vaccine  
XX compositions. There is evidence that the immune response to whole  
XX antigens is directed largely toward variable regions of the antigen,  
XX allowing for immune escape due to mutations. The groups for inclusion in  
XX an group-based vaccine may be selected from conserved regions of viral or  
XX tumour-associated antigens, which therefore reduces the likelihood of  
XX escape mutants. Furthermore, immunosuppressive groups that may be present  
XX in whole antigens can be avoided with the use of group-based vaccines.  
XX An additional advantage of an group-based vaccine approach is the ability  
XX to combine selected groups (CTL and HTL), and further, to modify the  
XX composition of the groups, achieving, for example, enhanced  
XX immunogenicity. Accordingly, the immune response can be modulated, as  
XX appropriate, for the target disease. Similar engineering of the response  
XX is not possible with traditional approaches. ABP1501 to ABP25412  
XX represent peptide sequences used in the exemplification of the present  
XX invention.

QY Sequence 8 AA;

Query Match 45.5%; Score 5; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7

DB 2 GKKKK 6

Query Match 45.5%; Score 5; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7

DB 2 GKKKK 6

Claim 32: Page 288; 448pp; English.

The present invention describes a composition (I) comprising a prepared  
human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
sequence selected from 51 defined amino acid sequences (ABL25347 to  
ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
may be used for immunising subjects against HIV-1 infections. The use of  
group-based vaccines has several advantages over traditional vaccines,  
particularly when compared to the use of whole antigens in vaccine  
compositions. There is evidence that the immune response to whole  
antigens is directed largely toward variable regions of the antigen,  
allowing for immune escape due to mutations. The groups for inclusion in  
an group-based vaccine may be selected from conserved regions of viral or  
tumour-associated antigens, which therefore reduces the likelihood of  
escape mutants. Furthermore, immunosuppressive groups that may be present  
in whole antigens can be avoided with the use of group-based vaccines.  
An additional advantage of an group-based vaccine approach is the ability  
to combine selected groups (CTL and HTL), and further, to modify the  
composition of the groups, achieving, for example, enhanced  
immunogenicity. Accordingly, the immune response can be modulated, as  
appropriate, for the target disease. Similar engineering of the response  
is not possible with traditional approaches. ABP1501 to ABP25412  
represent peptide sequences used in the exemplification of the present  
invention.

ABP22687	
ID	ABP22687 standard; Peptide: 8 AA
XX	
AC	ABP22687:
XX	
DI	15-JUL-2002 (first entry)
XX	
DE	HIV A11 motif gag peptide #66.
XX	
KW	HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr; vpx; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW	antigen; vaccine; HIV infection; immunisation; virucide.
XX	
CS	Human immunodeficiency virus type 1.
XX	
PN	WG200124810 A1.
XX	
PD	12-APR-2001.
XX	
PF	05-OCT-2000; 2000WO-US27766.
XX	
PR	05-OCT-1999; 99US 0412863.
XX	
PA	(EPIM-) EPIMMUNE INC.
XX	
PI	Settle A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI	Baker DM, Cellis E, Kubo RT, Grey HM;
XX	
DR	WPI; 2001-354857/47.
XX	
PT	Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT	peptide groups, useful for vaccinating against HIV-1.
XX	
PS	Claim 32; Page 314; 448pp; English.
XX	
CC	The present invention describes a composition (I) comprising a prepared
CC	human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC	sequence selected from 51 defined amino acid sequences (ABL25347 to
CC	ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC	may be used for immunising subjects against HIV-1 infections. The use of
CC	group-based vaccines has several advantages over traditional vaccines,
CC	particularly when compared to the use of whole antigens in vaccine
CC	compositions. There is evidence that the immune response to whole
CC	antigens is directed largely toward variable regions of the antigen,
CC	allowing for immune escape due to mutations. The groups for inclusion in
CC	an group-based vaccine may be selected from conserved regions of viral or
CC	tumour-associated antigens, which therefore reduces the likelihood of
CC	escape mutants. Furthermore, immunosuppressive groups that may be present
CC	in whole antigens can be avoided with the use of group-based vaccines.
CC	An additional advantage of an group-based vaccine approach is the ability
CC	to combine selected groups (CTL and HTL), and further, to modify the
CC	composition of the groups, achieving, for example, enhanced
CC	immunogenicity. Accordingly, the immune response can be modulated, as
CC	appropriate, for the target disease. Similar engineering of the response
CC	is not possible with traditional approaches. ABP11501 to ABP25412
CC	represent peptide sequences used in the exemplification of the present
CC	invention.
XX	
SQ	Sequence 8 AA:
XX	
Query Match	45.5%; Score 5; DB 22; Length 8;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	3 GCKKK 7
DB	
	2 GCKKK 6
RESULT 22	
ABP22868	
ID	ABP22868 standard; Peptide: 8 AA.
XX	

AC ABU22808;  
 DT 15-JUL-2002 (first entry)  
 DE HIV All motif gag peptide #187.  
 DE HIV; HIV-1; human immunodeficiency virus; env; gag; pol; tat; rev; vif; vpr; vpx; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virulence.  
 KW  
 XX Human immunodeficiency virus type 1.  
 CS  
 XX  
 XX WO200124410-A1.  
 PN 12-APR-2001.  
 XX  
 PD  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX  
 PF  
 XX 05-OCT-1999; 99US-0412863.  
 XX  
 PR  
 XX (EPIM-) EPIMUNE INC.  
 PA  
 XX Sette A, Sidney J, Southwood S, Livingston RB, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 PR WPI: 2001-354887/37.  
 CR  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 PT  
 PS Claim 32; Page 336; 448pp; English.  
 XX  
 CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to  
 CC ABP25397). (ii) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of a group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HIV), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABU1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB 2 GKKKK 6  
 I I I I I  
 RESULT 23  
 ID AAU12533 standard; Peptide: 8 AA.  
 XX  
 AC AAU12533;  
 XX  
 DT 27-SEP-2001 (first entry)

XX Human HIV-1 Th-CTL overlapping epitope #40.  
 DE  
 XX  
 KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;  
 KW Human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;  
 KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;  
 KW Vaccinia ankara.  
 XX  
 OS Homo sapiens.  
 CS  
 XX Human immunodeficiency virus type 1.  
 PN WO200156355-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US03540.  
 XX  
 PR 04-FEB-2000; 2000US-0497497.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Haynes BF, Liao H;  
 PR WPI: 2001-488827/53.  
 CR  
 XX Vaccine for immunizing against human immunodeficiency virus has mixture  
 PT or linear array of peptides comprising immunodominant T-helper epitopes  
 PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes -  
 XX  
 PS Disclosure; Page 27; 33pp; English.  
 XX  
 CC The present invention relates to human immunodeficiency virus (HIV)  
 CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.  
 CC The vaccine comprises a mixture or linear array of peptides, or its  
 CC variants, where the peptides contain immunodominant T-helper (Th)  
 CC epitopes and major histocompatibility complex (MHC) cytotoxic T-  
 CC lymphocyte (CTL) epitopes and the linear array of peptides are  
 CC preferably expressed in modified Vaccinia ankara. The vaccine is useful  
 CC for immunising a patient against HIV and focuses immune response on many  
 CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with  
 CC linear arrays of CTL epitopes can be used as either primes or boosts of  
 CC peptides or of each other to optimally give CTL anti-HIV responses. The  
 CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558  
 CC represent the amino acid sequences of the Th-CTL epitopes and HIV  
 CC immunogenic peptides used in the invention.  
 XX  
 SQ Sequence 8 AA:  
 Query Match 45.5%; Score 5; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9,3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 DB 1 GKKKK 5  
 I I I I I  
 RESULT 24  
 ID ABU57482 standard; Peptide: 8 AA.  
 XX  
 AC ABU57482;  
 XX  
 DT 08-APR-2003 (first entry)  
 XX  
 DE HIV cytotoxic lymphocyte epitope #46.  
 XX  
 KW MHC; major histocompatibility complex; human; cytostatic; anti-HIV;  
 KW antiinflammatory; dermatological; antihistaminic; antidiabetic; virucide;  
 KW antiarthritic; antitumor; antitubercular; antiparasitic; AIDS;  
 KW antipsoriasis; immunosuppressive; inflammatory bowel disease; measles;  
 KW Crohn's disease; ulcerative colitis; scleroderma; type 1 diabetes; pox;  
 KW rheumatoid arthritis; psoriasis; atopic dermatitis; asthma; Chicken pox;

KW malignant melanoma; carcinoma; cancer; leukaemia; lymphoma; hepatitis;  
 KW rheila; herpes; human immunodeficiency virus.  
 XX Human immunodeficiency virus.  
 CS W:27027231-A2.  
 XX 19 SEP-2002.  
 XX 13-MAR-2002: 2002WC-DK00169.  
 XX 14-MAR-2001: 2001DK-0000435.  
 XX 14-MAR-2001: 2001DK-0000436.  
 XX 14-MAR-2001: 2001DK-0000443.  
 XX 14-MAR-2001: 2001US-275447P.  
 XX 14-MAR-2001: 2001US-275448P.  
 XX 14-MAR-2001: 2001US-275470P.  
 XX (DAK-) LAKOCYTOMATION DENMARK AS.  
 PA (DYNA-) DYNAL BIOTECH ASA.  
 XX Winther L, Petersen LO, Buus S, Schreiner G, Roub E, Aamleim M.  
 XX WPI: 2002 759637/82.  
 XX New Major Histocompatibility Complex (MHC) molecule construct, useful  
 PT for treating, preventing, stabilizing or alleviating a disease  
 PT involving MHC recognizing cells e.g., cancer  
 XX Disclosure: Figure 37: 304pp: English.  
 XX This invention relates to a new Major Histocompatibility Complex (MHC)  
 CC molecule construct comprising a carrier molecule to which one or more  
 CC MHC molecules are attached either directly or via one or more entities.  
 CC The construct of the invention may have cytostatic, antiinflammatory,  
 CC dermatological, antitumoral, antidiabetic, anti-HIV, virucide,  
 CC antiparasitic, antitumor, antirheumatic, antiallergic,  
 CC antiproliferative and immunosuppressive activities and may be used in gene  
 CC therapy. The MHC molecule construct is useful as a therapeutic  
 CC composition in vivo or ex vivo therapy for treating, preventing,  
 CC stabilizing or alleviating a disease involving MHC recognising cells,  
 CC for monitoring MHC recognising cells or establishing a prognosis of a  
 CC disease or diagnosing a disease, or determining the status of a disease  
 CC or the effectiveness of a medication against a disease, involving MHC  
 CC recognising cells, e.g., chronic inflammatory bowel disease, such as  
 CC Crohn's disease or ulcerative colitis, sarcoidosis, type 1 diabetes,  
 CC rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant  
 CC melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the  
 CC uterus, cervical cancer, prostate cancer, brain cancer, head and neck  
 CC cancer, leukaemia, cutaneous lymphoma, epidermal carcinoma, colorectal  
 CC cancer, bladder cancer, rejection related diseases, graft versus host-  
 CC related disease, or a viral disease associated with hepatitis. Acquired  
 CC immunodeficiency Syndrome (AIDS), measles, pox, chicken pox, rabies or  
 CC herpes. The MHC molecule construct is also useful for flow cytometry,  
 CC histology or cytology. The present sequence represents a peptide  
 CC used to create the MHC molecule construct of the invention.  
 XX  
 XX Sequence 8 AA:  
 SQ  
 Query Match 45.5%; Score 5; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 IIII  
 DB 1 GKKKK 5  
 RESULT 25  
 ARG79866  
 ID ARG79866 standard; Peptide: 8 AA.  
 XX  
 AC ARG79866;

XX 15-NOV-2002 (first entry)  
 XX MHC class I molecule, viral epitope #114.  
 CE Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.  
 XX Human immunodeficiency virus.  
 OS W:200262368 A2.  
 XX 15-AUG-2002.  
 PD 22-JAN-2002: 2002WC-US02033.  
 PF 02-FEB-2001: 2001US-0776232.  
 XX (CTL-) CTL IMMUNOTHERAPIES CORP.  
 PA Kundiq TM, Simard JUL.  
 XX WPI: 2002-657506/70.  
 DR Inducing or sustaining immunological cytotoxic T lymphocyte response in  
 XX a mammal, useful for treating a mammal with malignant tumour or  
 PT infectious disease, by directly administering an antigen to the  
 PT lymphatic system of the mammal.  
 XX Disclosure: Page 21: 73pp: English.  
 XX The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans.  
 CC ARG79753-ABG6659 represent viral epitopes on major histocompatibility  
 CC complex (MHC) class I molecules, used in the method of the invention.  
 XX  
 XX Sequence 8 AA:  
 SQ  
 Query Match 45.5%; Score 5; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 IIII  
 DB 1 GKKKK 5  
 RESULT 26  
 ABP96665  
 ID ABP96665 standard; peptide; 8 AA.  
 XX  
 AC ABP96665;  
 XX 29-MAY-2003 (first entry)  
 DT HIV p17 protein neutralising epitope related peptide SEQ ID NO:3.  
 DE HIV; human immunodeficiency virus; p17; neutralising epitope;  
 XX vaccine; infection; antibody; immune response; immunostimulation.  
 KW  
 AC

US Human immunodeficiency virus type 1

XX WO2003016337-A1

XX 27-FEB-2003

XX 05 AUG 2002: 2002WO-1H0394

XX 07 AUG-2001: 2001TT-T060796

PR 02 NOV 2001: 2001IT-T001042

XX (MEDE-) MEDISTEA INT SRL

XX Caruso A, Franzone JS

PI WPI: 2003-248147/25

XX New isolated polypeptide based on the neutralising epitope of the p17 protein of HIV, useful for the diagnosis, prevention and treatment of the human acquired immune deficiency syndrome

XX Claim 4: Page 28: 37pp: English

XX The present invention describes an isolated polypeptide (1) capable of reacting specifically with a neutralising antibody anti-p17 of human immunodeficiency virus (HIV), which comprises an amino acid sequence which corresponds to the neutralising epitope of the protein p17 of HIV that is the sequence lying between position 9 and position 22 of the protein p17 of HIV. Also described: (1) a pharmaceutical vaccine or inoculum composition comprising (1) and a carrier, (2) a monoclonal or polyclonal antibody directed against (1), and (3) a pharmaceutical composition comprising the antibody of (2) and a carrier. (1) has anti-HIV activity, and can be used in vaccines. (1) is useful for the preparation of a medicament capable of generating an immune response neutralising the biological activity of the protein p17 of HIV in a subject to which it is administered, or as a specific reagent for the purification of neutralising antibodies anti-p17 of HIV from a sample of biological sample. The antibodies are useful for the preparation of a therapeutic or prophylactic medicament capable of inhibiting the immunostimulating activity of the protein p17 of HIV produced in the course of an HIV infection. The polypeptide and antibody are also useful as specific reagents in a test for detecting the presence of neutralising antibodies anti-p17 of HIV in a sample of biological material. The present sequence represents a specifically obtained HIV p17 protein neutralising epitope related to that from the present invention.

XX Sequence 8 AA:

Query Match 45.5% Score 5; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Matches 5; Conservative 0; Mismatches 0; Gaps 0;

OY 3 GKKKK 7

DB 2 GKKKK 6

RESULT 27

AAW78854

ID AAW78854 standard; peptide: 9 AA

XX AAW78854

XX 26 MAR 2004 (updated)

ET 27 MAR 1996 (first entry)

XX HIV gag p17.5 cytotoxic T lymphocyte epitope

XX HIV gag p17.5 cytotoxic T cell epitopes; helper T cell epitopes

KW lymphocytic viruses; parasitic; tumours; antitumor treatment

XX disease prevention

XX human immunodeficiency virus

US human immunodeficiency virus

XX WO9522317 A1

XX 24 AUG 1995

XX 16-FEB-1995: 95WO-US02121

XX 16-FEB-1994: 94US 0197484

XX (CYTE-) CYTEL CORP

PI Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;

XX WPI: 1995-302545/39

XX Compn. inducing cytotoxic T lymphocyte response to pref. viral, bacterial, parasitic or tumour antigens - useful in the treatment and prevention of diseases associated with the antigen e.g. hepatitis B

XX Disclosure, Page 17: 109pp: English

XX A compsn. which induces a cytotoxic T lymphocyte (CTL) response to an antigen (Ag) in a mammal comprises, a CTL Ag response inducing peptide (i.e. AAW78824-R78853) and a lipid conjugated helper T cell inducing peptide. The compsn. induces a CTL response to bacterial, viral or tumour Ags, and is therefore useful in the treatment and prevention of diseases associated with the Ag.

XX (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 9 AA:

Query Match 45.5% Score 5; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GKKKK 7

DB 1 GKKKK 5

RESULT 28

AAW54640

ID AAW54640 standard; peptide: 9 AA

XX AAW54640

XX 25-SEP-1996 (first entry)

XX Peptide from HIV-1 gag p17 20-29

XX Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;

KW vaccine; treatment

XX Synthetic

XX WO9613378 A1

XX 02-APR-1998

XX 25-SEP-1997: 97WO NL00536

XX 26 SEP 1996: 96EP-C202701

XX (UYLE-) RIJKSENIV LEIDEN

PI Deilheut JW, Konink F

XX WPI: 1998-25061/20

XX Increasing uptake and presentation of antigen(s) - by adding mannose residues(s) to antigen for increasing T cell response, useful in,

PI e.g. vaccines against viral infection(s)



XX Disclosures: Page 28: 47pp; English.

XX

CC The peptides AAY5459-W54809 are examples of peptides 1-10 which, at least

CC : (preferably 2) mannose can be attached to each use that uptake as

CC antigens by antigen presenting cells. Optase of a host main sytiated

CC peptides will increase the T cell response, when as uptake of antigen host

CC peptides blocks the T cell response. Blockant binding of immunosence

CC autoantigens can be used in treatment of type 1 diabetes, rheumatoid

CC arthritis, graft rejection etc. also to inhibit T cell med

CC responsiveness. Vaccines containing mannose, and peptides used to

CC prevent or treat infections by: a) bacterial viruses, fungi, helminths

CC and parasites.

XX

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 10; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY < GKKKK 7

DB 5 GKKKK 9

RESULT 29

AAY5444

ID AAY5444 standard: Protein: 9 AA.

XX

XX AAY5444.

XX

DT 19 JAN 2000 (first entry)

XX

DE HIV-1 p17 protein (aa 20-28) binds HLA-A1.

XX

KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;

KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;

KW human immunodeficiency virus; hepatitis B virus; papilloma virus;

KW melanoma; malaria; parasite.

XX

XX Synthetic.

XX Human immunodeficiency virus type 1.

XX FR277626-A1.

XX

PD 08-OCT-1999.

XX

PF 07-APR-1998; 98FR-0004323.

XX

PR 07-APR-1999; 98FR-0004323.

XX

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

PA (INSP ) INST PASTEUR LILLE.

XX

PI Le Gal FA, Guillet JG, Gabery SH, Gras MH, Melnyk O, Tartar A;

XX

DR WPL: 1999-58115/50.

XX

PI New lipopeptide containing lipid regions and two epitopes, all

PI separated by peptide spacers that impart hydrophilicity, useful in

PI vaccines.

XX

PS Disclosures: Page 21: 35pp; French.

XX

XX The invention relates to the generation of a lipopeptide comprising at

CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)

CC epitope and at least one lipid residue with (i) the epitopes and lipid

CC portion and (ii) the epitopes, being separated independently by peptide

CC spacers. These spacers comprise sequences of amino acids which carry an

CC overall electrical charge in neutral media to ensure that the

CC lipopeptide is hydrophilic. The peptides AAY5301-Y53549 represents

CC examples of peptide epitopes used to generate the lipopeptides. These are

CC used in therapeutic or prophylactic compositions and vaccines to induce

CC specific immune responses against human immunodeficiency, hepatitis B or

CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC used in therapeutic or prophylactic compositions and vaccines to induce

CC specific immune responses against human immunodeficiency, hepatitis B or

CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY < GKKKK 7

DB 5 GKKKK 9

RESULT 30

AAY5349

ID AAY5349 standard: Protein: 9 AA.

XX

XX AAY5349.

XX

DT 18 JAN 2000 (first entry)

XX

DE HIV-1 p17 protein (aa 24-32) binds HLA-B8.

XX

KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;

KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;

KW human immunodeficiency virus; hepatitis B virus; papilloma virus;

KW melanoma; malaria; parasite.

XX

XX Synthetic.

XX Human immunodeficiency virus type 1.

XX FR277625-A1.

XX

PD 08-OCT-1999.

XX

PF 07-APR-1998; 98FR-0004323.

XX

PR 07-APR-1999; 98FR-0004323.

XX

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

PA (CNRS ) CNRS CENT NAT RECH SCI.

PA (INSP ) INST PASTEUR LILLE.

XX

PI Le Gal FA, Guillet JG, Gabery SH, Gras MH, Melnyk O, Tartar A;

XX

DR WPL: 1999-58115/50.

XX

PI New lipopeptide containing lipid regions and two epitopes, all

PI separated by peptide spacers that impart hydrophilicity, useful in

PI vaccines.

XX

PS Disclosures: Page 21: 35pp; French.

XX

XX The invention relates to the generation of a lipopeptide comprising at

CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)

CC epitope and at least one lipid residue with (i) the epitopes and lipid

CC portion and (ii) the epitopes, being separated independently by peptide

CC spacers. These spacers comprise sequences of amino acids which carry an

CC overall electrical charge in neutral media to ensure that the

CC lipopeptide is hydrophilic. The peptides AAY5301-Y53549 represents

CC examples of peptide epitopes used to generate the lipopeptides. These are

CC used in therapeutic or prophylactic compositions and vaccines to induce

CC specific immune responses against human immunodeficiency, hepatitis B or

CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX

XX Sequence 9 AA:

XX

Query Match 45.5%, Score 5; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e-05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      3 GKKKK 7
DB      11111
        1 GKKKK 5

RESULT 31
AAV45448
ID      AAY45448 Standard: Peptide: 9 AA
XX
XX
AC      AAY45448;
DT      01 DEC 1999 (first entry)
DE      Immunogenic peptide having a human leukocyte antigen binding motif: #59.
XX
XX      Human leukocyte antigen; binding: immunogenic; glycoprotein; MHC: HLA;
KW      immune response; T cell activation; major histocompatibility complex;
KW      cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW      prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW      vaccine; immunisation.
XX
XX      Synthetic.
XX      Homo sapiens.
XX
XX      W05945954 AL.
XX
XX      16 SEP 1999.
XX
XX      13 MAR 1998; 98WO-US05039.
XX
XX      23 MAR 1998; 98WO-US05049.
XX
XX      (EPIM-) EPIMMUNE INC.
XX
XX      Sette A, Kube RT, Sidney G, Cellis E, Grey HM. Southwest S;
XX      WPI: 1999 551214/46.
XX
XX      New immunogenic peptides with HLA binding motif useful in treatment
XX      and diagnosis of cancers and viral diseases
XX      claim 1; Page 29; 150pp; English.
XX
XX      AAY45448 to AAY48214 represent specifically obtained immunogenic peptides
XX      having a human major histocompatibility complex (MHC) class I false
XX      known as human leukocyte antigen (HLA); binding motif. The immunogenic
XX      peptides can bind to a specific HLA allele of the HLA A subtypes
XX      HLA-A2.1, AL, A3.2 or A24.1 or HLA-B*07:01 and induce a cytotoxic T cell
XX      response against the antigen from which the peptide is derived.
XX      Cytotoxic T lymphocytes (CTLs) which destroy antigen presenting cells are
XX      normally induced by an antigen in the form of a peptide fragment bound
XX      to a HLA molecule, rather than the intact foreign antigen itself, and
XX      are particularly important in tumour rejection and in fighting viral
XX      infections. The peptides are therefore useful therapeutically to treat
XX      or prevent viral infections and cancers in mammals (especially humans)
XX      e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX      They can be administered as vaccines to elicit an immune response in
XX      individuals susceptible or otherwise at risk of viral infection or
XX      cancer, or used to treat chronic or acute conditions. They are also
XX      useful diagnostically, and can be used to induce a cytotoxic T cell
XX      response, by contacting a cytotoxic T cell with the peptide e.g. to
XX      produce CTLs ex vivo for infusion back into a patient. The
XX      polypeptides encoding the immunogenic peptides are also useful
XX      therapeutically and for immunisation as above.
XX      Sequence 9 AA:

Query Match      45.5%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GKKKK 7
DB      11111
        1 GKKKK 5

RESULT 32
AAV40273
ID      AAY40273 Standard: Peptide: 9 AA
XX
XX
AC      AAY40273;
DT      19-NOV-1999 (first entry)
DE      Amino acid sequence of a HIV 1 epitope.
XX
XX      Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
KW      CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
KW      vaccine; tumor; infection; immune response; cytokine profile;
KW      acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
KW      autoimmune disease.
XX
XX      Human immunodeficiency virus type 1.
XX
XX      FR2774687-A1.
XX
XX      13-AUG-1999.
XX
XX      06-FEB-1998; 98FR-0001439.
XX
XX      06-FEB-1998; 98FR-0001439.
XX
XX      (INRM ) INSRM INST NAT SANTE & RECH MEDICALE.
XX      (INSP ) INST PASTEUR LILLE.
XX
XX      Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;
XX      WPI: 1999-510734/43.
XX
XX      New lipopeptide comprising C-terminal interferon-gamma fragment with
XX      attached lipophilic groups, used as interferon mimic, e.g. for treating
XX      cancer or virus infection
XX      Disclosure: Page 38; 53pp; French.
XX
XX      AAY40123-Y40179 represent epitopes that are able to activate cytotoxic
XX      T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
XX      B epitopes recognized by corresponding antibodies. The epitopes may be
XX      used in the composition of the invention. The specification describes a
XX      lipopeptide that has a peptide part derived from mammalian interferon
XX      gamma (IFNg) and one or more lipophilic parts comprising a linear or
XX      branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The
XX      lipopeptide mimics the activity of IFNg. Compositions comprising the
XX      lipopeptide are used to treat or prevent any condition that responds
XX      to IFNg, and as adjuvant for vaccines (particularly those directed
XX      against tumors, viral or parasitic infections), to stimulate or
XX      (re)orient the immune response between types 1 and 2 cytokine profiles.
XX      Particular applications are treatment of infections (particularly
XX      viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
XX      hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
XX      (particularly of kidney, cutaneous T cells or ovary, chronic
XX      myelogenous leukemia or mesothelioma), allergy; and autoimmune
XX      diseases.
XX      Sequence 9 AA:

Query Match      45.5%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches      5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GKKKK 7
DB      11111
        1 GKKKK 5

RESULT 33

```

```

AAV40308
ID AAY40308 standard; Peptide: 9 AA.
XX
AC AAY40308;
XX
DZ 19-NOV-1999 (first entry)
XX
DE Amino acid sequence of a HIV-1 epitope.
XX
KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
KW vaccine; tumor; infection; immune response; cytokine profile;
KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
KW autoimmune disease.
XX
OS human immunodeficiency virus type 1.
XX
PN FR2774687-A1.
XX
PD 13-NOV-1999.
XX
PF 06-FEB-1998; 98FR-0001439.
XX
PR 06-FEB-1998; 98FR-0001439.
XX
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP ) INST PASTEUR LILLE.
XX
PI Thiam K, Guillet JG, Ver Waerde C, Aubault C, Gras MH, Loring E;
PI WPI: 1999 510734/43.
XX
DR New lipopeptide comprising C-terminal interferon gamma treatment with
PI attached lipophilic groups, used as interferon mimic, e.g. for treating
PI cancer or virus infection.
XX
PS Disclosure: Page 39; 53pp; French.
XX
AA AAY40123-Y40179 represent epitopes that are able to activate cytotoxic
CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
CC B epitopes recognized by corresponding antibodies. The epitopes may be
CC used in the composition of the invention. The specification describes a
CC lipopeptide that has a peptide part derived from mammalian interferon
CC gamma (IFN $\gamma$ ) and one or more lipophilic parts comprising a linear or
CC branched, (un)saturated 4-200 hydrocarbon chain of a steroid. The
CC lipopeptide mimics the activity of IFN $\gamma$  preparations comprising the
CC lipopeptide are used to treat or prevent any condition that responds
CC to IFN $\gamma$ , and as adjuvant for vaccines (particularly those directed
CC against tumors, viral or parasitic infections), to stimulate or
CC (re)orient the immune response between types 1 and 2 cytokine profiles.
CC Particular applications are treatment of infections (particularly
CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
CC hepatitis), but also bacterial, fungal, parasitic or helminthic; cancers
CC (particularly of kidney, cutaneous T cells or hairy, chronic
CC myelogenous leukemia or mesothelioma); allergy and autoimmune
CC diseases.
XX
SQ Sequence 9 AA;
XX
Query Match 45.5%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9 3e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 3 GGRKK 7
DB 11111
5 GGRKK 5
XX
RESULT 34
AAY26765
ID AAY26765 standard; peptide: 9 AA.
XX
AC AAY26765;
XX
DZ 19-SEP-1999 (first entry)
XX
DE HIV-derived lipopeptide epitope #70 for mixed micelles.
XX
KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
KW melanoma; Plasmodium falciparum; malaria.
XX
OS Synthetic.
OS Human immunodeficiency virus type 1.
XX
PN FR2771640-A1.
XX
PD 04-JUN-1999.
XX
PF 03-DEC-1997; 97FR-0015246.
XX
PR 03-DEC-1997; 97FR-0015246.
XX
PA (CNRS ) CNRS CENT NAT RECH SCI.
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INSP ) INST PASTEUR LILLE.
XX
PI Bossus M, Bourgault VL, Gras-Masse H, Guillet JG, Lippens G;
PI Tartar A, Wieruszski JM;
XX
PI WPI: 1999-349509/30.
XX
DR Immunogenic lipopeptide micelles - comprising lipopeptides
PI containing cytotoxic and helper T-lymphocyte epitopes
XX
PS Disclosure: Page 33; 60pp; French.
XX
AA The invention relates to the generation of mixed micelles or
CC microaggregates for inducing an immune response comprise: (a) a first
CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
CC and at least one lipid unit; and (b) a second lipopeptide comprising at
CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
CC different from that of the first lipopeptide. This peptide represents
CC an example of a lipopeptide epitope used in the invention and is derived
CC from a human immunodeficiency virus type 1 (HIV-1) protein. The
CC immunogenic lipopeptide micelles are used in vaccines, especially
CC against HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma
CC or Plasmodium falciparum malaria.
XX
SQ Sequence 9 AA;
XX
Query Match 45.5%; Score 5; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9 3e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 3 GGRKK 7
DB 11111
5 GGRKK 5
XX
RESULT 35
AAY26800
ID AAY26800 standard; peptide: 9 AA.
XX
AC AAY26800;
XX
DZ 14-SEP-1999 (first entry)
XX
DE HIV-derived lipopeptide epitope #70 for mixed micelles.
XX
KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
KW melanoma; Plasmodium falciparum; malaria.
XX

```

OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 PN FR2771640-A1.  
 XX  
 XX 04-JUN-1999.  
 XX  
 XX 01-DEC-1997; 97FR-0015246.  
 XX  
 XX 03-DEC-1997; 97FR-0015246.  
 XX  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (INSP ) INST PASTEUR LILLE.  
 XX  
 XX Bosses M, Bourgault VL, Gras-Masse H, Guillet-DS, Lippens G;  
 PI Tartat A, Wieruszski JM;  
 XX WPI: 1999-345509/30.  
 XX  
 XX Immunogenic lipopeptide micelles comprising lipopeptides  
 PI containing cytotoxic and helper T-lymphocyte epitopes  
 XX  
 XX Disclosure: Page 34; 60pp; French.  
 XX  
 XX The invention relates to the generation of mixed micelles or  
 CC microaggregates for inducing an immune response comprising: (a) a first  
 CC lipopeptide comprising at least one CTL (cytotoxic T lymphocyte) epitope  
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at  
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit,  
 CC different from that of the first lipopeptide. This peptide represents  
 CC an example of a lipopeptide epitope used in the invention and is derived  
 CC from a human immunodeficiency virus type 1 (HIV 1) protein. The  
 CC immunogenic lipopeptide micelles are used in vaccines, especially  
 CC against HIV, hepatitis B virus (HBV), papilloma viruses, P53, melanoma  
 CC or Plasmodium falciparum malaria.  
 XX  
 XX Sequence 9 AA;  
 SO

Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKKKK 7  
 DE 1 GKKK 5  
 IIII

RESULT 46  
 AAY10176  
 ID AAY10176 standard; Peptide: 9 AA.  
 XX  
 AC AAY10176;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE 1 cell epitope/MHC ligand SEQ ID NO:106.  
 XX  
 KW Cytotoxic T lymphocyte response; CTL; antigen; lymphatic system;  
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 KW malignant melanoma; viral disease; Hepatitis; AIDS.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO9902183-A2.  
 PN  
 XX 21 JAN-1999.  
 PD  
 XX 10 JUL 1998; 98WO-US:4289.  
 XX  
 XX 10-DEC-1997; 97US-0988320.  
 XX  
 XX 10-JUL-1997; 97CA-2209815.  
 XX

XX (CTL1-) CTL IMMUNOTHERAPIES CORP.  
 XX Kuendig TM, Simard JLL;  
 XX WPI: 1999-120514/10.  
 XX  
 XX Inducing a cytotoxic T lymphocyte response - by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 PT sustained CTL response, used to treat, e.g. AIDS  
 XX  
 XX Disclosure: Page 27; 19pp; English.  
 XX  
 XX The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g. a differentiation antigen, a tumour-specific multilineage antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10071 to AAY10639 represent examples of peptide  
 CC antigens given in the present invention.  
 XX  
 XX Sequence 9 AA;  
 SO

Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 DE 5 GKKKK 9  
 IIII

RESULT 37  
 AAY10575  
 ID AAY10575 standard; Peptide: 9 AA.  
 XX  
 AC AAY10575;  
 XX  
 DT 12-MAY-1999 (first entry)  
 XX  
 DE HLA Class I motif peptide SEQ ID NO:505.  
 XX  
 KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;  
 KW malignant melanoma; viral disease; hepatitis; AIDS.  
 XX  
 OS Synthetic.  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO9902183-A2.  
 PN  
 XX 21-JAN-1999.  
 PD  
 XX 10-JUL-1998; 98WO-US14289.  
 XX  
 XX 10-DEC-1997; 97US-0988320.  
 XX  
 XX 10-JUL-1997; 97CA-2209815.  
 XX  
 XX (CTL1-) CTL IMMUNOTHERAPIES CORP.  
 XX Kuendig TM, Simard JLL;  
 XX WPI: 1999-120514/10.  
 XX

PT Inducing a cytotoxic T lymphocyte response by maintaining a level  
 PT of antigen in the lymphatic system of a mammal so as to provide a  
 E3 sustained CTL response, used to treat, e.g., AIDS  
 XX Disclosure: Page 47; 199pp; English.  
 XX The present invention describes a method of inducing and/or sustaining  
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain  
 CC the immunologic CTL response. The method can be used for the delivery of  
 CC e.g., a differentiation antigen, a tumour specific multipeptide antigen,  
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor  
 CC gene antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g., malignant melanoma or infectious disease,  
 CC e.g., viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating  
 CC through the body. AAY10073 to AAY1569 represent examples of peptide  
 CC antigens given in the present invention.

Sequence 9 AA;

Query Match 45.5%; Score 5; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 ID 1 1 1 1  
 DB 5 GGKKK 9

RESULT 48  
 ABP1448:  
 ID ABP1448; standard; Peptide: 9 AA

AC ABP14481

DT 15-JUL-2002 (first entry)

DE HIV A27 super motif gag peptide #26.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

PN WC200124810-A1.

PU 12-APR-2001.

PF 05-OCT-2000; 2000WO-US27766.

PR 05-OCT-1999; 99US-0412863.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

DR WPI; 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1

PS Claim 32; Page 165; 448pp; English.

CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,

CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

Sequence 9 AA;

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9; 3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 ID 1 1 1 1  
 DB 5 GGKKK 9

RESULT 39  
 ABP17150:  
 ID ABP17150; standard; Peptide: 9 AA.

AC ABP171501

DT 15-JUL-2002 (first entry)

DE HIV B27 super motif gag peptide #26.

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

PN WC200124810-A1.

PU 12-APR-2001.

PF 05-OCT-2000; 2000WO-US27766.

PR 05-OCT-1999; 99US-0412863.

PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;

DR WPI; 2001-354887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 220; 446pp; English.

CC The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25447 to  
 CC ABL25497). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CII and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ARP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 9 AA;  
 Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 IIIL  
 DB 4 GKKKK 8

RESLI: 40  
 ABP20400  
 ID ABP20400 standard; Peptide: 9 AA  
 AC ARI-20400;

DT 15 JUL-2002 (first entry)

XX HIV A03 motif gag peptide #63.

LE HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX W0200124410-A1.

PN 12-APR-2001.

XX C5-CCT-2000; 2500WD-US27766.

XX C5-CCT-1999; 990S-0412463.

XX (EPIM) EPIMMUNE INC.

XX Settle A, Sidney J, Southwood S, Livingston S, Chesnut R;  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.

PI Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PI peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 288; 448pp; English.

XX The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus 1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen.

CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CII and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ARP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX  
 SQ Sequence 9 AA;

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 IIIL  
 DB 1 GKKKK 5

RESLI: 41

ABP20552  
 ID ABP20552 standard; Peptide: 9 AA.

XX ABP20552;

XX 15-JUL-2002 (first entry)

DE HIV A03 motif gag peptide #215.

KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus type 1.

XX W0200124810-A1.

PN 12-APR-2001.

XX C5-CCT-2000; 2500WD-US27766.

XX C5-CCT-1999; 990S-0412463.

XX (EPIM) EPIMMUNE INC.

XX Settle A, Sidney J, Southwood S, Livingston S, Chesnut R;  
 PI Baker DM, Cells E, Kubo RT, Grey HM;  
 XX WPI: 2001-354887/37.

PI Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PI peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 291; 448pp; English.

XX The present invention describes a composition (i) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group based vaccines.  
 CC An additional advantage of an group based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 7

DB 1 GKKKK 5

RESULT 42

ABP20742  
 ID ABP20742 standard; Peptide: 9 AA

AC ABP20742;

DT 15-JUL-2002 (first entry)

DE HIV A13 motif gag peptide #405.

XX HIV; HIV-1; human immunodeficiency virus; env; gag; nef; vif;  
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

CS Human immunodeficiency virus type 1

PN W0200124810-A1

PD 12-APR-2001

PF 05-OCT-2000; 2000W0-US27766

PR 05-OCT-1999; 99US-0412663

PA (EPIM) : EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;

PR WPI: 2001-054887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1

PS Claim 42; Page 294; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumor-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC immunogenicity. Accordingly, the immune response can be modulated, as

CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 9 AA:

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 7

DB 5 GKKKK 9

RESULT 43

ABP22667  
 ID ABP22667 standard; Peptide: 9 AA

AC ABP22667;

DT 15-JUL-2002 (first entry)

DE HIV A13 motif gag peptide #46.

XX HIV; HIV-1; human immunodeficiency virus; env; gag; nef; vif;  
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

CS Human immunodeficiency virus type 1

PN W0200124810-A1

PD 12-APR-2001

PF 05-OCT-2000; 2000W0-US27766

PR 05-OCT-1999; 99US-0412663

PA (EPIM) : EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;

PR WPI: 2001-054887/37.

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1

PS Claim 42; Page 433; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumor-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 9 AA:  
 Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 Db 1 GKKKK 5

# RESULT 44

ABP22764

ID ABP22764 standard; Peptide: 9 AA.

AC ABP22764;

XX ABP22764;

XX 15-JUL-2002 (first entry)

XX HIV All motif gag peptide #143.

XX HIV: HIV-1; human immunodeficiency virus: env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

SN WO200124810 A1.

PN 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27765.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI: 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)  
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 335; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present

CC invention.  
 XX SQ Sequence 9 AA:

Query Match 45.5%; Score 5; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKKKK 7  
 Db 1 GKKKK 5

# RESULT 45

ABP22885

ID ABP22885 standard; Peptide: 9 AA.

AC ABP22885;

XX ABP22885;

XX 15-JUL-2002 (first entry)

XX HIV All motif gag peptide #264.

XX HIV: HIV-1; human immunodeficiency virus: env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

PN WO200124810 A1.

XX 12-APR-2001.

XX 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

XX (EPIM-) EPIMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI: 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 338; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (1)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 9 AA:



Query Match 45.5% Score 5; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 7  
 IIII  
 DB 5 GKKKK 9

RESULT 4b  
 AAB59211  
 ID AAB59211 standard; peptide; 9 AA.

XX AC AAB59211;  
 XX DT 25-MAR-2001 (first entry)  
 XX CE Peptide #2 used in invention.  
 XX KW Nucleic acid imaging.  
 XX CS Synthetic.

XX PN WC200075125-A1.  
 XX PD 14-OCT-2000.  
 XX PF 25-MAY-2003; 2003WO-US14439.

XX PR 03 JUN-1999; 94US-0324665.  
 XX PA (GENO) GEN HOSPITAL CORP.  
 XX PI Bogdanov A., Tung C., Weissleder R.

XX DR WPI: 2001-080571/09.  
 XX PT New nucleic acid-imaging compounds comprising a base-binding group, a phosphate-binding group, and a metal-binding group for quantitative assessment of the biodistribution of introduced nucleic acid.

XX PS Example 2; Page 14; 24pp; English.  
 XX CC The present invention relates to a nucleic acid binding compound comprising a base-binding group, a phosphate-binding group, and a metal-binding group. The nucleic acid binding compound is useful for noninvasive imaging for the quantitative assessment of the biodistribution of introduced nucleic acid.  
 XX SQ Sequence 9 AA;

Query Match 45.5% Score 5; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 IIII  
 DB 4 GKKKK 8

RESULT 47  
 AB057445  
 ID AB057445 standard; Peptide; 9 AA.

XX AC AB057445;

XX DT 09-APR-2003 (first entry)

XX DE HIV cytotoxic lymphocyte epitope #9.

KW MHC: major histocompatibility complex; human cytostatic anti HIV; antinflammatory; dermatological; antidiabetic; virucide;

KW antiarteriosclerotic; antiulcer; antirheumatic; antiarthritic; AIDS;  
 KW antiproliferative; immunosuppressive; inflammatory bowel disease; measles;  
 KW Crohn's disease; ulcerative colitis; sclerosis; type I diabetes; pox;  
 KW rheumatoid arthritis; psoriasis; atopic dermatitis; asthma; chicken pox;  
 KW malignant melanoma; carcinoma; cancer; leukaemia; lymphoma; hepatitis;  
 KW rubella; herpes; human immunodeficiency virus.  
 XX Human immunodeficiency virus.

XX WO200272631-A2.

XX PC 19-SEP-2002.

XX PF 13-MAR-2002; 2002WO DK03169.

XX PR 14-MAR-2001; 2001DK-0000435.

XX PR 14-MAR-2001; 2001DK-0000436.

XX PR 14-MAR-2001; 2001DK-0000441.

XX PR 14-MAR-2001; 2001US-275447P.

XX PR 14-MAR-2001; 2001US-275448P.

XX PR 14-MAR-2001; 2001US-275470P.

XX PA (DAKO) DAKOCYTOMATION DENMARK AS.

XX PA (DYNA-) DYNAL BIOTECH ASA.

XX EI Winther L., Petersen LO., Ruus S., Schoeller J., Ruub E., Aamellem O;

XX WIPI: 2002-759837/82.

XX PT New Major Histocompatibility Complex (MHC) molecule construct, useful for treating, preventing, stabilizing or alleviating a disease involving MHC recognizing cells e.g., cancer.

XX PS Disclosure; Figure 37; 304pp; English.

XX CC This invention relates to a new Major Histocompatibility Complex (MHC) molecule construct comprising a carrier molecule to which one or more MHC molecules are attached either directly or via one or more entities. The construct of the invention may have cytostatic, antinflammatory, dermatological, antiallergic, antidiabetic, anti-HIV, virucide, antiarteriosclerotic, antiulcer, antirheumatic, antiarthritic, antiproliferative and immunosuppressive activities and may be used in gene therapy. The MHC molecule construct is useful as a therapeutic composition in vivo or ex vivo therapy, for treating, preventing, stabilizing or alleviating a disease involving MHC recognizing cells, for monitoring MHC recognizing cells or establishing a prognosis of a disease or diagnosing a disease, or determining the status of a disease or the effectiveness of a medicament against a disease, involving MHC recognizing cells, e.g., chronic inflammatory bowel disease such as Crohn's disease or ulcerative colitis, sclerosis, type I diabetes, rheumatoid arthritis, psoriasis, atopic dermatitis, asthma, malignant melanoma, renal carcinoma, breast cancer, lung cancer, cancer of the uterus, cervical cancer, prostate cancer, brain cancer, head and neck cancer, leukaemia, cutaneous lymphoma, hepatic carcinoma, colorectal cancer, bladder cancer, rejection-related disease, Graft-versus-host-related disease, or a viral disease associated with hepatitis. Acquired immunodeficiency Syndrome (AIDS), measles, pox, chicken pox, rubella or herpes. The MHC molecule construct is also useful for flow cytometry, histology or cytology. The present sequence represents a peptide used to create the MHC molecule construct of the invention.

XX SQ Sequence 9 AA;

Query Match 45.5% Score 5; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
 IIII  
 DB 5 GKKKK 9

RESULT 48

ABR82016  
 ID: ABR82016 standard: protein; 9 AA.  
 XX AC ABR82016;  
 XX AC  
 XX DT 05 DEC-2002 (first entry)  
 XX DE CP02 enzyme immunogenic region peptide (residues 33-48).  
 XX KW CP02: carboxypeptidase G2; gene-directed enzyme producing therapy; enzyme;  
 KW immunogenicity; antibody-directed enzyme producing therapy; cytostatic;  
 KW ACEP1; GDEPT.  
 XX OS Pseudomonas sp.  
 XX PN US2002090709-A1.  
 XX PD 11 JUL 2002.  
 XX PF 05-JUL-2001; 2001US-0898461.  
 XX PR 07 JUL 2002; 2000US-216689P.  
 XX PA (REGG/) BEGENT R H J.  
 XX PA (CHES/) CHESTER K.  
 XX PA (MINT/) MINTON N P.  
 XX PA (REES/) REES A R.  
 XX PA (SHAR/) SHARMA S K.  
 XX PA (SPEN/) SPENCER D I R.  
 XX P1 Bequent RHJ, Chester K, Minton NP, Rees AP, Sharma SK, Spencer DR.  
 XX WP1: 2002 681730/73.  
 XX Novel carboxypeptidase G2 enzyme used in antibody directed enzyme  
 P1 producing therapy and gene-directed enzyme producing therapy, comprises  
 P1 immunogenic regions modified to reduce or alter immunogenicity to  
 P1 immune system.  
 XX Claim 1; Page 12; 23pp; English.  
 XX The invention provides a Pseudomonas derived carboxypeptidase G2 (CPG2)  
 CC enzyme in which an immunogenic residue is modified to reduce or alter  
 CC immunogenicity to a mammalian immune system, with a retaining CPG2  
 CC activity, or a CPG2 enzyme where the C-terminal of the enzyme comprises  
 CC an extension such as histidine, myc tag, etc. and the CPG2 enzyme is  
 CC useful in therapy, particularly antibody directed enzyme producing therapy  
 CC (ADEPT) and gene-directed enzyme producing therapy (GDEPT). A fusion  
 CC protein comprising an antibody fused to the CPG2, as useful in ADEPT  
 CC therapy, or used in the provision of vectors such as viral vectors for  
 CC GDEPT therapies. ADEPT therapy has use in the treatment of tumours  
 CC associated with tumour specific markers, which may be targeted for an  
 CC antibody. Sequences ABR82012-16 represented immunogenic region peptides of  
 CC the CPG2 enzyme, that can be modified to reduce or alter immunogenicity.  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 45.5%; Score 5; DB 23; Length 4;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 EGKK 6  
 DB 1 EGKK 5  
 RESULT 45  
 ABR79858  
 ID: ABR79858 standard: Peptide; 9 AA.  
 XX AC ABR79858;  
 XX AC  
 XX DT 15-NOV-2002 (first entry)  
 XX KW Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.

XX MHC class I molecule, viral epitope #106.  
 DE Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 XX epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.  
 XX Human immunodeficiency virus.  
 OS  
 XX WO200262368-A2.  
 XX PN 15-AUG-2002.  
 XX PD 22-JAN-2002; 2002WO-USQ2033.  
 XX PF 02-FEB 2001; 2001US-0776232.  
 XX PR (CTL1-) CTL IMMUNOTHERAPIES CORP.  
 XX PA Kurlig TM, Simard JDL;  
 XX P1 WP1: 2002-657506/70.  
 XX DR Inducing or sustaining immunological cytotoxic T lymphocyte response in  
 XX a mammal, useful for treating a mammal with malignant tumour or  
 PT infectious disease, by directly administering an antigen to the  
 PT lymphatic system of the mammal.  
 XX PS Disclosure; page 21; 73pp; English.  
 XX The invention relates to a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal  
 CC comprising administering directly to the lymphatic system of the mammal:  
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
 CC method is useful for inducing and/or sustaining CTL response in a mammal.  
 CC This is particularly useful for treating a mammal having a malignant  
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
 CC malaria, measles or tuberculosis), or in an animal having a  
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,  
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans.  
 CC ABR79753; ABR80159 represent viral epitopes on major histocompatibility  
 CC complex (MHC) class I molecules, used in the method of the invention.  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 45.5%; Score 5; DB 23; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GGKK 7  
 DB 5 GGKK 9  
 RESULT 50  
 ABR80258  
 ID: ABR80258 standard: Peptide; 9 AA.  
 XX AC ABR80258;  
 XX AC  
 XX DT 15-NOV-2002 (first entry)  
 XX DE MHC class I molecule, viral epitope #506.  
 XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
 KW acquired immune deficiency syndrome; AIDS.

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XX Viridae.
XX
XX W-2002266-A2.
XX
XX
XX 16-AUG 2002.
XX
XX 22 JAN-2002; 2002W0-USC2034.
XX
XX 02-FEB-2001; 2001US-0776232.
XX
XX (C111 ) C11 IMMUNOTHERAPIES (APP.
XX
XX Kundiq TM, Simard JUL.
XX
XX W61; 2002-657506/70.
XX
XX Inducing or sustaining immunological cytotoxic T lymphocyte response in
XX a mammal, useful for treating a mammal with malignant tumour or
XX infectious disease, by directly administering an antigen to the
XX lymphatic system of the mammal.
XX
XX Disclosure: Page 41; 73pp; English.
XX
XX The invention relates to a method of inducing and/or sustaining an
XX immunological cytotoxic T lymphocyte (CTL) response in a mammal
XX comprising administering directly to the lymphatic system of the mammal:
XX (a) an antigen in the form of a polypeptide; (b) a vector comprising a
XX nucleic acid encoding the antigen; or (c) a non-peptide antigen. The
XX method is useful for inducing and/or sustaining CTL response in a mammal.
XX This is particularly useful for treating a mammal having a malignant
XX tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious
XX disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),
XX malaria, measles or tuberculosis), or in an animal having a
XX predisposition to these diseases; the mammal may be dogs, cats, mice,
XX cattle, sheep, pigs, goats, rabbits, or preferably humans.
XX AM074753-A5380319 represent viral epitopes on major histocompatibility
XX complex (MHC) class I molecules, used in the method of the invention.
XX
XX Sequence 9 AA:
XX
XX Query Match 45.5%, Score 51, ID: 216, Length 97
XX Best Local Similarity 100.0%, Pos. No. 9 to 95
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 5 GAKKK 7
XX 5 KKKK 9
XX

```

Search completed: September 30, 2003 11:07:00  
 Job time: 47.1667 secs

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OM proteins - protein search, using SW mode.

Run on: September 30, 2003, 10:07:44 - Search time 11.6433 seconds  
(without alignment)  
90,440 Million cell updates/sec

Title: US-09-787-443-19

Perfect score: 11

Sequence: 1 AEGSKKKKRA 1:

Scoring table: Q120

Gapop 60.0 - Gapext 60.0

Searched: 293308 seqs, 96166682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 204

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

Database:

PIR\_76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	4	46.4	15	2	129501			calnexin protein A
2	4	46.4	15	2	42960			calnexin protein A
3	3	27.3	9	2	157676			specrin alpha cha
4	3	27.3	10	2	102790			hypothetical prote
5	3	27.3	10	2	877990			cytochrome oxid
6	3	27.3	11	2	100029			338 protein 4218
7	3	27.3	11	2	102790			tracylglycerol li
8	3	27.3	11	2	857574			T-cell receptor V-
9	3	27.3	11	2	852294			tubulin 2 beta-3 c
10	3	27.3	12	2	86902			33 protein - wheat
11	3	27.3	12	2	864573			hypothetical prote
12	3	27.3	12	2	848204			zinc-metallophosph
13	3	27.3	12	2	860757			enterotoxin C11
14	3	27.3	12	2	A3900			hydrolin 1 - Arica
15	3	27.3	12	2	S10626			lipovitellin - Afr
16	3	27.3	12	2	S57570			T-cell receptor V-
17	3	27.3	12	2	PH1189			T-cell receptor al
18	3	27.3	12	2	PH1180			T-cell receptor al
19	3	27.3	12	2	PH1175			T-cell receptor al
20	3	27.3	12	2	PH1481			T-cell receptor be
21	3	27.3	13	3	JIJ03			trepanosin d-13 -
22	3	27.3	13	2	G24565			K thymocytin ca
23	3	27.3	13	2	JO1350			hypothetical prote
24	3	27.3	13	2	PH1585			14 H chain V-D 1 r
25	3	27.3	14	2	S27140			hypothetical prote
26	3	27.3	14	2	S14864			acetyl coenzyme M
27	3	27.3	14	2	PA0109			protein p115 - Aca
28	3	27.3	14	2	PA0045			protein p115 - Aca
29	3	27.3	14	2	PH1623			14 H chain V-D 1 r

30	3	27.3	15	2	S26524			T-cell receptor al
31	3	27.3	15	2	S26534			T-cell receptor al
32	3	27.3	15	2	J06101			fibrinogen alpha c
33	3	27.3	15	2	A36786			pineloyl-CoA synth
34	3	27.3	15	2	S47387			T-cell antigen rec
35	3	27.3	15	2	A27504			histone H2A - mous
36	3	27.3	15	2	H26501			lipoprotein lipase
37	2	18.2	8	1	LFSAHE			probable msra lead
38	2	18.2	8	2	PI0184			capsid protein vp-
39	2	18.2	8	2	110077			hypothetical prote
40	2	18.2	8	2	S19288			acylase - Kluyvera
41	2	18.2	8	2	S63493			dissimilatory sulf
42	2	18.2	8	2	S21273			cellulase (EC 3.2
43	2	18.2	8	2	B39745			endoglycosylcerami
44	2	18.2	8	2	D61512			variant surface gl
45	2	18.2	8	2	A21440			calliPMRFamide 8 -
46	2	18.2	8	2	H41978			acetylcholinestera
47	2	18.2	8	2	A41117			Ig heavy chain CRD
48	2	18.2	8	2	PT0279			phosphatidylethano
49	2	18.2	8	2	PN0043			T-cell receptor be
50	2	18.2	8	2	PT0595			T-cell receptor be
51	2	18.2	8	2	PT0530			T-cell receptor be
52	2	18.2	8	2	PT0527			T-cell receptor be
53	2	18.2	8	2	PT0509			T-cell receptor be
54	2	18.2	8	2	PT0639			T-cell receptor be
55	2	18.2	8	2	PT0613			T-cell receptor be
56	2	18.2	8	2	PT0557			T-cell receptor be
57	2	18.2	8	2	PT0554			T-cell receptor be
58	2	18.2	8	2	PT0716			T-cell receptor be
59	2	18.2	8	2	PT0725			T-cell receptor be
60	2	18.2	8	2	PT0588			T-cell receptor be
61	2	18.2	8	2	A35180			neutral proteinase
62	2	18.2	8	2	PC4372			telomeric and tetr
63	2	18.2	8	2	T48890			hypothetical prote
64	2	18.2	8	4	155411			hypothetical histo
65	2	18.2	9	1	YFPG			thymic factor - pi
66	2	18.2	9	2	S59902			glutathione transf
67	2	18.2	9	2	A60957			thymocyte growth p
68	2	18.2	9	2	A61230			caldesmonin, car
69	2	18.2	9	2	D28854			fibrinopeptide B -
70	2	18.2	9	2	E28854			fibrinopeptide B -
71	2	18.2	9	2	F28854			fibrinopeptide B -
72	2	18.2	9	2	D24180			fibrinogen beta ch
73	2	18.2	9	2	S30494			cat gene leader pe
74	2	18.2	9	2	H4362			chloramphenicol O-
75	2	18.2	9	2	A60522			sperm-activating p
76	2	18.2	9	2	S79329			sperm-activating p
77	2	18.2	9	2	Q0RB			delta sleep-induci
78	2	18.2	9	2	H45020			probable minipolyp
79	2	18.2	9	2	S02484			probable membrane
80	2	18.2	9	2	S66608			quinoline 2-oxidor
81	2	18.2	9	2	PI0139			orf AB protein - S
82	2	18.2	9	2	S19523			carbon-monoxide de
83	2	18.2	9	2	S70334			endosperm protein,
84	2	18.2	9	2	A57444			neuropeptide Grb-A
85	2	18.2	9	2	B57444			neuropeptide Grb-A
86	2	18.2	9	2	C57444			neuropeptide Grb-A
87	2	18.2	9	2	A41978			calliPMRFamide 1 -
88	2	18.2	9	2	A44787			calliPMRFamide 10
89	2	18.2	9	2	D44787			calliPMRFamide 13
90	2	18.2	9	2	B41978			calliPMRFamide 2 -
91	2	18.2	9	2	C41978			calliPMRFamide 3 -
92	2	18.2	9	2	D41978			calliPMRFamide 4 -
93	2	18.2	9	2	E41978			calliPMRFamide 5 -
94	2	18.2	9	2	F41978			calliPMRFamide 6 -
95	2	18.2	9	2	G41978			calliPMRFamide 7 -
96	2	18.2	9	2	B20569			serum amyloid P-co
97	2	18.2	9	2	A53797			3',5'-cyclic-GMP p
98	2	18.2	9	2	150633			c-rel protein - ch
99	2	18.2	9	2	PT0225			Ig heavy chain CDR
100	2	18.2	9	2	PC2197			zymogen granule me
101	2	18.2	9	2	C60070			gastrin - domestic
102	2	18.2	9	2	S56636			alpha-2-macroglobu

104	2	18.2	9	2	PHO136	late gl 19 protein	176	2	18.2	10	2	PT0245	Ig heavy chain CRD
104	2	18.2	9	2	PT0670	T-cell receptor be	177	2	18.2	10	2	PT0289	Ig heavy chain CRD
105	2	18.2	9	2	PT0634	T-cell receptor be	178	2	18.2	10	2	PT0309	Ig heavy chain CRD
106	2	18.2	9	2	PT0562	T-cell receptor be	179	2	18.2	10	2	PT0310	Ig heavy chain CRD
107	2	18.2	9	2	PT0706	unidentified 48.7K	180	2	18.2	10	2	H45482	platelet activatin
108	2	18.2	9	2	PT0935	T-cell receptor be	181	2	18.2	10	2	S23370	T-cell receptor al
109	2	18.2	9	2	PT0937	T-cell receptor be	182	2	18.2	10	2	S23371	T-cell receptor al
110	2	18.2	9	2	PT0938	T-cell receptor be	183	2	18.2	10	2	F49033	T-cell receptor ga
111	2	18.2	9	2	PT0938	T-cell receptor be	184	2	18.2	10	2	S68638	T-cell receptor ga
112	2	18.2	9	2	PT0937	52.1K protein sf	185	2	18.2	10	2	S26506	acetylcholinestera
113	2	18.2	9	2	PT0937	pep tachykinin	186	2	18.2	10	2	S71948	collagen alpha 1(V
114	2	18.2	10	2	GM0412	cat 2 rat V-prot	187	2	18.2	10	2	PT0212	matrix metalloprot
115	2	18.2	10	2	PT0513	leucosulfakinin II	188	2	18.2	10	2	PT0212	T-cell receptor al
116	2	18.2	10	2	S65388	hydroxylase redu	189	2	18.2	10	2	PT0664	T-cell receptor be
117	2	18.2	10	2	S41190	cytochrome-c oxida	190	2	18.2	10	2	PT0215	T-cell receptor be
118	2	18.2	10	2	PT0215	typtase (EC 3.4.2	191	2	18.2	10	2	F41946	T-cell receptor be
119	2	18.2	10	2	PT0215	prosin (EC 3.4.23	192	2	18.2	10	2	S65387	T-cell receptor ga
120	2	18.2	10	2	S33844	alpha 2 macroglob	193	2	18.2	10	2	PT0212	cytochrome-c oxida
121	2	18.2	10	2	PT0212	inhibin beta-A era	194	2	18.2	10	2	PH0944	T-cell receptor be
122	2	18.2	10	2	PT0212	lydlin 2 - bullro	195	2	18.2	10	2	PH0926	T-cell receptor be
123	2	18.2	10	2	PT0212	beta neomorphin	196	2	18.2	10	2	S15245	T-cell receptor be
124	2	18.2	10	2	PT0212	triacylglycerol II	197	2	18.2	10	2	PA0116	gene B-50 protein
125	2	18.2	10	2	PT0212	sperm-activation p	198	2	18.2	10	2	PS0220	ferredoxin-NADP re
126	2	18.2	10	2	PT0212	sperm-activation p	199	2	18.2	10	2	S74147	ferredoxin-NADP re
127	2	18.2	10	2	PT0212	sperm-activation p	200	2	18.2	11	1	GM001	glyceroldehyde-3-P
128	2	18.2	10	2	PT0212	sperm-activation p	201	2	18.2	11	1	S66196	leucosulfakinin -
129	2	18.2	10	2	PT0212	sperm-activation p	202	2	18.2	11	1	A33917	alcohol dehydrogen
130	2	18.2	10	2	PT0212	sperm-activation p	203	2	18.2	11	1	PT0682	dihydroorotase (EC
131	2	18.2	10	2	PT0212	sperm-activation p	204	2	18.2	11	1	C53652	photosystem 1 17.5
132	2	18.2	10	2	PT0212	sperm-activation p	205	2	18.2	11	1	YH01	rhIR protein - Pse
133	2	18.2	10	2	PT0212	sperm-activation p	206	2	18.2	11	1	YH01	morphogenetic neur
134	2	18.2	10	2	PT0212	sperm-activation p	207	2	18.2	11	1	YH01	morphogenetic neur
135	2	18.2	10	2	PT0212	sperm-activation p	208	2	18.2	11	1	YH01	morphogenetic neur
136	2	18.2	10	2	PT0212	sperm-activation p	209	2	18.2	11	1	YH01	morphogenetic neur
137	2	18.2	10	2	PT0212	sperm-activation p	210	2	18.2	11	1	S42449	ant1 protein - pha
138	2	18.2	10	2	PT0212	sperm-activation p	211	2	18.2	11	1	C58501	42K bile stone pro
139	2	18.2	10	2	PT0212	sperm-activation p	212	2	18.2	11	1	PT0395	hypothetical prote
140	2	18.2	10	2	PT0212	sperm-activation p	213	2	18.2	11	1	PT0395	beta-glucosidase (
141	2	18.2	10	2	PT0212	sperm-activation p	214	2	18.2	11	1	S66406	quinoline 2-oxidor
142	2	18.2	10	2	PT0212	sperm-activation p	215	2	18.2	11	1	S58244	pyrroloquinoline q
143	2	18.2	10	2	PT0212	sperm-activation p	216	2	18.2	11	1	S04875	nifs protein - Bra
144	2	18.2	10	2	PT0212	sperm-activation p	217	2	18.2	11	1	E60691	phycoerythrin 8K1
145	2	18.2	10	2	PT0212	sperm-activation p	218	2	18.2	11	1	S33519	probable secreted
146	2	18.2	10	2	PT0212	sperm-activation p	219	2	18.2	11	1	T06383	hypothetical prote
147	2	18.2	10	2	PT0212	sperm-activation p	220	2	18.2	11	1	S19775	wound-induced prot
148	2	18.2	10	2	PT0212	sperm-activation p	221	2	18.2	11	1	S41747	chaperonin 10 homo
149	2	18.2	10	2	PT0212	sperm-activation p	222	2	18.2	11	1	A38590	transforming prote
150	2	18.2	10	2	PT0212	sperm-activation p	223	2	18.2	11	1	A61512	variant surface gl
151	2	18.2	10	2	PT0212	sperm-activation p	224	2	18.2	11	1	A35594	buccalin - Califor
152	2	18.2	10	2	PT0212	sperm-activation p	225	2	18.2	11	1	A60656	perisulfakinin - A
153	2	18.2	10	2	PT0212	sperm-activation p	226	2	18.2	11	1	S65395	chemical-sense-rel
154	2	18.2	10	2	PT0212	sperm-activation p	227	2	18.2	11	1	141978	callifmramide 9 -
155	2	18.2	10	2	PT0212	sperm-activation p	228	2	18.2	11	1	D37196	bradykinin-potenti
156	2	18.2	10	2	PT0212	sperm-activation p	229	2	18.2	11	1	S65231	CCK-B gastrin rece
157	2	18.2	10	2	PT0212	sperm-activation p	230	2	18.2	11	1	PT0349	Ig heavy chain CRD
158	2	18.2	10	2	PT0212	sperm-activation p	231	2	18.2	11	1	PT0349	Ig heavy chain CRD
159	2	18.2	10	2	PT0212	sperm-activation p	232	2	18.2	11	1	PH1343	Ig heavy chain DJ
160	2	18.2	10	2	PT0212	sperm-activation p	233	2	18.2	11	1	S51732	T-cell receptor al
161	2	18.2	10	2	PT0212	sperm-activation p	234	2	18.2	11	1	S60354	retinal oxidase -
162	2	18.2	10	2	PT0212	sperm-activation p	235	2	18.2	11	1	PN0044	protein kinase C 1
163	2	18.2	10	2	PT0212	sperm-activation p	236	2	18.2	11	1	PT0209	T-cell receptor al
164	2	18.2	10	2	PT0212	sperm-activation p	237	2	18.2	11	1	PT0218	T-cell receptor be
165	2	18.2	10	2	PT0212	sperm-activation p	238	2	18.2	11	1	141946	T-cell receptor ga
166	2	18.2	10	2	PT0212	sperm-activation p	239	2	18.2	11	1	C49037	tcr gamma V-J regi
167	2	18.2	10	2	PT0212	sperm-activation p	240	2	18.2	11	1	PD0441	translation elonga
168	2	18.2	10	2	PT0212	sperm-activation p	241	2	18.2	11	1	S17447	urinary protein -
169	2	18.2	10	2	PT0212	sperm-activation p	242	2	18.2	11	1	S65377	cytochrome-c oxida
170	2	18.2	10	2	PT0212	sperm-activation p	243	2	18.2	11	1	S78422	ribosomal protein
171	2	18.2	10	2	PT0212	sperm-activation p	244	2	18.2	11	1	PH0947	T-cell receptor be
172	2	18.2	10	2	PT0212	sperm-activation p	245	2	18.2	11	1	S52304	gene rsSTR4 protei
173	2	18.2	10	2	PT0212	sperm-activation p	246	2	18.2	11	1	A34243	H-hyosporin - Ja
174	2	18.2	10	2	PT0212	sperm-activation p	247	2	18.2	11	1	A61575	Trimeresurus serin
175	2	18.2	10	2	PT0212	sperm-activation p	248	2	18.2	11	1	S19015	hypothetical prote

249	2	18.2	11	4	154081	retinoic acid rece	322	2	18.2	13	2	S22995	hypothetical prote
250	2	18.2	12	2	PN0577	tyrosine 3-monooxy	323	2	18.2	13	2	H36042	oxfx protein - Esc
251	2	18.2	12	2	PN0578	tyrosine 3-monooxy	324	2	18.2	13	2	H64124	hypothetical prote
252	2	18.2	12	2	PN0579	tyrosine 3-monooxy	325	2	18.2	13	2	S36668	hypothetical prote
253	2	18.2	12	2	PN0580	tyrosine 3-monooxy	326	2	18.2	13	2	PC2371	probable endopepti
254	2	18.2	12	2	PN0581	tyrosine 3-monooxy	327	2	18.2	13	2	A01825	botulinum toxins -
255	2	18.2	12	2	PN0576	tyrosine 3-monooxy	328	2	18.2	13	2	S36887	ribosomal protein
256	2	18.2	12	2	A29169	phospholipase A2 (	329	2	18.2	13	2	S41209	F420-non-reducing-
257	2	18.2	12	2	C49215	urease (EC 3.5.1.5	330	2	18.2	13	2	PN0176	acidic ribosomal p
258	2	18.2	12	2	S65409	6-ostore H2H - huma	331	2	18.2	13	2	PA0023	protein QA300052 -
259	2	18.2	12	2	S15815	translation, e-longa	332	2	18.2	13	2	S00316	photosystem I prot
260	2	18.2	12	2	S65649	protoporphyrinogen	333	2	18.2	13	2	S09733	protein P18 - comm
261	2	18.2	12	2	S71034	p-t-B protein - Sal	334	2	18.2	13	2	H44557	tetrahydroberberin
262	2	18.2	12	2	S43013	hypothetical prote	335	2	18.2	13	2	PS0325	unidentified 6.3/4
263	2	18.2	12	2	D28551	hypothetical prote	336	2	18.2	13	2	P00700	protein QF200053 -
264	2	18.2	12	2	S49547	hypothetical prote	337	2	18.2	13	2	PA0089	lignin peroxidase
265	2	18.2	12	2	S36899	ribosomal protein	338	2	18.2	13	2	S04013	equinoxilin 1A - s
266	2	18.2	12	2	T46794	hypothetical prote	339	2	18.2	13	2	PC1149	carboxylesterase (
267	2	18.2	12	2	PA00025	protein QA300025 -	340	2	18.2	13	2	A26999	CD61 homolog - cha
268	2	18.2	12	2	S70337	napiin small chain	341	2	18.2	13	2	H58533	hemolytic protein
269	2	18.2	12	2	S28215	glucosyl endo-1,3-be	342	2	18.2	13	2	S09019	osteoclast functio
270	2	18.2	12	2	PS0213	28K protein 4472 -	343	2	18.2	13	2	A33660	glialdular kallikre
271	2	18.2	12	2	P00730	unidentified 5.4/3	344	2	18.2	13	2	A54326	hypothetical prote
272	2	18.2	12	2	PN0170	alcohol dehydrogen	345	2	18.2	13	2	S52356	hypothetical prote
273	2	18.2	12	2	PN0162	malate dehydrogena	346	2	18.2	13	2	PT0263	Ig heavy chain CRD
274	2	18.2	12	2	T46656	hypothetical prote	347	2	18.2	13	2	S57567	T cell receptor V-
275	2	18.2	12	2	C33099	148K exoantigen	348	2	18.2	13	2	S47382	T-cell antigen rec
276	2	18.2	12	2	A13099	163K exoantigen -	349	2	18.2	13	2	S47383	T-cell antigen rec
277	2	18.2	12	2	S16204	4 phosphofructokin	350	2	18.2	13	2	S47388	T-cell antigen rec
278	2	18.2	12	2	A09985	gamma-crystallin	351	2	18.2	13	2	S47389	T-cell antigen rec
279	2	18.2	12	2	A43261	coagulation factor	352	2	18.2	13	2	S47374	T-cell antigen rec
280	2	18.2	12	2	S24830	dimethylamino mo	353	2	18.2	13	2	H56046	urinary tract ston
281	2	18.2	12	2	PT0253	Ig heavy chain CRD	354	2	18.2	13	2	C56046	sperm motility inh
282	2	18.2	12	2	PT0339	Ig heavy chain CRD	355	2	18.2	13	2	S66235	tubulin alpha-chai
283	2	18.2	12	2	S21205	Ig heavy chain V ;	356	2	18.2	13	2	S65612	Ig kappa-1 chain J
284	2	18.2	12	2	S43170	kinesin light chai	357	2	18.2	13	2	R20907	Ig H chain V-D-J r
285	2	18.2	12	2	S47363	T cell antigen rec	358	2	18.2	13	2	PH1636	Ig kappa chain J r
286	2	18.2	12	2	PH1181	T-cell receptor al	359	2	18.2	13	2	A33933	Ig kappa chain J r
287	2	18.2	12	2	PH1186	T-cell receptor al	360	2	18.2	13	2	H26406	Ig kappa chain J r
288	2	18.2	12	2	PH1172	T-cell receptor al	361	2	18.2	13	2	S22761	Ig lambda-2 chain
289	2	18.2	12	2	A45033	T-cell receptor de	362	2	18.2	13	2	PH0796	T-cell receptor al
290	2	18.2	12	2	C49033	T-cell receptor de	363	2	18.2	13	2	PH0787	T-cell receptor al
291	2	18.2	12	2	A60526	insulin-like growt	364	2	18.2	13	2	PH0799	T-cell receptor al
292	2	18.2	12	2	P23907	Ig kappa-2 chain J	365	2	18.2	13	2	PH0783	T-cell receptor al
293	2	18.2	12	2	PH1606	Ig H chain V-D-J r	366	2	18.2	13	2	PH0786	T-cell receptor al
294	2	18.2	12	2	PH1611	Ig H chain V-D-J r	367	2	18.2	13	2	PH0805	T-cell receptor al
295	2	18.2	12	2	S25039	Ig heavy chain V ;	368	2	18.2	13	2	PH0928	T-cell receptor be
296	2	18.2	12	2	A42324	cytochrome P450c27	369	2	18.2	13	2	A47630	Ig kappa chain J r
297	2	18.2	12	2	B42523	hexokinase (EC 2.7	370	2	18.2	13	2	S74130	NADH oxidase - Glu
298	2	18.2	12	2	PH0940	T-cell receptor be	371	2	18.2	13	2	A86126	hypothetical prote
299	2	18.2	12	2	PH0946	T-cell receptor be	372	2	18.2	13	2	S01904	H+-transporting tw
300	2	18.2	12	2	PC4377	telomeric and tetr	373	2	18.2	13	2	PS0277	glyceraldehyde-3-p
301	2	18.2	12	2	S71680	lebetin 1 isoform	374	2	18.2	14	1	NTPG14	hypochalamic tetra
302	2	18.2	12	2	A59375	microcin B17 - Esc	375	2	18.2	14	1	OMWAV	mastoparan - yello
303	2	18.2	12	2	A53252	pollen mator aller	376	2	18.2	14	1	OMVHMM	mastoparan M - hor
304	2	18.2	12	2	141235	glutamine-tRNA lig	377	2	18.2	14	1	OMVHXX	mastoparan X - hor
305	2	18.2	12	2	S21163	NAD ADP-ribosyltra	378	2	18.2	14	1	OMVHP2	mastoparan C - Eur
306	2	18.2	12	4	PC2122	aminotransferase c	379	2	18.2	14	1	OMWAPP	polistes mastopara
307	2	18.2	13	1	XAV19B	angiotensin-conver	380	2	18.2	14	1	NTKNIM	alpha-conotoxin MI
308	2	18.2	13	1	MTCMAD	melanotropin alpha	381	2	18.2	14	2	PC2373	probable IMP dehyd
309	2	18.2	13	1	MTHOAD	melanotropin alpha	382	2	18.2	14	2	A33798	D-amino-acid oxida
310	2	18.2	13	1	N7KN2G	alpha-conotoxin GI	383	2	18.2	14	2	C40944	hypothetical prote
311	2	18.2	13	1	NTKNAS	alpha conotoxin SI	384	2	18.2	14	2	JN0389	histamine-releasein
312	2	18.2	13	2	A32734	enkephalin precurs	385	2	18.2	14	2	JN0390	histamine-releasein
313	2	18.2	13	2	S48210	collagen alpha 1(V	386	2	18.2	14	2	A58963	alpha-conotoxin Cn
314	2	18.2	13	2	A23695	myosin heavy chain	387	2	18.2	14	2	S15130	hemoglobin beta ch
315	2	18.2	13	2	S15755	actin 7 - soybean	388	2	18.2	14	2	S19803	ubiquitin - potato
316	2	18.2	13	2	A59778	lactose phosphotra	389	2	18.2	14	2	S15132	histone H4-1 precu
317	2	18.2	13	2	S50173	alpha-2 collagen -	390	2	18.2	14	2	A35377	GTP-binding protei
318	2	18.2	13	2	A61351	bradykinin-like pe	391	2	18.2	14	2	R29743	translation initia
319	2	18.2	13	2	A60409	hombesin-like pept	392	2	18.2	14	2	A42473	ermK leader peptid
320	2	18.2	13	2	T08533	hypothetical prote	393	2	18.2	14	2	A32654	fibrinopeptide A -
321	2	18.2	13	2	154984	aeq 46.5 protein -	394	2	18.2	14	2	JH0328	probrusin tetradece

495	2	18.2	14	2	S29632	xyran 1,4-beta-xyl	468	2	18.2	15	2	S26527	T-cell receptor al
496	2	18.2	14	2	S59495	formate dehydrogen	469	2	18.2	15	2	S26528	T-cell receptor al
497	2	18.2	14	2	S54945	gene C protein - E	470	2	18.2	15	2	A28497	neurotensin-relate
498	2	18.2	14	2	H54006	hypothetical prote	471	2	18.2	15	2	149407	placental calcium-
499	2	18.2	14	2	S58866	metalinum neurotox	472	2	18.2	15	2	P00681	photosystem I 19.0
500	2	18.2	14	2	S36892	ribosomal protein	473	2	18.2	15	2	P00692	photosystem I 18.5
501	2	18.2	14	2	S74126	superoxide dismuta	474	2	18.2	15	2	140665	ilvBN leader pepti
502	2	18.2	14	2	P00613	photosystem II oxy	475	2	18.2	15	2	P00545	capsid protein VP1
503	2	18.2	14	2	P01411	protein GAL1054	476	2	18.2	15	2	S02381	probable membrane
504	2	18.2	14	2	P01497	seed protein ES-21	477	2	18.2	15	2	A60929	dichloromethane de
505	2	18.2	14	2	A01002	photosystem II oxy	478	2	18.2	15	2	C48401	ribosomal protein
506	2	18.2	14	2	G44957	photosystem II oxy	479	2	18.2	15	2	PC4213	bphB protein - Com
507	2	18.2	14	2	P00147	omega-glucosidase	480	2	18.2	15	2	B60929	dichloromethane de
508	2	18.2	14	2	P00151	omega-glucosidase	481	2	18.2	15	2	B35389	urease (EC 3.5.1.5
509	2	18.2	14	2	S13803	chaperone, TCP1-re	482	2	18.2	15	2	A35389	urease (EC 3.5.1.5
510	2	18.2	14	2	P00258	18K protein 3228	483	2	18.2	15	2	E41383	32K variable histo
511	2	18.2	14	2	S35267	acetyl-CoA carboxy	484	2	18.2	15	2	C41383	32K variable histo
512	2	18.2	14	2	B34135	2NA-binding protei	485	2	18.2	15	2	S29386	nigerythrin - Desu
513	2	18.2	14	2	E33698	214K exoantigen (v	486	2	18.2	15	2	C43334	orf3', to aadR -
514	2	18.2	14	2	S23476	collagen alpha cha	487	2	18.2	15	2	S03353	plastocyanin - MIC
515	2	18.2	14	2	A56642	zeosultakinin-1-	488	2	18.2	15	2	PC2374	unidentified 22K p
516	2	18.2	14	2	S14356	mastoparan B - hor	489	2	18.2	15	2	A60156	cellulase (EC 3.2.
517	2	18.2	14	2	S12904	protein kinase (EC	490	2	18.2	15	2	S36893	ribosomal protein
518	2	18.2	14	2	S43629	cytochrome-c oxida	491	2	18.2	15	2	S36897	ribosomal protein
519	2	18.2	14	2	S11074	alcohol dehydrogen	492	2	18.2	15	2	S36896	ribosomal protein
520	2	18.2	14	2	P10492	Ig heavy chain CR2	493	2	18.2	15	2	A61145	dihydrofolate redu
521	2	18.2	14	2	S57564	T cell receptor V-	494	2	18.2	15	2	A40634	orf19, 3' of eryk -
522	2	18.2	14	2	S29674	T cell receptor V-	495	2	18.2	15	2	PA0036	glycine cleavage s
523	2	18.2	14	2	S47465	T cell antigen rec	496	2	18.2	15	2	PA0040	malate dehydrogena
524	2	18.2	14	2	S22369	T-cell receptor al	497	2	18.2	15	2	PA0002	photosystem II oxy
525	2	18.2	14	2	E49339	T-cell receptor be	498	2	18.2	15	2	PA0038	protein OA100030 -
526	2	18.2	14	2	S58426	spectrin-delta: ANK b	499	2	18.2	15	2	PA0046	protein OA100044 -
527	2	18.2	14	2	A47471	leukotriene B-4 12	500	2	18.2	15	2	PA0034	protein OA300024 -
528	2	18.2	14	2	S64244	sperm motility inh							
529	2	18.2	14	2	F48394	glycoprotein compo							
530	2	18.2	14	2	I45474	thiobiospondin 2 -							
531	2	18.2	14	2	S36678	dodecenoyl-CoA Del							
532	2	18.2	14	2	PH1594	Ig H chain V-D-3 F							
533	2	18.2	14	2	PH1598	Ig H chain V-D-1 F							
534	2	18.2	14	2	PH1448	T cell receptor al							
535	2	18.2	14	2	PH0600	T cell receptor al							
536	2	18.2	14	2	PH0795	T-cell receptor al							
537	2	18.2	14	2	PH0834	T-cell receptor al							
538	2	18.2	14	2	PH0776	T-cell receptor al							
539	2	18.2	14	2	PH1450	T-cell receptor al							
540	2	18.2	14	2	PT0310	T cell receptor al							
541	2	18.2	14	2	PH0742	T cell receptor be							
542	2	18.2	14	2	PH0747	T-cell receptor be							
543	2	18.2	14	2	D35141	T-cell receptor de							
544	2	18.2	14	2	S35141	T-cell receptor de							
545	2	18.2	14	2	S35141	T-cell receptor de							
546	2	18.2	14	2	E49037	Tcr delta chain V							
547	2	18.2	14	2	PC7379	unidentified 27.2K							
548	2	18.2	14	2	A37789	heat shock cognate							
549	2	18.2	14	2	PH0345	T-cell receptor be							
550	2	18.2	14	2	S29478	Na+/K+-exchanging							
551	2	18.2	14	2	A12150	glucose 1 dehydrog							
552	2	18.2	14	2	A15218	hemoglobin beta ch							
553	2	18.2	15	1	SFR1	scotophobin - rat							
554	2	18.2	15	1	NTKNAG	alpha-conotoxin G1							
555	2	18.2	15	1	LEFWL	leu leader peptide							
556	2	18.2	15	2	S21241	oligo-1,6-glucosid							
557	2	18.2	15	2	S21241	alpha-glucosidase							
558	2	18.2	15	2	S21241	glucan 1,4 alpha-g							
559	2	18.2	15	2	S24159	leukocyte elastase							
560	2	18.2	15	2	PC2215	fibrinogenolytic p							
561	2	18.2	15	2	S57201	basic proteinase I							
562	2	18.2	15	2	A54397	ubiquitin-carrier							
563	2	18.2	15	2	P00232	cystatin G1-4a - m							
564	2	18.2	15	2	I52734	gene c-KI ras prot							
565	2	18.2	15	2	A22789	platelet derived g							
566	2	18.2	15	2	A22789	T cell receptor al							
567	2	18.2	15	2	S26516								

## ALIGNMENTS

## RESULT 1

129501  
 fibrinopeptide A kanaroc  
 C:Species: Macropus sp. (kanaroc)  
 C:Date: 21-Nov-1987 #sequence\_revision 08-Jun-1990 #text\_change 18-Aug-2000  
 C:Accession: 129501  
 R:Blombaeck, B.; Blombaeck, M.; Hann, C.  
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and  
 A:Reference number: A29501;  
 A:Accession: 129501  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <RI/O>  
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 36.4%; Score 4; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.4e-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEGG 4

IIII

Db 9 AEGG 12

## RESULT 2

129501  
 fibrinopeptide A - wombat  
 C:Species: Vombatidae gen. sp. (wombat)  
 C:Date: 21-Nov-1987 #sequence\_revision 08-Jun-1990 #text\_change 18-Aug-2000  
 C:Accession: F29501  
 R:Blombaeck, B.; Blombaeck, M.; Hann, C.  
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and  
 A:Reference number: A29501  
 A:Accession: F29501  
 A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-15 <BLD>  
C:Superfamily: fibrinogen alpha chain; fibrinogen doublet ring homology

Query Match 46.4% Score 3: 100.0% DB 2: Length 15;  
Best Local Similarity 100.0% Pred. No. 5 AEG 2;  
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 4  
DB 9 AEG 12

RESULT 5  
PC7076

Spectrin alpha chain, non-erythroid - mouse (fragment)  
N:Alternate names: lodrin alpha chain  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Aug-2000 #sequence\_revision 18 Aug 2000 #text\_change 18-Aug-2000  
C:Accession: PC7076

K:Tsukita, A.; Kawakami, T.; Gehda, T.; Sakai, I.; Kamo, M.; Matsui, T.; Watanabe, Y.  
Electrophoresis 21, 1853-1871, 2000  
A:Title: Proteome analysis of mouse brain. Two-dimensional electrophoresis profiles of b  
A:Reference number: PC7072  
A:Accession: PC7076  
A:Molecule type: protein  
A:Residues: 1-9 <TSU>  
A:Experimental source: strain C57BL/6J SIV, brain; brain; striatum  
C:Keywords: brain

Query Match 27.3% Score 3: 100.0% DB 2: Length 9;  
Best Local Similarity 100.0% Pred. No. 2 AEG 0;  
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
DB 5 KKK 8

RESULT 4  
PC7097

Hypothetical protein (tpi 57 region) - bacteriophage phiK5 T (fragment)  
C:Species: Bacteriophage phiK5 T  
C:Date: 28 Apr 1993 #sequence\_revision 28 Apr 1993 #text\_change 17 Mar 1999  
C:Accession: PC7397

K:Kasamides, G.; Davidson, R.R.; Hillier, A.  
Appl. Environ. Microbiol. 56, 944-947, 1990  
A:Title: Molecular characterization of bacteriophage phiK5 T (tphi 57 region) and its  
activity.  
A:Reference number: A47397; MUID:96253170; PEG 2000 18  
A:Accession: PC7397  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <LAK>  
A:Cross-References: GB:M34497

Query Match 27.3% Score 3: 100.0% DB 2: Length 10;  
Best Local Similarity 100.0% Pred. No. 1 AEG 0;  
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KMR 10  
DB 7 KMR 9

RESULT 5  
S77990

Cytochrome c oxidase (EC 1.9.3.1) chain VIII - bovine heart (fragment)  
C:Species: Bos taurus (biquey line)  
C:Date: 17-Sep-1997 #sequence\_revision 17 Sep 1997 #text\_change 18 Jan 1998  
C:Accession: S77990

R:Arnold, S.; Lee, J.; Kim, M.; Socha, K.; Scheller, R.; Gaspard, D.; Kozlowski, R.  
Submitted to the Protein Sequence Database, June 1997

A:Reference number: S77980  
A:Accession: S77990  
A:Molecule type: protein  
A:Residues: 1-16 <ARN>  
A:Experimental source: heart; liver  
C:Genetics:  
A:Genome: nuclear  
C:Function:  
A:Pathway: oxidative phosphorylation; respiratory chain  
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner mem

Query Match 27.3% Score 3: 100.0% DB 2: Length 10;  
Best Local Similarity 100.0% Pred. No. 3.7e+03;  
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 4  
DB 4 AEG 5

RESULT 5  
P00029

33K protein 3218 - rice (strain Nohonbare) (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C:Accession: P00029

K:Tsukita, A.; Miyatake, N.  
Submitted to JIPID, April 1993  
A:Reference number: PEG206  
A:Accession: P00029  
A:Molecule type: protein  
A:Residues: 1-11 <TSU>  
A:Experimental source: brain  
C:Comment: molecular weight 33K, pI 6.0.

Query Match 27.3% Score 3: 100.0% DB 2: Length 11;  
Best Local Similarity 100.0% Pred. No. 4e+03;  
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 3 EGG 5

RESULT 7  
PC2173

triacylglycerol lipase (EC 3.1.1.3) II - Rhizopus niveus (strain IFO 4759) (fragmen  
C:Species: Rhizopus niveus  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C:Accession: PC2173

R:Kohno, M.; Kujiyama, W.; Hashimoto, Y.; Morita, Y.  
Biosci. Biotechnol. Biochem. 58, 1007-1012, 1994  
A:Title: Purification, characterization, and crystallization of two types of lipase  
A:Reference number: PC2171; MUID:94319059; PMID:7765029  
A:Accession: PC2173  
A:Molecule type: protein  
A:Residues: 1-10:11 <KCH>  
C:Comment: This enzyme catalyzes the hydrolysis of the ester bonds of triacylglycer  
C:Comment: This enzyme is produced from lipase I by limited proteolysis due to the  
C:Keywords: carboxylic ester hydrolase

Query Match 27.3% Score 3: 100.0% DB 2: Length 11;  
Best Local Similarity 100.0% Pred. No. 4e+03;  
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5  
DB 3 GKK 5

RESULT 8  
S57675

11e11 recombinant alpha chain teton - human (fragment)





DL 9 GKK 11

A:Residues: 1-12 <ROR>  
A:Cross-references: EMBL:Z49954; NID:9887488; PTDN:CAA90225.1; PID:q887489  
C:Keywords: T-cell receptor

RESULT 14

Hyd in 1 African clawed frog  
A:Species: Xenopus laevis (African clawed frog)  
C:Date: 09-Mar-1990 #sequence\_revision 09 Mar 1990 #text\_change 31 Mar 1997  
C:Accession: A33900; S30176  
R:Rouille, Y.; Michel, G.; Chauvet, M.; Chang, J.; Acton, R.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5272-5275, 1989  
A:Title: Hydrius, hydrosomic neurohypophyseal peptides: osmoregulatory adaptation in a  
A:Reference number: A33900; MCID:8915779; PMID:2757509  
A:Accession: A33900  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <ROU>  
R:Iwanuro, S.; Hayashi, H.; Kikuyama, S.  
Biochim. Biophys. Acta 1176, 143-147, 1993  
A:Title: An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenopus  
A:Reference number: S30176; MCID:94200145; PMID:8452872  
A:Accession: S30176  
A:Molecule type: protein  
A:Residues: 1-12 <IWA>  
C:Keywords: neuroptide

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5  
DB 9 GKK 11

RESULT 15

S10625  
T:Epovirellin - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 18-Feb-1994 #sequence\_revision 16 Nov 1995 #text\_change 16-Nov-1995  
C:Accession: S10626  
R:Wallace, R.A.; Hoch, K.L.; Carnevali, R.  
J. Mol. Biol. 213, 407-409, 1990  
A:Title: Placement of small lipovirellin subunit's within the virion-egocin precursor is X  
A:Reference number: S10624; MCID:9027575; PMID:2022256  
A:Accession: S10625  
A:Molecule type: protein  
A:Residues: 1-12 <WAL>

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 5  
DB 10 GKK 12

RESULT 16

S57570  
T-cell receptor V- $\beta$  junctional alpha chain region (Cw3/Cas3) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Oct-1995 #sequence\_revision 17 Nov 1995 #text\_change 05 Nov 1995  
C:Accession: S57570  
R:Barrows, S.R.; Sillins, S.L.; Moss, B.J.; Kamao, K.; Misko, I.S.; Arquet, V.P.  
Submitted to the EMBL Data Library, June 1995  
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b  
A:Reference number: S57494  
A:Accession: S57570  
A:Status: preliminary  
A:Molecule type: mRNA

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MKA 11  
DB 3 MKA 5

RESULT 17

PH1189  
T-cell receptor alpha chain V region (Cw3/C2C3) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1189  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell rec  
A:Reference number: S26512; MCID:92364546; PMID:1380061  
A:Accession: PH1189  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 5 EGG 7

RESULT 18

PH1180  
T-cell receptor alpha chain V region (Cw3/5B8) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1180  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell rec  
A:Reference number: S26512; MCID:92364546; PMID:1380061  
A:Accession: PH1180  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 27.3% Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 5 EGG 7

RESULT 19

PH1175  
T-cell receptor alpha chain V region (Cw3/Cas3) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C:Accession: PH1175  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell rec  
A:Reference number: S26512; MCID:92364546; PMID:1380061  
A:Accession: PH1175  
A:Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>

Query Match 27.3%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 5 EGG 7

## RESULT 20

PH1481  
T-cell receptor beta chain (clone AZ4/HE12) mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C:Accession: PH1481  
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, D.; Panuotier, C.; Regnault, A.; Kieffer, J.; Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex peptides  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1481  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
A:Note: The authors translated the cDNA obtained for residue 2 as Ala and not for residue 3  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 27.3%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
DB 4 AEG 6

## RESULT 21

PH1585  
Tremorogen a-13 - jelly fungus (Tremella mesenterica)  
C:Species: Tremella mesenterica  
C:Date: 03-Aug-1984 #sequence\_revision 03-Aug-1984 #text\_change 07-Nov-1997  
C:Accession: A01641  
R:Sakaguchi, Y.; Yoshida, M.; Isigai, A.; Saitoh, A.  
Science 212, 1525-1527, 1981  
A:Title: Peptide sex hormones inducing aggregation and formation in compatible mating partners  
A:Reference number: A94256  
A:Accession: A01641  
A:Molecule type: protein  
A:Residues: 1-13 <SAK>  
C:Comment: Tremorogen a-13 is produced by the a-mating type cells and induces formation of compatible mating partners  
C:Keywords: extracellular protein; hormone; lipopeptide; pheromone; prolylated cysteine  
A:Binding site: farnesyl (Cys) (covalent) #status experimental  
A:Modified site: methyl ester carboxyl end (Cys) #status absent

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 1 EGG 3

## RESULT 22

G22565  
R-phycoerythrin gamma-B chain - red alga (Gastrocyclonium coulteri) (fragment)  
C:Species: Gastrocyclonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: G22565

R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 268, 4856-4863, 1993

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601; PMID:3886644

A:Accession: G22565

A:Molecule type: protein

A:Residues: 1-13 <KLO>

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
DB 2 AEG 4

## RESULT 23

QJ1350  
hypothetical protein, 1.3K (rps16 5' region) - Emerizella nidulans  
C:Species: Emerizella nidulans, Aspergillus nidulans  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Sep-1997  
C:Accession: QJ1350  
R:Bradshaw, R.E.; Pillar, T.M.  
Gene 108, 157-162, 1991  
A:Title: Isolation and nucleotide sequence of the ribosomal protein S16-encoding gene  
A:Reference number: QJ1349; MUID:92104500; PMID:1761226  
A:Accession: QJ1350  
A:Molecule type: DNA  
A:Residues: 1-13 <BRA>  
A:Cross-references: GB:M65259; NID:g168087; PID:g168089  
A:Experimental source: strain K153

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6  
DB 9 GKK 11

## RESULT 24

PH1585  
Iq B Chain V-D-J region (wild-type clone 9) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1585  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1585

A:Molecule type: DNA

A:Residues: 1-13 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.3%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 5 EGG 7

## RESULT 25

S27140  
hypothetical protein 1 estrogen receptor 5'-region - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Mar-1994 #sequence\_revision 12-May-1995 #text\_change 18-Aug-2000  
C:Accession: S27140

R:Keaveney, M.; Klug, J.; Gannon, F.  
DNA Seq. 2, 347-358, 1992

A:Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene

A:Reference number: S27140; MUID:93375998; PMID:1476547

A:Accession: S27140

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-14 <K&A>

A:Cross-references: EMBL:X62452; NID:G1211; PUBMED:1294

C:Superfamily: unassigned leader peptides

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MRA 11

DB 1 MRA 3

RESULT 26

S17864  
methy: coenzyme M reductase (EC 1.8.1.7) alpha chain - Methanobacterium thermoautotrophicum

C:Species: Methanobacterium thermoautotrophicum

A:Variety: Strain Marburg

C:Date: 19-Mar-1997 #sequence\_revision 13-Sep-1998 #text\_change 30-Oct-1998

C:Accession: S17864

R:Kosper, S.; Linder, D.; Ellermann, J.; Thauer, R.K.

Eur. J. Biochem. 194, 871-877, 1990

A:Title: Two genetically distinct methyl coenzyme M reductases in Methanobacterium thermophilum

A:Reference number: S13864; MUID:91099473; PMID:226566

A:Accession: S13864

A:Molecule type: protein

A:Residues: 1-14 <K&S>

A:Experimental source: strain Marburg

C:Keywords: methanogenesis; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7

DB 12 KKK 14

RESULT 27

PA0109

porin por 18 - Arabidopsis thaliana (flower)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 07-Apr-1995 #sequence\_revision 26-May-1995 #text\_change 30-Jun-1995

C:Accession: PA0109

R:Kamo, M.; Kawakami, T.; Tsugita, A.

submitted to JIPID, March 1995

A:Reference number: PA0109

A:Accession: PA0109

A:Molecule type: protein

A:Residues: 1-14 <K&M>

A:Experimental source: root

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6

DB 11 GKK 13

RESULT 28

PA0045

porin por1 - Arabidopsis thaliana (flower)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995

C:Accession: PA0045

R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A:Description: Separation and characterization of Arabidopsis proteins by two-dimen

A:Reference number: PA0045

A:Accession: PA0045

A:Molecule type: protein

A:Residues: 1-14 <K&M>

A:Experimental source: root

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6

DB 11 GKK 14

RESULT 29

PH1626

Ig H chain V-D-J region (clone B-less 118) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1626

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1626

A:Molecule type: DNA

A:Residues: 1-14 <L&V>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.3% Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MRA 11

DB 2 MRA 4

RESULT 30

S26524

T-cell receptor alpha chain V region (clone Cw3/5B8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

A:Variety: Clone Cw3/5B8

C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999

C:Accession: S26524

R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.

J. Exp. Med. 176, 439-447, 1992

A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell rec

A:Reference number: S26512; MUID:92364546; PMID:1380061

A:Accession: S26524

A:Molecule type: mRNA

A:Residues: 1-15 <C&S>

A:Cross-references: EMBL:X67975

A:Experimental source: cytolytic T-lymphocyte, clone Cw3/5B8

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4

DB 5 EGG 7



C:Keywords: carboxylic ester hydrolase

Query Match 27.1% Score 2; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 OK 5

DB 1 1

4 OK 5

RESULT 47

LFNAME

Probable msra leader peptide - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis

C>Date: 30-Sep-1991 #sequence\_revision 10 Sep 1991 #text\_change 16-Jul-1999

C:Accession: S1157

R:Ross, J. L.; Eady, E. A.; Cove, J. H.; Canfield, W. L.; Baumberg, S.; Wootton, J. C.

Mol. Microbiol. 4, 1207-1214, 1990

A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member of the

A:Reference number: S1157; M0105104710; PMID:2239255

A:Accession: S1157

A:Molecule type: DNA

A:Residues: 1-8 <ROS>

A:Cross-references: EMBL:X52065; N10047600; F11N:25A6333; F11P:4541653

C:Superfamily: probable msra leader peptide

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 OK 10

DB 1 1

5 OK 6

RESULT 48

FL0184

capsid protein VP-1 - murine poliovirus (fragment)

C:Species: murine poliovirus; Theiler's murine encephalomyelitis virus

C>Date: 20-Feb-1995 #sequence\_revision 20 Feb 1995 #text\_change 20 Feb 1995

C:Accession: FL0184

R:Zurbriggen, A.; Hoque, J. M.; Fujiwara, R. S.

J. Exp. Med. 170, 2037-2049, 1989

A:Title: Alteration of amino acid 101 within capsid protein VP-1 enhances the pathogenicity

A:Reference number: FL0184; M0105066446; PMID:2473766

A:Accession: FL0184

A:Molecule type: genomic RNA

A:Residues: 1-8 <OK>

C:Keywords: capsid protein

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 OK 4

DB 1 1

2 OK 3

RESULT 49

FL0377

hypothetical protein N - Methylophilus methylotrophus (fragment)

C:Species: Methylophilus methylotrophus

C>Date: 16-Jul-1999 #sequence\_revision 16 Jul 1999 #text\_change 27-Jul-2000

C:Accession: FL0377

R:Richtoseder, A. Y.; McIntire, W. S.; Matthews, F. S.; Johnston, M. B.

J. Bacteriol. 176, 4073-4080, 1994

A:Title: Organization of the methylamine utilization (mnu) genes in Methylophilus methyl

A:Reference number: FL0377; M0105429242; PMID:21167

A:Accession: FL0377

A>Status: preliminary

A:Molecule type: DNA

A:Cross-references: translated from GH/EMBL/GenBank

A:Residues: 1-8 <CHI>

A:Cross-references: EMBL:L26407; N1004561931; PIDN:AAB46955.1; PID:9561933

A:Experimental source: strain W3A1

C:Genetics:

A:Gene: mauN

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 OK 10

DB 1 1

1 OK 2

RESULT 40

SL9238

acylase - Kluyvera cryocrescens

C:Species: Kluyvera cryocrescens

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C:Accession: SL9238

R:Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991

A:Title: Chemical modification of serine at the active site of penicillin acylase f

A:Reference number: SL9238; M01052104664; PMID:1764029

A:Accession: SL9238

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <MAR>

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 OK 5

DB 1 1

7 OK 8

RESULT 41

S63493

dissimilatory sulfite reductase gamma chain, membrane-bound and soluble - Desulfovibrio

C:Species: Desulfovibrio desulfuricans

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999

C:Accession: S63493; S63494

R:Steuber, J.; Arendsen, A. F.; Hagen, W. R.; Kroneck, P. M. H.

Eur. J. Biochem. 233, 873-879, 1995

A:Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio

A:Reference number: S63493; M01056085152; PMID:8521853

A:Accession: S63493

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <STE>

A:Accession: S63494

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <ST2>

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2

DB 1 AE 2

RESULT 42

S21273

cellulase (EC 4.2.1.4) - Clostridium thermocellum (fragment)

N:Alternate names: endo-1,4-beta-glucanase

C:Species: Clostridium thermocellum

C>Date: 04-Nov-1992 #sequence\_revision 04-Dec-1992 #text\_change 22-Nov-1996

C:Accession: S21273  
 R:Komunie, M.P.M.; Fauth, U.; Kobayashi, T.; Huskinson, N.S.; Barker, P.J.; Demain, A.L.  
 Biochem. J. 283, 69-73, 1992  
 A:Title: Purification and characterization of a low molecular weight cellulase from *Glomus intraradicalis*  
 A:Reference number: S21273; MUID:92231850; PMID:156737  
 C:Accession: S21273  
 A:Molecule type: protein  
 A:Residues: 1-8 <R>  
 C:Function:  
 A:Description: hydrolysis of 1,4-beta-D-glucosidase; 1,4-glucosidase; polysaccharide degradation  
 A:Pathway: cellulose degradation  
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 18.2% Score 2: DB 2: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.8e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 4  
 DB 5 AE 6

RESULT 43  
 B39745  
 endoglycosyltransferase (EC 3.2.1.22) from *Neisseria meningitidis* sp. (fragment)  
 C:Species: *Neisseria meningitidis*  
 C:Date: 30 Dec 1994 #sequence\_revision 30-Dec-1994 #text\_change 11-Dec-1994  
 C:Accession: B39745  
 R:Kato, M.; Ikegami, Y.; Yamada, T.  
 J. Biol. Chem. 265, 7919-7926, 1991  
 A:Title: Activator proteins for glycosyltransferase hydrolysis by endoglycosyltransferases. Evidence using these activator proteins  
 A:Reference number: B39745; MUID:91210421; PMID:1856127  
 C:Accession: B39745  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <R>  
 C:Keywords: glycosidase; hydrolase

Query Match 18.2% Score 2: DB 2: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.8e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KA 11  
 DB 7 KA 8

RESULT 44  
 B61512  
 variant surface glycoprotein M181 from *Trypanosoma brucei* (fragment)  
 C:Species: *Trypanosoma brucei*  
 C:Date: 24 Oct 1994 #sequence\_revision 28-Oct-1994 #text\_change 07-May-1995  
 C:Accession: B61512  
 R:Reed, A.A.; Cross, G.A.M.  
 Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A:Title: Glycopeptides from variant surface glycoproteins of *Trypanosoma brucei*. C-terminal  
 A:Reference number: B61512; MUID:81172844; PMID:7161104  
 C:Accession: B61512  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <R>  
 C:Keywords: glycoprotein

Query Match 18.2% Score 2: DB 2: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.8e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EA 3  
 DB 1  
 2 EA 3

RESULT 45  
 A21440  
 variant surface glycoprotein pSL1 from *Trypanosoma brucei* (fragment)  
 C:Species: *Trypanosoma brucei*  
 C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 20-Mar-1998  
 C:Accession: A21440  
 R:Parsons, M.; Weis, K.G.; Watkins, K.P.; Agabian, N.  
 Cell 38, 309-316, 1984  
 A:Title: *Trypanosoma* mRNAs share a common 5' spliced leader sequence.  
 A:Reference number: A21440; MUID:84282716; PMID:6088073  
 C:Accession: A21440  
 A:Molecule type: mRNA  
 A:Residues: 1-8 <R>  
 A:Cross-references: GB:K02195; MUID:dl62150; PID:gl62151  
 C:Keywords: glycoprotein

Query Match 18.2% Score 2: DB 2: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.8e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GG 4  
 DB 7 GG 8

RESULT 46  
 H41978  
 calliphorin 8 from *Calliphora vomitoria*  
 C:Species: *Calliphora vomitoria*  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Mar-1999  
 C:Accession: H41978  
 R:Dave, H.; Johsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; T.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992  
 A:Title: Isolation, structure, and activity of Phe-Met-Arg-Phe-NH-2 neuropeptides  
 A:Reference number: H41978; MUID:92196111; PMID:1549595  
 C:Accession: H41978  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <R>  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.8e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MR 10  
 DB 6 MR 7

RESULT 47  
 A41117  
 acetylcholinesterase (EC 3.1.1.7) venom - Asian cobra (fragment)  
 C:Species: *Naja naja oxiana* (Asian cobra, Oxus cobra)  
 C:Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 23-Jun-1993  
 C:Accession: A41117  
 R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Ravikumar, A.; Hucho, F.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991  
 A:Title: Anionic subsites of the catalytic center of acetylcholinesterase from *Torpax*  
 A:Reference number: A41117; MUID:91296772; PMID:2068091  
 C:Accession: A41117  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <R>  
 C:Keywords: carboxylic ester hydrolase

Query Match 18.2% Score 2: DB 2: Length 8:  
 Best Local Similarity 100.0% Pred. No. 2.8e-05;  
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2  
 DB 1

```

Db          2 AB 3

RESULT 48
PT0279
Ig heavy chain CRO3 region (clone 4-91A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0279
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shaze, S.; Eaton, A.J.; Kovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:199932
A:Accession: PT0279
A:Molecule type: DNA
A:Residues: 1-8 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match          18.2%   Score 23   DB 23   Length 83
Best Local Similarity 100.0%   Pred. No. 2.8e+05
Matches      2:   Conservative  0:   Mismatches  0:   Indels  0:   Gaps  0:

UY      3 GG 4
      11
DB      7 GG 8

RESULT 49
PN0043
phosphatidylethanol amine-binding protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C:Accession: PN0043
S:Kato, H.
Kawasaki, I.; Kaishu, 22, 245-259, 1996
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: PN0041
A:Accession: PN0043
A:Molecule type: protein
A:Residues: 1-8 <KAT>
A:Experimental source: neuroblastoma cells
C:Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked
C:Keywords: Brain

Query Match          18.2%   Score 23   DB 23   Length 83
Best Local Similarity 100.0%   Pred. No. 2.8e+05
Matches      2:   Conservative  0:   Mismatches  0:   Indels  0:   Gaps  0:

UY      4 GK 5
      11
DB      7 GK 8

RESULT 50
PT0595
T cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0595
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711554
A:Accession: PT0595
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match          18.2%   Score 23   DB 23   Length 83
Best Local Similarity 100.0%   Pred. No. 2.9e+05

```

```

Matches      2:   Conservative  0:   Mismatches  0:   Indels  0:   Gaps  0:

UY      2 EG 4
      11
DB      4 EG 5

```

Search completed: September 30, 2003, 10:09:53  
 Job time : 12.4167 secs



GenCore version 5.1.6  
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1M protein - protein search, using sw mod-1

Run on: September 30, 2003, 10:07:04 : Search time: 6.25 seconds

(without alignments)  
82,767 million total updates/sec

Title: US-09-787-443-19

Perfect score: 11

Sequence: AEGGKKKKMRA 11

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767

Minimum hit seq length: 8

Maximum hit seq length: 15

Post-processing: Listing first 500 summaries

Database: SwissProt\_41\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	15	PIR4_SYNCA	P14463 syncytin ca
2	3	27.3	9	DL_NEPRI	P24816 nephrin
3	3	27.3	9	NEP_HV7c	P12481 human nephrin
4	3	27.3	10	COX2_HUMAN	P92982 cytochrome c
5	3	27.3	11	PKC1_CARM	P82684 cytochrome c
6	3	27.3	12	RS19_CARM	P82684 cytochrome c
7	3	27.3	12	V14K_WRSV	P82684 cytochrome c
8	3	27.3	13	TA12_TREME	P21470 tremella me
9	3	27.3	14	FIBA_HERSE	P14452 equus cabal
10	3	27.3	14	MAST_FALID	P42716 parapolybia
11	3	27.3	14	MCRX_METIM	P58815 methanobact
12	3	27.3	15	FIBA_AKAPL	P12801 anas platyr
13	3	27.3	15	ONCL1_HMY	P12801 anas platyr
14	3	27.3	15	UC26_MALZE	P40626 zea mays (m
15	3	27.3	15	ALL1_CARMA	P41819 carcinus ma
16	3	27.3	15	ALL1_CARMA	P41819 carcinus ma
17	2	18.2	8	CLP_HV7c	P82684 cytochrome c
18	2	18.2	8	FAR5_CALVO	P41863 calliphora
19	2	18.2	8	LM12_LUEMI	P22496 locusta mig
20	2	18.2	8	LMPS_STAEF	P23211 staphylococ
21	2	18.2	8	NS3_MYCTU	P41552 mycobacteri
22	2	18.2	8	UC26_MALZE	P40626 zea mays (m
23	2	18.2	8	UF06_MOUSE	P18644 mus musculu
24	2	18.2	8	WPL_PEARF	P83195 perkinsus a
25	2	18.2	9	DS1P_RABIT	P01158 oryctolagus
26	2	18.2	9	FAR1_CALVO	P41856 calliphora
27	2	18.2	9	FAR2_CALVO	P41857 calliphora
28	2	18.2	9	FAR3_CALVO	P41858 calliphora
29	2	18.2	9	FAR3_PENMO	P84116 penaeus mon
30	2	18.2	9	FAR4_CALVO	P41859 calliphora
31	2	18.2	9	FAR4_PENMO	P84119 penaeus mon
32	2	18.2	9	FAR5_AKAPL	P41863 calliphora
33	2	18.2	9	FAR5_CALVO	P41860 calliphora

P82661	panagrellus
P41861	calliphora
P83279	macrobrachi
P41862	calliphora
P41865	calliphora
P41868	calliphora
P19346	erythrocebu
P19344	papio anubi
P19343	papio hamad
P19342	theropithec
P83350	sarcophaga
P82992	rhodopseudo
P36884	staphylococ
P41952	sarcophaga
P19095	mustelus ca
P24047	stomopneute
P01255	sus scrofa
P81736	leucophaea
P31929	homo sapien
P31934	homo sapien
P81355	clostridium
P81731	heilicoverpa
P80331	oncorhynch
P80431	rattus norv
P80432	rattus norv
P80336	oryctolagus
P11735	locusta mig
P81012	schizaphis
P41867	calliphora
P01358	homo sapien
P02728	homo sapien
P09039	leucophaea
P40325	comamonas t
P49325	bacillus th
Q10997	haemocytaria
P19118	nicotiana p
P81738	leucophaea
P81739	leucophaea
P81740	leucophaea
P81741	leucophaea
P32118	homo sapien
P38007	chlamydia t
P80717	dictyoglomu
P83147	bacteroides
P30424	bothrops in
P81095	bacillus su
P56571	rattus norv
P41864	calliphora
P81018	oncorhynch
P04428	leucophaea
P36885	periplaneta
P00580	klebsiella
P01163	homo sapien
P49820	canis fami
P55173	pseudomonas
P41837	periplaneta
P80464	comamonas t
P13179	chondipura
P83328	oncorhynch
Q05055	tetrahymena
P56246	litoria ran
P83327	oncorhynch
P47733	locusta mig
Q24426	lotus japon
Q46490	clover yell
Q47881	elm yellows
P80863	bacillus su
P31144	homo sapien
P04561	cyprinus ca
P15987	glycine max
P82386	litoria ran
P82387	litoria ran

107	3	18.2	13	1	5	MAE_PSEUDO	242931	use.d-443-19	180	2	18.2	15	1	POCB_VIG	P20034	sus scrofa
108	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	181	2	18.2	15	1	PLAS_MICAE	P10625	microcystis
109	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	182	2	18.2	15	1	RL11_STRAU	Q9X520	streptomyces
110	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	183	2	18.2	15	1	RS20_BACST	P59681	bacillus st
111	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	184	2	18.2	15	1	RS20_BACST	P59682	bacillus st
112	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	185	2	18.2	15	1	SCUT_RAT	P01155	rattus norv
113	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	186	2	18.2	15	1	SCUT_RAT	P01155	rattus norv
114	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	187	2	18.2	15	1	TAL1_REBR	P34070	tremella br
115	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	188	2	18.2	15	1	TRPA_LEUMA	P81753	leucophaea
116	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	189	2	18.2	15	1	UC11_MAI2E	P80607	zea mays (m
117	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	190	2	18.2	15	1	UC11_MAI2E	P80620	zea mays (m
118	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	191	2	18.2	15	1	UC17_MAI2E	P80623	zea mays (m
119	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	192	2	18.2	15	1	UC27_MAI2E	P80633	zea mays (m
120	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	193	2	18.2	15	1	UC27_MAI2E	P80633	zea mays (m
121	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	194	2	18.2	15	1	UC28_MAI2E	P80634	zea mays (m
122	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	195	2	18.2	15	1	UN04_PINPS	P81673	pinus pinas
123	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	196	2	18.2	15	1	URE1_MORMO	P17337	morganelia
124	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	197	2	18.2	15	1	URE2_MORMO	P17338	morganelia
125	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	198	2	18.2	15	1	VORA_MEITM	P80907	methanobact
126	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	199	2	18.2	15	1	VORA_MEITM	Q02006	rhodospseud
127	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	200	2	18.2	15	1	YAA3_RHOPA	P86991	thunnus alb
128	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	201	2	18.2	15	1	ACT1_THUAL	P80709	carcinus ma
129	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	202	2	18.2	15	1	ACT1_THUAL	P14086	gryllus bim
130	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	203	2	18.2	15	1	AKHG_GRYBI	P14595	tabanus atr
131	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	204	2	18.2	15	1	AKHG_GRYBI	P81815	carcinus ma
132	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	205	2	18.2	15	1	AKHG_GRYBI	P81818	carcinus ma
133	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	206	2	18.2	15	1	AKHG_GRYBI	P81820	carcinus ma
134	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	207	2	18.2	15	1	AKHG_GRYBI	P81821	carcinus ma
135	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	208	2	18.2	15	1	AKHG_GRYBI	P82152	cydia pomon
136	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	209	2	18.2	15	1	AKHG_GRYBI	P82154	cydia pomon
137	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	210	2	18.2	15	1	AKHG_GRYBI	P41840	calliphora
138	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	211	2	18.2	15	1	AKHG_GRYBI	P82155	cydia pomon
139	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	212	2	18.2	15	1	AKHG_GRYBI	P41841	calliphora
140	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	213	2	18.2	15	1	AKHG_GRYBI	P82156	cydia pomon
141	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	214	2	18.2	15	1	AKHG_GRYBI	P82157	cydia pomon
142	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	215	2	18.2	15	1	AKHG_GRYBI	P81809	carcinus ma
143	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	216	2	18.2	15	1	AKHG_GRYBI	P81811	carcinus ma
144	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	217	2	18.2	15	1	AKHG_GRYBI	Q10582	bothrops ja
145	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	218	2	18.2	15	1	AKHG_GRYBI	P81886	porphyromon
146	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	219	2	18.2	15	1	AKHG_GRYBI	P13268	enterococcu
147	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	220	2	18.2	15	1	AKHG_GRYBI	P30369	macropus eu
148	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	221	2	18.2	15	1	AKHG_GRYBI	P8785	canis purpu
149	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	222	2	18.2	15	1	AKHG_GRYBI	P80430	rattus norv
150	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	223	2	18.2	15	1	AKHG_GRYBI	P13269	enterococcu
151	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	224	2	18.2	15	1	AKHG_GRYBI	P41872	panagrellus
152	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	225	2	18.2	15	1	AKHG_GRYBI	P83316	penaeus mon
153	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	226	2	18.2	15	1	AKHG_GRYBI	P83275	macrobrachi
154	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	227	2	18.2	15	1	AKHG_GRYBI	P41486	homarus ame
155	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	228	2	18.2	15	1	AKHG_GRYBI	P41487	homarus ame
156	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	229	2	18.2	15	1	AKHG_GRYBI	P83277	macrobrachi
157	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	230	2	18.2	15	1	AKHG_GRYBI	P43171	ascaris suu
158	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	231	2	18.2	15	1	AKHG_GRYBI	P81010	fusarium so
159	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	232	2	18.2	15	1	AKHG_GRYBI	P02729	homo sapien
160	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	233	2	18.2	15	1	AKHG_GRYBI	P21140	leucophaea
161	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	234	2	18.2	15	1	AKHG_GRYBI	P21141	leucophaea
162	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	235	2	18.2	15	1	AKHG_GRYBI	P21142	leucophaea
163	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	236	2	18.2	15	1	AKHG_GRYBI	P21143	leucophaea
164	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	237	2	18.2	15	1	AKHG_GRYBI	P19987	leucophaea
165	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	238	2	18.2	15	1	AKHG_GRYBI	P19988	leucophaea
166	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	239	2	18.2	15	1	AKHG_GRYBI	P19989	leucophaea
167	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	240	2	18.2	15	1	AKHG_GRYBI	P19990	leucophaea
168	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	241	2	18.2	15	1	AKHG_GRYBI	P13049	leucophaea
169	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	242	2	18.2	15	1	AKHG_GRYBI	P15507	bos laurus
170	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	243	2	18.2	15	1	AKHG_GRYBI	P82455	oriconetes
171	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	244	2	18.2	15	1	AKHG_GRYBI	P81707	brassica na
172	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	245	2	18.2	15	1	AKHG_GRYBI	P82692	periplaneta
173	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	246	2	18.2	15	1	AKHG_GRYBI	P82618	periplaneta
174	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	247	2	18.2	15	1	AKHG_GRYBI	P08939	pandalus bo
175	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	248	2	18.2	15	1	AKHG_GRYBI	P37985	erwinia chr
176	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	249	2	18.2	15	1	AKHG_GRYBI	P33564	mycobacteri
177	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	250	2	18.2	15	1	AKHG_GRYBI	P82929	bos laurus
178	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	251	2	18.2	15	1	AKHG_GRYBI	P56575	rattus norv
179	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	252	2	18.2	15	1	AKHG_GRYBI	P30687	homo sapien
180	2	18.2	13	1	1	BPAT_LEUMA	281754	leucophaea	253	2	18.2	15	1	AKHG_GRYBI	P40096	homo sapien



399	1	9.1	10	1	UPA4_HUMAN	1	400-4	homo sapien	472	1	9.1	12	1	HEPL_RACSE	P83054 bacteroides
400	1	9.1	10	1	UPA5_HUMAN	1	400-4	homo sapien	473	1	9.1	12	1	HS9A_RAT	P82995 rattus norv
401	1	9.1	10	1	UPA6_HUMAN	1	400-4	homo sapien	474	1	9.1	12	1	LICH_BACLI	P82907 bacillus li
402	1	9.1	10	1	UPA7_HUMAN	1	400-4	homo sapien	475	1	9.1	12	1	LM11_LUCMI	P22395 locusta mig
403	1	9.1	10	1	UPA8_HUMAN	1	400-4	homo sapien	476	1	9.1	12	1	NO40_SFRO	O24369 sesbania ro
404	1	9.1	10	1	UPA9_HUMAN	1	400-4	homo sapien	477	1	9.1	12	1	NO40_SFRO	P55960 glycine max
405	1	9.1	10	1	UPA10_HUMAN	1	400-4	homo sapien	478	1	9.1	12	1	NO40_SFRO	P54713 canis fami
406	1	9.1	10	1	UPA11_HUMAN	1	400-4	homo sapien	479	1	9.1	12	1	OPS3_DROVI	P17645 drosophila
407	1	9.1	10	1	UPA12_HUMAN	1	400-4	homo sapien	480	1	9.1	12	1	PA21_MICFM	P25072 micurus fu
408	1	9.1	10	1	UPA13_HUMAN	1	400-4	homo sapien	481	1	9.1	12	1	PA28_VIPBO	P31859 vipera beru
409	1	9.1	10	1	UPA14_HUMAN	1	400-4	homo sapien	482	1	9.1	12	1	PA28_VIPBO	P80903 methanobact
410	1	9.1	10	1	UPA15_HUMAN	1	400-4	homo sapien	483	1	9.1	12	1	PA28_VIPBO	P82619 periplaneta
411	1	9.1	10	1	UPA16_HUMAN	1	400-4	homo sapien	484	1	9.1	12	1	PPK4_PERFU	P84690 periplaneta
412	1	9.1	10	1	UPA17_HUMAN	1	400-4	homo sapien	485	1	9.1	12	1	PPK4_PERFU	P80662 physcomitre
413	1	9.1	10	1	UPA18_HUMAN	1	400-4	homo sapien	486	1	9.1	12	1	PSK3_PHYPA	P81555 periplaneta
414	1	9.1	10	1	UPA19_HUMAN	1	400-4	homo sapien	487	1	9.1	12	1	PSK3_PHYPA	P58805 conus spuri
415	1	9.1	10	1	UPA20_HUMAN	1	400-4	homo sapien	488	1	9.1	12	1	RFL1_CONSP	P36207 conus spuri
416	1	9.1	10	1	UPA21_HUMAN	1	400-4	homo sapien	489	1	9.1	12	1	RFL1_CONSP	P01371 tremella me
417	1	9.1	10	1	UPA22_HUMAN	1	400-4	homo sapien	490	1	9.1	12	1	TAJ10_TREME	P82652 hoplobatrach
418	1	9.1	10	1	UPA23_HUMAN	1	400-4	homo sapien	491	1	9.1	12	1	TAJ10_TREME	P82653 hoplobatrach
419	1	9.1	10	1	UPA24_HUMAN	1	400-4	homo sapien	492	1	9.1	12	1	TAJ10_TREME	P08613 kassina mac
420	1	9.1	10	1	UPA25_HUMAN	1	400-4	homo sapien	493	1	9.1	12	1	TAJ10_TREME	P08614 kassina mac
421	1	9.1	10	1	UPA26_HUMAN	1	400-4	homo sapien	494	1	9.1	12	1	TAJ10_TREME	P08611 kassina sen
422	1	9.1	10	1	UPA27_HUMAN	1	400-4	homo sapien	495	1	9.1	12	1	TAJ10_TREME	P56572 rattus norv
423	1	9.1	10	1	UPA28_HUMAN	1	400-4	homo sapien	496	1	9.1	12	1	TAJ10_TREME	P81359 ciostridium
424	1	9.1	10	1	UPA29_HUMAN	1	400-4	homo sapien	497	1	9.1	12	1	TAJ10_TREME	P55954 caenorhabdi
425	1	9.1	10	1	UPA30_HUMAN	1	400-4	homo sapien	498	1	9.1	12	1	TAJ10_TREME	P04558 catostomus
426	1	9.1	10	1	UPA31_HUMAN	1	400-4	homo sapien	499	1	9.1	12	1	TAJ10_TREME	P04559 catostomus
427	1	9.1	10	1	UPA32_HUMAN	1	400-4	homo sapien	500	1	9.1	12	1	TAJ10_TREME	P01147 gillichthys
428	1	9.1	10	1	UPA33_HUMAN	1	400-4	homo sapien							
429	1	9.1	10	1	UPA34_HUMAN	1	400-4	homo sapien							
430	1	9.1	10	1	UPA35_HUMAN	1	400-4	homo sapien							
431	1	9.1	10	1	UPA36_HUMAN	1	400-4	homo sapien							
432	1	9.1	10	1	UPA37_HUMAN	1	400-4	homo sapien							
433	1	9.1	10	1	UPA38_HUMAN	1	400-4	homo sapien							
434	1	9.1	10	1	UPA39_HUMAN	1	400-4	homo sapien							
435	1	9.1	10	1	UPA40_HUMAN	1	400-4	homo sapien							
436	1	9.1	10	1	UPA41_HUMAN	1	400-4	homo sapien							
437	1	9.1	10	1	UPA42_HUMAN	1	400-4	homo sapien							
438	1	9.1	10	1	UPA43_HUMAN	1	400-4	homo sapien							
439	1	9.1	10	1	UPA44_HUMAN	1	400-4	homo sapien							
440	1	9.1	10	1	UPA45_HUMAN	1	400-4	homo sapien							
441	1	9.1	10	1	UPA46_HUMAN	1	400-4	homo sapien							
442	1	9.1	10	1	UPA47_HUMAN	1	400-4	homo sapien							
443	1	9.1	10	1	UPA48_HUMAN	1	400-4	homo sapien							
444	1	9.1	10	1	UPA49_HUMAN	1	400-4	homo sapien							
445	1	9.1	10	1	UPA50_HUMAN	1	400-4	homo sapien							
446	1	9.1	10	1	UPA51_HUMAN	1	400-4	homo sapien							
447	1	9.1	10	1	UPA52_HUMAN	1	400-4	homo sapien							
448	1	9.1	10	1	UPA53_HUMAN	1	400-4	homo sapien							
449	1	9.1	10	1	UPA54_HUMAN	1	400-4	homo sapien							
450	1	9.1	10	1	UPA55_HUMAN	1	400-4	homo sapien							
451	1	9.1	10	1	UPA56_HUMAN	1	400-4	homo sapien							
452	1	9.1	10	1	UPA57_HUMAN	1	400-4	homo sapien							
453	1	9.1	10	1	UPA58_HUMAN	1	400-4	homo sapien							
454	1	9.1	10	1	UPA59_HUMAN	1	400-4	homo sapien							
455	1	9.1	10	1	UPA60_HUMAN	1	400-4	homo sapien							
456	1	9.1	10	1	UPA61_HUMAN	1	400-4	homo sapien							
457	1	9.1	10	1	UPA62_HUMAN	1	400-4	homo sapien							
458	1	9.1	10	1	UPA63_HUMAN	1	400-4	homo sapien							
459	1	9.1	10	1	UPA64_HUMAN	1	400-4	homo sapien							
460	1	9.1	10	1	UPA65_HUMAN	1	400-4	homo sapien							
461	1	9.1	10	1	UPA66_HUMAN	1	400-4	homo sapien							
462	1	9.1	10	1	UPA67_HUMAN	1	400-4	homo sapien							
463	1	9.1	10	1	UPA68_HUMAN	1	400-4	homo sapien							
464	1	9.1	10	1	UPA69_HUMAN	1	400-4	homo sapien							
465	1	9.1	10	1	UPA70_HUMAN	1	400-4	homo sapien							
466	1	9.1	10	1	UPA71_HUMAN	1	400-4	homo sapien							
467	1	9.1	10	1	UPA72_HUMAN	1	400-4	homo sapien							
468	1	9.1	10	1	UPA73_HUMAN	1	400-4	homo sapien							
469	1	9.1	10	1	UPA74_HUMAN	1	400-4	homo sapien							
470	1	9.1	10	1	UPA75_HUMAN	1	400-4	homo sapien							
471	1	9.1	10	1	UPA76_HUMAN	1	400-4	homo sapien							

## ALIGNMENTS

RESULT :

FIBRA\_SYN'A

ID FIBRA\_SYN'A STANDARD PRI: 15 AA.

AC P14463

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Fibrinogen: alpha chain (Contains: Fibrinopeptide A) (Fragment).

GN FGA.

CS Syncerus caffer (Cape buffalo).

OC Bakartylia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:

OC Bovidae: Bovinae: Syncerus.

CX NCBI\_TaxID: 9923.

RN [1]

RP SEQUENCE:

KX MEDLINE: 6729145, PubMed: 6033721.

KA Dogliotti R.F., Schubert D., Schwartz S.A.:

\*Amino acid sequence studies on artiodactyl fibrinopeptides. I.

\*Dromedary camel, male deer, and cape buffalo.\*;

RL Arch. Biochem. Biophys. 118:456-467(1967).

CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET

CC AGGREGATION.

CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA &amp; BETA

CC CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

KW Blood coagulation; Plasma.

FT PEPTIDE 1 15 FIBRINOPEPTIDE A.

FT NON\_TER 15 15

SQ SEQUENCE 15 AA: 1480 MW: 4598EA5F0B41CC6 CRC64;

Query Match 36.4% Score 4; DB 1; Length 15;

Best Local Similarity 100.0%, Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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GX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC Tissue-corpora cardiaca;
RA Predel R., Kellner R., Gaele S.;
RT "Myotropic neuropeptides from the retroectoderm complex of the stick
insect, Carausius morosus (Phasmatodea: Isometopidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC 1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTIONS. ACTIVITY
(MYOTROPIC ACTIVITY).
CC 2- MASS SPECTROMETRY: MW: 2255; METHOD=MALDI
CC 3- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR INTERPLOT: IPR001484; PYROKININ.
DR PROSITE: PS00519; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOLECULES 11
SQ SEQUENCE 11 AA: 1236 MW: 264522 EBB491A8 CRC64;

Query Match 27.3% Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 1
2 EGG 4

RESULT 5
RS19_TUBHP
ID RS19_TUBHP STANDARD: PRI: 12 AA.
AC Q56251;
DT 10-MAY-2000 (Rel. 39, Created)
BT 10-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE 40S ribosomal protein S19 (fragment).
GN RPS19 OR RPS19.
OS Tomato big bud phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Actinobacteriales;
OC Actinobacteriales; Actinobacteriales;
GX NCBI_TaxID=35770;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94350802; PubMed-8071178;
RA Gunderson D.E., Lee T.M., Kehler S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC 1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH THE 16S RIBOSOMAL RNA.
CC 2- TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 3- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed, altered by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@sib-sib.ch).
CC .....
DR EMBL: L27034; AAA83952.1;
DR HAMAP: MF_00531; 1.
DR InterPro: IPR002222; Ribosomal S19.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 12 AA: 1470 MW: 408886 E98339A3 CRC64;

Query Match 27.3% Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKM 9
DB 1

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DB 7 KKM 9

RESULT 7
V14K_WSSV
ID V14K_WSSV STANDARD: PRI: 12 AA.
AC P82006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE 14.5 kDa structural polyprotein (fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
GX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=Scott, Carolina;
RX MEDLINE: 20214217; PubMed:10752552;
RA Wang Q., Poulos B.P., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
virus.";
RL Arch. Virol. 145:263-274(2000).
CC 1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
CC NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA: 1242 MW: 248804 FFD21A338 CRC64;

Query Match 27.3% Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5
DB 4 GKK 6

RESULT 8
TAL3_TREME
ID TAL3_TREME STANDARD: PRI: 13 AA.
AC P01370;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE Tremmerogen A-13.
OS Tremella mesenterica (Jelly fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
GX NCBI_TaxID=5217;
RN [1]
RP SEQUENCE.
RA Sakaqami Y., Yoshida M., Isogai A., Suzuki A.;
RT "Peptide sex hormones inducing conjugation tube formation in
compatible mating-type cells of Tremella mesenterica.";
RL Science 212:1525-1527(1981).
CC 1- FUNCTION: TREMEROGEN A-13 IS PRODUCED BY THE A MATING-TYPE CELLS.
CC AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.
DR PIR: A01641; JTIJG3.
KW Lipoprotein; Prenylation; Pheromone.
FT LIPID 13
FT FARNESYL 13
SQ SEQUENCE 13 AA: 1204 MW: 680304 A9697BA864 CRC64;

Query Match 27.3% Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 1 EGG 3

RESULT 9
FIBA_HORSE
ID FIBA_HORSE STANDARD: PRI: 14 AA.
AC P14452;

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BT 01-JAN-1990 (Rel. 13, Created)
DI 01-JAN-1990 (Rel. 13, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN EGA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID:9796;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Gressdahl N. J.
RT "Studies on fibrinopeptides from mammals."
RL Acta Chem. Scand. 15:1789-1791(1955).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SET COAT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 14 FIBRINOPEPTIDE A.
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1517 MW: 459266.024567 Da;
Query Match 27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EGG 4
DI 1
DI 9 EGG 11
RESULT 10
MAST_PART:
ID MAST_PART STANDARD: PRT: 14 AA.
AC P42716;
DI 01-NOV-1995 (Rel. 32, Created)
DI 01-NOV-1995 (Rel. 32, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparasin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hymenoptera; Proctophora;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespidae;
OC Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID: 31921;
RN [1]
RP SEQUENCE.
RA Tosi T., Vasileara T., Nakajima T.
RT "Isolation and sequential analysis of peptides in the venom secret
RT Parapolybia indica."
RL Fisiol. Jap. 39:105-111(1988).
CC -1- FUNCTION: Mast cell degranulating peptide. A peptide of 13 peptides
CC that couple to phospholipase C.
KW Mast cell degranulation; Activation.
FT RES 14 14 AMITILIN.
SQ SEQUENCE 14 AA: 1619 MW: 163760.056104 Da;
Query Match 27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KKM 9
DI 1
DI 4 KKM 5

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RESULT 11

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MCRX_METTM STANDARD: PRT: 14 AA.
ID MCRX_METTM
AC P58815;
DI 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase II alpha subunit (EC 1.8.1.1) (MCR II
DE alpha) (Fragment).
GN MRTA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriacea; Methanothermobacter.
OX NCBI_TaxID:75929;
RN [1]
RP SEQUENCE.
RA MEDLINE:91099370; PubMed 2269306;
RA Rospert S., Linder D., Eilermann J., Thauer R.K.
RT "Two genetically distinct methyl-coenzyme M reductases in
RT Methanobacterium thermoautotrophicum strain Marburg and delta H.":
RL Eur. J. Biochem. 194:871-877(1990).
CC -1- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreosine phosphate
CC to methane and an heterodisulfide.
CC -1- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP -> CH(4) + CoM-S-S-HTP.
CC -1- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)
CC TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
CC Porphyrinoid.
CC -1- PATHWAY: Methanogenesis; last step.
CC -1- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
CC -1- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE, LATE GROWTH CELLS
CC CONTAINS MOSTLY MCR I.
KW Methanogenesis; Oxidoreductase; Multiene family.
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1718 MW: D317CCC562F00E29 CRC64;
Query Match 27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKM 7
DI 1
DI 12 KKM 14
RESULT 12
FIBA_AKAP1
ID FIBA_AKAP1 STANDARD: PRT: 15 AA.
AC P28901;
DI 01-NOV-1989 (Rel. 12, Created)
DI 01-OCT-1989 (Rel. 12, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Anser; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID:8839;
RN [1]
RP SEQUENCE.
RA MEDLINE:85168194; PubMed:3983613;
RA Min Y., Ping Z., Yaoshi Z.
RT "Purification and primary structures of duck fibrinopeptides A and
RT B."
RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

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100  RESIDUE FOR THE FORMATION OF THE SITE 101.
KW  PIR: J101C11: J101C11.
FT  FIBRIN PERLEIDE A.
FT  FIBRIN PERLEIDE B.
FT  PYRROGLUTAMINE CARBOXYL-ACTA.
FT  NON TER 15 15
SQ  SEQUENCE 15 AA: 1580 MW: 17465.446404143604.

Query Match 27.3% Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 10 EGG 12

RESULT 14
ALL9_CARMA
ID ALL9_CARMA STANDARD; PRT: 15 AA.
AC P81812;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Oncorhynchus mykiss (Rainbow trout) (Salmo salar L.).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID:8022;
RN 1;
KW  FUNCTION, SUBCELLULAR LOCATION, ANTI-TOXIN SPECIFICITY.
RP  TISSUE-SKIN;
SA  Fernandes J.M.G., Smith V.J., Kemp G.J.
SA  Purification and N-terminal sequencing of a 15 kDa antifibrinolytic
SA  peptide from skin secretions of rainbow trout.
SA  Submitted (MAY 2002) to the SWISS Prot data bank.
CC  FUNCTION: Has antibacterial activity against gram positive
CC  bacteria: P. citreus.
CC  SUBCELLULAR LOCATION: Secreted.
CC  TISSUE SPECIFICITY: SKIN.
DR  GO:0005576; Extracellular; NAS.
DR  GO:0005795; Fibrinolytic; peptidase activity; NAS.
DR  GO:0006095; Pexenobiotic metabolism; NAS.
KW  Antibiotic.
FT  UNSURE 4 4
FT  UNSURE 7 9
FT  NON TER 15 15
SQ  SEQUENCE 15 AA: 1601 MW: 4502.246604143604.

Query Match 27.3% Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6
DB 4 GKK 5

RESULT 14
9C2C_MAIZE
ID 9C2C_MAIZE STANDARD; PRT: 15 AA.
AC P81626;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated corn (Spot 436)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes;
OC Spermatophyta; Magnoliophyta; Equisetidae; Liliopsida; Poales;
OC Poaceae; Panicoideae; Andropogoneae.
NCBI_TaxID:4577;

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RN  SEQUENCE.
RP  TISSUE: Neuropteric.
SA  Touzel P., Richard F., Marin C., Damerval C., Huet J.-C.,
SA  Pernollet J.-C., Zivy M., de Vienne D.
SA  The maize two dimensional gel protein database: towards an integrated
SA  genome analysis program.
RC  16001; Appl. Genet. 93(1997):205(1996).
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKN/AN
CC  PROTEIN IS 4.1, ITS MW IS 45.3 KDA.
CC  -1- SIMILARITY: TO ALA-ME; SYNTHETASES.
DR  MAIZE 2D PAGE PAGE 26; COLEOPTILE.
DR  MAIZE DB: 123952;
FT  NON TER 15 15
FT  NON TER 15 15
SQ  SEQUENCE 15 AA: 1597 MW: 17465.446404143604.

Query Match 27.3% Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 10 EGG 12

RESULT 15
ALL16_CARMA
ID ALL16_CARMA STANDARD; PRT: 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Brachyura;
OC Brachyura; Portunidea; Portunidae; Carcinus.
NCBI_TaxID:6759;
RN 1;
KW  FUNCTION.
RP  SEQUENCE.
RC  TISSUE-Cerebral ganglion, and thoracic ganglion;
RX  MESLINE-98121193; EMBL-9461295;
RA  Dave H., Johnson A.H., Maestro J.L., Scott A.G., Jaros P.P.,
RA  Thorpe A.
RA  Isolation and identification of multiple neuropeptides of the
RA  allatostatins superfamily in the shore crab Carcinus maenas.
RA  Eur. J. Biochem. 250:727-734(1997).
CC  -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC  -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW  Neuropeptide; Amidation; Multigene family.
FT  MOD_RES 5 8
FT  MOD_RES 5 8
SQ  SEQUENCE 8 AA: 613 MW: 70286B45AB476878 CRC64;

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GG 4
DB 1 GG 2

RESULT 16
ALL19_CARMA
ID ALL19_CARMA STANDARD; PRT: 8 AA.
AC P81812;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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CC Eumalacostraca; Eucarida; Decapoda; Pycnogonata; Brachyura;  
 CC MEDLINE-92196111; PubMed 1549595;  
 CC NCBI\_TaxID-6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Cerebral ganglion, and Thoracic ganglion.  
 RA MEDLINE-98121193; PubMed-9461295;  
 RA Dove H., Johnsen A.H., Maestri E., Scott A.G., Orchard I.,  
 RA Thorpe A.,  
 RA "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab, *Cancerus magellanicus*."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC [1] FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC [1] SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation; Multigene family.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA: 781 MW: 702879CD8476876 CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EG 4  
 DB 1 EG 2

RESULT 17  
 ID CLIP\_THICU STANDARD; PRT; 8 AA.  
 AC P83488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Chemotroph-specific protein (Framcort)  
 OS Thiobacillus cuprinus  
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 CC Comamonadaceae; Thiomonas.  
 CC NCBI\_TaxID-35860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN DSM 5494;  
 RA Martin L., Amaro A.M., Jerez J.A., Anzils R., Anad J.P.P.  
 RA Submitted (SEP-1995) to the SwissProt data bank.  
 CC [1] MISCELLANEOUS: FOUND SPECIFICALLY IN TUBES FILLED  
 CC WITH CHEMOLITHOTROPHICALLY.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA: 785 MW: 9146666C21667565

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3  
 DB 6 EG 7

RESULT 18  
 ID FARB\_CALVO STANDARD; PRT; 8 AA.  
 AC P41863;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliphramide 8.  
 OS Calliphora vomitoria (Blue blowfly)  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Gastrophila;  
 CC Calliphoridae; Calliphora.  
 CC NCBI\_TaxID-27454;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-thoracic ganglion;  
 RA MEDLINE-92196111; PubMed 1549595;  
 RA Dove H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.,  
 RA "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliphramides) from the blowfly  
 RT Calliphora vomitoria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC [1] SIMILARITY: BELONGS TO THE FARP (FAMFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 UR PIR: H41978; H41978  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA: 957 MW: 72040699CAA44DD8 CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10  
 DB 6 MR 7

RESULT 19  
 ID LMT2\_LOCM1 STANDARD; PRT; 8 AA.  
 AC P22356;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Locustamyotropin 2 (COM MI-2).  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 CC NCBI\_TaxID-7004;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE-Corpus cardiaca;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RA "Isolation, identification and synthesis of locustamyotropin II, an  
 RT additional neuropeptide of locusta migratoria. Member of the  
 RT cephalomyotropic peptide family."  
 RL Insect Biochem. 20:479-484(1990).

CC [1] FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).

CC [1] SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

UR InterPro: IPR001484; Pyrokinin.

DR PROSITE: PS00549; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD\_RES 8 8 AMIDATION.

SQ SEQUENCE 8 AA: 934 MW: 26341771A9CAA87B CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3  
 DB 1 EG 2

RESULT 20  
 ID LPMS\_STAEP STANDARD; PRT; 8 AA.  
 AC P32211;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Probable msrA leader peptide.  
 OS Staphylococcus epidermidis.  
 CC Plasmid p015050.

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UC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=968;
RX MEDLINE=9104:730; PubMed=2233255;
RA Ross J.L., Eady E.A., Cove J.H., Gunthill W.J., Baumberg S.,
RA Wootton J.C.;
RT "Inducible erythromycin resistance in staphylococci is encoded by a
RL member of the ATP-binding transport supergene family."
RL Mol. Microbiol. 4:1207-1214(1992);
CC -!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
CC PROTEIN.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR ENBL: X52085; CAA36303.1;
DR PIR: S11157; LFSAME.
KW Leader peptide; Plasmid.
SQ SEQUENCE 8 AA; 937 MW; FA37430E5F0A1A676094;
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 MR 10
DB 5 MR 6
RESULT 23
NS3_MOUSE
ID NS3_MOUSE STANDARD; PRT; 8 AA.
AC P81152;
DT 15-JUN-1999 (Rel. 38, Created)
DT 15-JUN-1999 (Rel. 38, Last sequence update)
DT 15-OCT-2003 (Rel. 40, Last annotation update)
DE 40 kDa non-secretory protein 3 (fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
[1]
RP SEQUENCE.
RC STRAIN H37Kv.
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS PRO database.
CC -!- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Kv.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 919 MW; 8D10C4E6793C24275741;
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 RA 11
DB 6 RA 7
RESULT 24
UC26_MAIZE
ID UC26_MAIZE STANDARD; PRT; 8 AA.
AC P80632;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 907)
DE (fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
[1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi P., Motin C., Damerval C., Huet J.-C.,
RA Pernoillet J.-C., Zivy M., de Vienne D.;
RT "The maize 2D dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7.0, ITS MW IS: 57.2 kDa.
DR Maize-2DPAGE; P80632; COLEOPTILE.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 990 MW; 9639D6DAB4176B1D CRC64;
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AE 2
DB 1 AE 2
RESULT 23
CF06_MOUSE
ID CF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE.
RC TISSUE:Fibroblast;
RX MEDLINE=95069907; PubMed 7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GG 4
DB 5 GG 6
RESULT 24
WPI_PERAT
ID WPI_PERAT STANDARD; PRT; 8 AA.
AC P83195;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Wall protein-1 (PWP-1) (Fragment).  
OS Perkinsus atlanticus.  
OC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.  
OX NCBI\_TaxID-106964;  
RN [1]  
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.  
RX MEDLINE-22044350; PubMed-12049410;  
RA Montes J.F., Durfort M., Llado A., Garcia Varela J.,  
RT Characterization and immunolocalization of a PWP proteinaceous  
RT component of the cell wall of the protozoan parasite Perkinsus  
RT atlanticus.  
RZ Parasitology 124:477-484(2002).  
CC -!- FUNCTION: Is a major protein component of the cell wall. May play  
CC a key role in the organization of the cell wall and in promoting  
CC the survival of this parasite.  
CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell  
CC wall components.  
CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental  
CC stages.  
KW Cell wall.  
FT NON\_TER  
SQ SEQUENCE 8 AA: 765 MW: F1787D08761AAB16 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 EG 3  
DB 4 EG 5  
RESULT 26  
ID DSIP\_RAB11 STANDARD; PRT; 9 AA.  
AC P01158;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DI 15-OCT-2001 (Rel. 40, Last annotation update)  
DE Delta sleep-inducing peptide (DSIP).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID-9986;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE-77185424; PubMed-862769.  
RA Monnier M., Didier L., Gachet R., Maier P.F., Toller H.J.,  
RA Schoenenberger G.A.;  
RT "The delta sleep inducing peptide (DSIP): Comparative properties of  
RT the original and synthetic nonapeptide.";  
RL Experientia 33:548-552(1977).  
RN [2]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE-79054421; PubMed-568769;  
RA Schoenenberger G.A., Maier P.F., Toller H.J., Wilson K., Monnier M.;  
RT "The delta EEG (sleep)-inducing peptide (DSIP): An amino-acid  
RT analysis, sequence, synthesis and activity of the nonapeptide.";  
RL Pflügers Arch. 376:119-129(1978).  
RN [3]  
RP REVIEW.  
RX MEDLINE-87175129; PubMed-3556726;  
RA Graf M.V., Kastin A.J.;  
RT "Delta-sleep-inducing peptide (DSIP): an update.";  
RL Peptides 7:1165-1187(1986).  
CC -!- FUNCTION: WHEN INFUSED INTO THE MESOENCEPHALIC VENTRICLE OF  
CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND  
CC REDUCED MOTOR ACTIVITIES.  
CC -!- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF  
CC OCCIPITAL VENOUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC  
CC STIMULATION OF THE THALAMUS.  
CC -!- DATABASE: NAME-Protein Spotlight;

CC NOTE-Issue 8 of March 2001;  
CC WWW-<http://www.expasy.org/spotlight/articles/sptlt008.html>.  
DR PIR; A01422; GDB.  
SQ SEQUENCE 9 AA: 849 MW: DDD365BDDAA8787D CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GG 4  
DB 3 GG 4  
RESULT 26  
ID FAR1\_CALVO STANDARD; PRT; 9 AA.  
AC P41856;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DI 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallipMRamide 1.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID-27454;  
RN [1]  
RP SEQUENCE.  
RX TISSUE-Rhotorac ganglion;  
RX MEDLINE-92196111; PubMed-1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated callipMRFamides) from the blowfly  
RT Calliphora vomitoria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
CC SALIVARY GLAND OF CALLIPHORA.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
CC PIR; A41978; A41978.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9  
SQ SEQUENCE 9 AA: 1169 MW: 29D00699CAB6C6C7 CRC64;  
Query Match 18.2%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 MR 10  
DB 7 MR 8  
RESULT 27  
ID FAR2\_CALVO STANDARD; PRT; 9 AA.  
AC P41857;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DI 01-NOV-1995 (Rel. 32, Last annotation update)  
DE CallipMRamide 2.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID-27454;  
RN [1]  
RP SEQUENCE.  
RX TISSUE-Thoracic ganglion;  
RX MEDLINE-92196111; PubMed-1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

RA Rehfeld J.F., Thorpe A.;  
 KT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 neuropeptides (designated calliferramides) from the blowfly  
 Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2325-2330(1992)  
 CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
 SALIVARY GLAND OF CALLIPHORA.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 CC PIR: B41978; B41978.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SEQUENCE 9 AA: 1128 MW: 250.6699kDa; GA7 100.4;  
 AMIDATION.

Query Match 18.2% Score 2: DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10  
 DB 7 MR 8

RESULT 2/4  
 FARP\_CALVO STANDARD; PRI: 9 AA.  
 AC B41978;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliferramide 3;  
 OS Calliphora vomitoria (Blue blowfly);  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Aestroidea;  
 CC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN 11

KT "Isolation, structure, and activity of the Met-Arg-Phe-NH2  
 neuropeptides (designated calliferramides) from the blowfly  
 Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2325-2330(1992)  
 CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED  
 SALIVARY GLAND OF CALLIPHORA.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 CC PIR: B41978; B41978.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SEQUENCE 9 AA: 1114 MW: 250.6699kDa; GA7 100.4;  
 AMIDATION.

Query Match 18.2% Score 2: DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10  
 DB 7 MR 8

RESULT 2/4  
 FARP\_PENMO STANDARD; PRI: 9 AA.  
 AC B41978;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide-FLP3 (AOPSRLEF amide);  
 OS Penaeus monodon (Penaeid shrimp).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN 11  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 KC TISSUE-Eyestalk;  
 RX MEDLINE:21956277; PubMed-11959015;  
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,  
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;  
 KT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 of the giant tiger prawn Penaeus monodon";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW 1121.2; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SEQUENCE 9 AA: 1105 MW: 320.07340685kDa; 776 CRC64;  
 AMIDATION.

Query Match 18.2% Score 2: DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10

DB 7 MR 8

## RESULT 3/

FARP\_CALVO STANDARD; PRI: 9 AA.  
 AC B41978;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Calliferramide 4;  
 OS Calliphora vomitoria (Blue blowfly);  
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Aestroidea;  
 CC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN 11

KT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 neuropeptides (designated calliferramides) from the blowfly  
 Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2325-2330(1992).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 FAMILY.  
 CC PIR: B41978; B41978.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 SEQUENCE 9 AA: 1182 MW: 317.0699kDa; 457 CRC64;  
 AMIDATION.

Query Match 18.2% Score 2: DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10

DB 7 MR 8

## RESULT 3/

FARP\_PENMO STANDARD; PRI: 9 AA.  
 AC B41978;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLH4 (SQSMRVR-amide)
OS Penaeus monodon (penaeid shrimp)
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Decapoda; Penaeidae
OC NCHI_TaxID=6687
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=21956277; PubMed=17559675;
RA Sittlerberg P., Pupem J., Krumholz C., Langguth S.,
RA Chavisanthangkura P., Sittlerberg W., Fong A.,
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 133B:325-337(2002).
CC -/- SUBCELLULAR LOCATION: Secreted.
CC -/- MASS SPECTROMETRY: MW 1119.8; MEINIG-MALLI.
CC -/- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1121 MW: DAUBD74068A776 CRC64:

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 5 MR 6

RESULT 32
FAR5_ASCSD STANDARD: PRT: 9 AA.
ID FAR5_ASCSD
AC 843170:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF5.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascarididae.
OC NCHI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE 95480462; PubMed=7451904
RA Cowden C., Stretton A.O.W.
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500(1995).
CC -/- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1052 MW: 340B85D8D64506 CRC64:

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GK 5
DB 2 GK 3

RESULT 33
FAR5_CALVO STANDARD: PRT: 9 AA.
ID FAR5_CALVO
AC 841860:

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 5.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Ephemeroptera; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OC NCHI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=9216611; PubMed=1549595;
RA Dure H., Johnson A.B., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -/- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1068 MW: 39D10699CAB6D867 CRC64:

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MR 10
DB 7 MR 8

RESULT 34
FAR5_PANKE STANDARD: PRT: 9 AA.
ID FAR5_PANKE
AC 882661:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropeptide PF5 (AMRNALVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OC NCHI_TaxID=5233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RX Motet C.L., Marks N.J., Hallon D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.
RT "Isolation, characterization and pharmacology of FMRamide-related
RT peptides (FARPs) from free-living nematode, Panagrellus redivivus."
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -/- FUNCTION: MYOACTIVE.
CC -/- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1077 MW: A0D112C72DB45406 CRC64:

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 2 MR 3

RESULT 35
FAR6_CALVO STANDARD: PRT: 9 AA.
ID FAR6_CALVO

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AC P41861:  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Callipmrfamide 6.  
 OS Calliphora vomitoria (Blue blowfly)  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora  
 CX NCBI\_TaxID:27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Thoracic ganglion;  
 RX MEDLINE:92196111; PubMed:1549595;  
 RA Dave H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated callipmrfamides) from the blowfly  
 RT Calliphora vomitoria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330 (1992)  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR: F41978; F41978.  
 KW Neuropeptide; Amidation.  
 FT MCD RES 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 1058 MW: 96619.96;AS-DEAD;AS-74;

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10  
 LB 7 MR 4

RESULT 0:  
 FARP MATCHES STANDARD; PRT; 9 AA.  
 AC P41861:  
 DT 24-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide F196 (FMRFamide)  
 OS Macrobathrus rosenbergi (Giant Fresh water fish)  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Eumalacostraca; Decapoda; Decapoda; Malacostraca;  
 OC Parameconidra; Palaemonidae; Macrobrachia  
 CX NCBI\_TaxID:79674;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RC TISSUE:Eviscalk;  
 RX MEDLINE:21107394; PubMed:1170812  
 RA Sathiyaraj P., Sathiyaraj W., Sathiyaraj S., Sathiyaraj N.,  
 RA Sathiyaraj W., Sathiyaraj W., Sathiyaraj W., Sathiyaraj W.,  
 RT "Three more novel FMRFamide like neuropeptides from the  
 RT eviscalk of the giant freshwater prawn Macrobrachium rosenbergi."  
 RL Peptides 22:191-197(2001).  
 CC -1- MASS SPECTROMETRY: MW 1081.7, Phe-Met-Arg-Phe-NH2  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR G07007218; Phe-Met-Arg-Phe-NH2 (FARP) (FMRFamide)  
 KW Neuropeptide; Amidation.  
 FT MCD RES 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 1081 MW: 2680.729;VQKRW;74;

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 4  
 LB 2 0 1 4

RESULT 1:  
 FARP MATCHES STANDARD; PRT; 9 AA.  
 AC P41861:  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Callipmrfamide 7.  
 OS Calliphora vomitoria (Blue blowfly)  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora  
 CX NCBI\_TaxID:27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Thoracic ganglion;  
 RX MEDLINE:92196111; PubMed:1549595;  
 RA Dave H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated callipmrfamides) from the blowfly  
 RT Calliphora vomitoria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR: G41978; G41978.  
 KW Neuropeptide; Amidation.  
 FT MCD RES 9 AMIDATION.  
 SQ SEQUENCE 9 AA: 1081 MW: E1D10699CAB6D86A CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best local Similarity 100.0%; Pred. No. 1.3e-05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10  
 LB 7 MR 8

RESULT 1:  
 FARP MATCHES STANDARD; PRT; 9 AA.  
 AC P41861:  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Callipmrfamide 10.  
 OS Calliphora vomitoria (Blue blowfly)  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora  
 CX NCBI\_TaxID:27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE:Thoracic ganglion;  
 RX MEDLINE:92196111; PubMed:1549595;  
 RA Dave H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated callipmrfamides) from the blowfly  
 RT Calliphora vomitoria."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR PIR: A44787; A44787.  
 KW Neuropeptide; Amidation.  
 FT MCD RES 9 AMIDATION.  
 FT UNSPEC 1 1 GR S OR A.  
 SQ SEQUENCE 9 AA: 1183 MW: 29006999CAB40457 CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MK 10
DB 7 MK 8

RESULT: 39
FARD_CALVO
ID FARD_CALVO STANDARD; PRT: 9 AA.
AC P41968;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 01-NOV-1995 (rel. 32, Last annotation update)
DE CalliPMPFamide 13.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Diptera; Oestroidea;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID-27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE-92196111; PubMed-1549595;
KA Dave H., Johnson A.H., Sewell J.C., Scott A.G., Orchard L.,
RA Reineid J.F., Thorpe A.;
RT "Isolation, structure, and activity of Fibrinogen-Ac-Phe-NR2
RT neuropeptides (designated calliPMPFamides) from the blowfly
RT Calliphora vomitoria.";
KL Proc. Natl. Acad. Sci. U.S.A. 93:2525-2530(1996).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMKFAIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: D44787; D44787.
KW Neuropeptide; Amidation.
FT MOD_RES 9 AMIDATION.
SQ SEQUENCE 9 AA: 1028 MW: 2201699678788068 C8764;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MK 10
DB 7 MK 8

RESULT 40
FIBB_ERYPA
ID FIBB_ERYPA STANDARD; PRT: 9 AA.
AC P19346;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS Erythrocybus patas (Red quebon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID-9538;
RN [1]
RP SEQUENCE.
RX MEDLINE-85289140; PubMed-3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT quensons, and baboons.";
KL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR: D28854; D28854.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA: 1076 MW: DDF6409C7287B06 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 3 EG 4

RESULT 42
FIBB_PAPHA

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CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR: D24180; D24180.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA: 1020 MW: 69FE7879C732CB1B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GC 4
DB 7 GC 8

RESULT 41
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT: 9 AA.
AC P19344;
DT 01-NOV-1990 (rel. 16, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID-9555;
RN [1]
RP SEQUENCE.
RX MEDLINE-84161822; PubMed-6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
KL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR: D28854; D28854.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA: 1076 MW: DDF6409C7287B06 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 3 EG 4

RESULT 42
FIBB_PAPHA

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ID FIBR_PAPHA STANDARD: PRT: 9 AA.
AC P19342:
DT 01-NOV-1990 (Rel. 16, Created);
DT 01-NOV-1990 (Rel. 16, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment);
GN FGB;
OS Papio hamadryas (Hamadryas baboon);
OC Eukaryota; Metazoa; Chordata; Gravidata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartida; Artiodactyla;
OC Cercopithecoidea; Papio;
OX NCBI_TaxID=9557;
RN [1];
RP SEQUENCE:
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT *Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons *;
RL J. Biochem. 94:1973-1978(1983);
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NON-IDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
SV PIR: E28854; E28854;
DR InterPro: IPR002181; Fibrinogen_C;
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL;
KW Blood coagulation; Plasma;
FT PEPTIDE 1 9 FIBRINOPEPTIDE B;
FT NON TER 1 9
SQ SEQUENCE 9 AA: 1057 MW; 10577.67224306 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 1
1 EG 4

RESULT 43
FIBR_TREGE STANDARD: PRT: 9 AA.
AC P19342:
DT 01-NOV-1990 (Rel. 16, Created);
DT 01-NOV-1990 (Rel. 16, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment);
GN FGB;
OS Theropithecus gelada (Gelada baboon);
OC Eukaryota; Metazoa; Chordata; Gravidata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catartida; Artiodactyla;
OC Cercopithecoidea; Theropithecus;
OX NCBI_TaxID=9565;
RN [1];
RP SEQUENCE:
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT *Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons *;
RL J. Biochem. 94:1973-1978(1983);
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NON-IDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

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CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen_C;
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL;
KW Blood coagulation; Plasma;
FT PEPTIDE 1 9 FIBRINOPEPTIDE B;
FT NON TER 1 9
SQ SEQUENCE 9 AA: 977 MW; 10577.67224306 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EG 3
DB 1
1 EG 4

RESULT 44
FIBL_SARBU STANDARD: PRT: 9 AA.
AC P8350:
DT 28-FEB-2003 (Rel. 41, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Neb-FMRamide 1;
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga;
OX NCBI_TaxID=7385;
RN [1];
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE=CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen J., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Naudman K.J., Huybrechts R., De Loof A., Schoofs L.;
RT Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRamide receptor *;
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002);
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1155 MW; 20510699CAB6C5A7 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 1
7 MR 8

RESULT 45
IPYR_RHOVI STANDARD: PRT: 9 AA.
AC P8292:
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPhase) (Fragment);
GN PPA;
OS Rhodospseudomonas viridis.

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RT the streptococcal plasmid pIP501.  
RL Plasmid 28:272-275(1992).  
CC  
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).  
CC  
DR EMBL: M58515; AAA26612.1;  
DR EMBL: M58516; AAA1528.1;  
DR EMBL: X02872; CAA26640.1;  
DR EMBL: X60827; CAA43217.1;  
DR EMBL: X65462; CAA46454.1;  
DR PIR: B24362; B24362.  
DR PIR: S30494; S30494.  
KW Leader peptide; Antibiotic resistance; Plasmid.  
SQ SEQUENCE 9 AA: 1074 MW: 5D9CAR5AAB05B333 CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6  
DB 2 KK 4

RESULT 47  
ID NSK1\_SARBU STANDARD; PRT; 9 AA.  
AC P41452;  
DT 01-NOV-1995 (rel. 32, Created)  
DT 01-NOV-1995 (rel. 32, Last sequence update)  
DT 01-FEB-1996 (rel. 33, Last annotation update)  
DE Neosulfakinin-I (NEH-SK-I).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
GX NCBI\_TaxID=73655;  
RN [1]  
RP SEQUENCE.  
RC TISSUE: Head;  
KC MEDLINE=9308111; PubMed 1360367;  
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;  
RI "Isolation and primary structure of two sulfakinin-like peptides from  
RI the fleshfly, Neobellieria bullata";  
RL Comp. Biochem. Physiol. 103C:135-142(1992).  
CC -!- FUNCTION: MYOTROPIC PEPTIDE.  
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
DR InterPro: IPR001651; Gastrin.  
DR PROSITE: PS00259; GASTRIN; 1.  
KW Neuropeptide; Amidation; Sulfation.  
FT MOD\_RES 4 4 4 SULFATION (POTENTIAL).  
FT MOD\_RES 4 4 9 AMIDATION (POTENTIAL).  
SQ SEQUENCE 9 AA: 1187 MW: 8B0A0691E86B5AAA CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10  
DB 7 MR 8

RESULT 48  
SAMP\_MUSCA  
ID SAMP\_MUSCA STANLARD; PRT; 9 AA.  
AC P19095;

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
Hyphomicrobiaceae; Blastochloris.  
NCBI\_TaxID=1079;  
CC  
CC  
CC SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.  
Gomez R., Losada M., Serrano A.;  
Submitted (JUN-2001) to the SWISS-PROT data bank.  
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS PROTEIN IS:  
23 kDa.  
CC -!- SIMILARITY: Belongs to the PRase family.  
DR HAMAP: MF\_00209; 1;  
DR InterPro: IPR001596; Pyrophosphatase.  
DR PROSITE: PS00387; PRASE; PARTIAL.  
KW Hydrolyase.  
FT NON\_TER 9 9  
FT SEQUENCE 9 AA: 1014 MW: 5BF4FAAF50RAA;14 CRE64;

Query Match 18.2% Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10  
DB 1 MR 2

RESULT 49  
LPCA\_STAAG  
ID LPCA\_STAAG STANDARD; PRT; 9 AA.  
AC P36884;  
DT 01-JUN-1994 (rel. 29, Created);  
DT 01-JUN-1994 (rel. 29, Last sequence update);  
DT 01-ACT-1994 (rel. 30, Last annotation update);  
DE Chloramphenicol resistance leader peptide.  
OS Streptococcus aureus, and  
OS Streptococcus agalactiae.  
GC Plasmid pSC86. Plasmid pSC87, Plasmid pSL123, and Plasmid pIP501.  
OG Bacteria; Firmicutes; Bacillales; Staphylococcus  
CX NCBI\_TaxID=1280, 1311;  
KN [1]  
RP SEQUENCE FROM N.A.  
KC SPECIES=S.aureus; STRAIN=446; PLASMID=pSC86;  
RX MEDLINE=92027652; PubMed-1429426;  
RA Schwarz S., Cardoso M.;  
RI "Nucleotide sequence and phylogeny of chloramphenicol  
RI acetyltransferase encoded by the plasmid pSC87 from Staphylococcus  
RI aureus";  
KL Antimicrob. Agents Chemother. 35:1761-1674(1993).  
LN [2]  
RN SEQUENCE FROM N.A.  
RP SPECIES=S.aureus; PLASMID=pSC86;  
RC MEDLINE=92388047; PubMed-1517170;  
RA Carosso M., Schwarz S.;  
RI "Nucleotide sequence and structural, total synthesis of a  
RI chloramphenicol acetyltransferase encoded by the plasmid pSC86 from  
RI Staphylococcus aureus";  
RJ J. Appl. Bacteriol. 72:289-293(1992)  
RN [3]  
RN SEQUENCE FROM N.A.  
RP SPECIES=S.aureus; PLASMID=pUR123;  
RC MEDLINE=86081739; PubMed-3865770;  
KA Brackner K., Matsuzawa H.;  
RI "Regulation of the inducible chloramphenicol acetyltransferase gene  
RI of the Staphylococcus aureus plasmid pUB12";  
RL EMBO J. 4:2295-2300(1985).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP SPECIES=S.agalactiae; PLASMID=pIP501;  
RC MEDLINE=93096867; PubMed-1461942;  
TX Tieu-Cuat P., de Cespedes G., Murad F.;  
RI "Nucleotide sequence of the chloramphenicol resistance determinant of

01 MAR 1990 (Rel. 16, Created)  
 02 MAR 1990 (Rel. 16, Last sequence update)  
 03 FEB 2003 (Rel. 41, Last annotation update)  
 04 SERUM amyloid P-component (SAP) (Fragment)  
 05 Mustelus canis (Smooth dogfish)  
 06 Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes  
 07 Elasmobranchii; Galeomorphi; Galeorhinidae; Chondrichthyes; Trachidae  
 08 Mustelus  
 09 NCBI\_TaxID 7812;  
 10 RN  
 11  
 12 MEDLINE=93160942; PubMed 9404720;  
 13 RA Money P.A., Takao T., Liu F.-S.,  
 14 RT "Isolation and characterization of two major serum proteins from the  
 15 dogfish, Mustelus canis, C-reactive protein and amyloid P  
 16 component";  
 17 J. Biol. Chem. 258:3889-3894 (1983).  
 18 CC  
 19 FUNCTION: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISC-  
 20 SHAPED ARRANGEMENT OF 5 NONCOVALENTLY BINDING SUBUNITS.  
 21 CC  
 22 SUBCELLULAR LOCATION: Secreted.  
 23 CC  
 24 DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT 1 WHICH IS FOUND  
 25 IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 26 CC  
 27 SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 28 ER PIR: B20569; B20569.  
 29 OR InterPro: IPR001759; PENTAXIN.  
 30 ER PROSITE: PS0289; PENTAXIN; PARTIAL.  
 31 KW Location: Amyloid; Glycoprotein; Plasma; Pentaxin  
 32 DOMAIN 1 59  
 33 FT NON\_TER 5 59  
 34 FT  
 35 SQ SEQUENCE 9 AA: 965 MW: 66597.60 Da; 965 aa; 18.2%  
 36  
 37 Query Match 18.2% Score 2; DB 1; Length 9;  
 38 Best Local Similarity 100.0%, Pred. No. 1.3e+05;  
 39 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 40  
 41 4 GK 5  
 42 11  
 43 4 GK 5  
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QY 4 GK 4  
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RESULT 50  
 ID THYF\_PIG STANDARD PRI: 9 AA  
 AC P01255;  
 DT 21-JUL-1984 (Rel. 61, Created)  
 DT 21-JUL-1984 (Rel. 61, Last sequence update)  
 DT 26-FEB-2003 (Rel. 41, Last annotation update)  
 DE Thymic factor;  
 OS Sus scrofa (Pig);  
 GC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;  
 CX NCBI\_TaxID:9823;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=78026571; PubMed:914862;  
 RA Pledau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;  
 RT "Structural study of circulating thymic factor: a peptide isolated  
 from pig serum. II. Amino acid sequence.";  
 JC J. Biol. Chem. 252:8045-8047(1977).  
 CC -1- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL  
 CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.  
 DR PIR: A01523; YFPG.  
 KW Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 9 AA: 876 MW: 105087.66 Da; 876 aa; 18.2%

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%, Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GK 4  
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 DB

Search completed: September 30, 2003, 10:26:08  
 Load time: 7.25 secs

RESULT 49  
 ID SAP\_SF\_VA STANDARD: PRI: 9 AA  
 AC P21347;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Sperm activating peptide (SAP)  
 OS Stromelysin variegatus (Sea urchin)  
 GC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinodermata;  
 CC Echinodermata; Echinodermata; Echinodermata; Echinodermata;  
 CC Stromelysin;  
 CX NCBI\_TaxID 7554;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BOND  
 TS TISSUE=EGG JELLY;  
 RX MEDLINE 92097763; PubMed:1756569;  
 RA Yoshino K. I., Takao T., Shimizu Y., Sato N.  
 RT "Determination of the amino acid sequence of a sperm activating  
 RT disulfide linkage containing sperm activating factor by tandem mass  
 RT spectrometry";  
 JC FEBS LETT. 294:179-182(1991).  
 CC -1- FUNCTION: CAUSE STIMULATION OF SPERM CELL FERTILIZATION AND MOTILITY  
 CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT DEPLETION OF  
 CC CAMP, GMP AND CALCIUM LEVELS IN SPERM CELLS AND TRANSIENT  
 CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE PUMP OF  
 CC ADENYLATE CYCLASE.  
 FT DISULFID 1 8  
 SQ SEQUENCE 9 AA: 1010 MW: 10490.66 Da; 1010 aa; 18.2%

Query Match 18.2% Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%, Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 GenCore Ltd.

OM protein - protein search, using SW model

Run on: September 30, 2003, 10:02:04 : Search time 31.6577 Seconds  
(with local alignment)

Title: US-09-787-443-19

Perfect score: 11

Sequence: 1 AEGCKKKMRA 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4659

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database:

1: SP archaea:\*

2: SP bacteria:\*

3: SP fungi:\*

4: SP human:\*

5: SP invertebrate:\*

6: SP mammal:\*

7: SP mhc:\*

8: SP organelle:\*

9: SP phage:\*

10: SP plant:\*

11: SP rodent:\*

12: SP virus:\*

13: SP vertebrate:\*

14: SP unclassified:\*

15: SP virus:\*

16: SP bacteriophage:\*

17: SP archaea:\*

Prod. No. is the number of results produced for the query. In this case, the number is higher than or equal to the score. The results are listed in the order of the score and are derived by analysis of the local alignment.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	9	2	Q4960 azotobacter
2	3	27.3	9	2	P72149 pseudomonas
3	3	27.3	9	4	Q9H184 homo sapien
4	3	27.3	9	11	Q99M34 mus musculus
5	3	27.3	10	6	Q7FS42 sus scrofa
6	3	27.3	10	6	Q7L153 saccharomye
7	3	27.3	10	9	Q48217 lactococcus
8	3	27.3	10	12	P90474 pseudorabies
9	3	27.3	11	2	Q8K81 escherichia
10	3	27.3	11	12	Q58428 psittacaru
11	3	27.3	11	14	Q9FS22 xenopus lae
12	3	27.3	12	4	Q9BQ07 homo sapien
13	3	27.3	12	6	Q9N258 poxvira pyoma
14	3	27.3	12	15	Q75729 human immun
15	3	27.3	12	15	Q41611 human immun
16	3	27.3	12	16	Q25174 helicobacte

17	3	27.3	13	4	Q5NR93	Q9nr93 homo sapien
18	3	27.3	13	8	Q9T569	Q9t569 zea mays (m
19	3	27.3	13	10	Q39380	Q39380 brassica ol
20	3	27.3	13	11	Q62355	Q62355 mus musculu
21	3	27.3	14	4	Q9NY40	Q9ny40 homo sapien
22	3	27.3	14	4	Q96050	Q96050 homo sapien
23	3	27.3	14	4	Q15222	Q15222 homo sapien
24	3	27.3	14	4	Q81VK4	Q81vk4 homo sapien
25	3	27.3	14	6	Q9TR83	Q9tr83 sus scrofa
26	3	27.3	14	15	Q8UT17	Q8ut17 human immun
27	3	27.3	15	4	Q9UC07	Q9uc07 homo sapien
28	3	27.3	15	6	Q9TR45	Q9tr45 bos taurus
29	3	27.3	15	6	Q9GLJ0	Q9glj0 sus scrofa
30	3	27.3	15	10	Q9SQ16	Q9sq16 oryza sativ
31	3	27.3	15	10	Q9FYV6	Q9fyv6 gossypium h
32	3	27.3	15	10	P82431	P82431 nicotiana t
33	3	27.3	15	10	P82439	P82439 nicotiana t
34	3	27.3	15	15	Q8USK4	Q8usk4 human immun
35	3	27.3	15	15	Q8UM88	Q8um88 human immun
36	2	18.2	8	2	Q9S6D5	Q9s6d5 escherichia
37	2	18.2	8	2	P72279	P72279 rhodococcus
38	2	18.2	8	2	Q9R712	Q9r712 escherichia
39	2	18.2	8	2	Q9AGP4	Q9agp4 arthrobacte
40	2	18.2	8	2	Q68485	Q68485 klebsiella
41	2	18.2	8	2	Q93SR0	Q93sr0 staphylococ
42	2	18.2	8	2	Q44463	Q44463 rhizobiales
43	2	18.2	8	2	Q32560	Q32560 escherichia
44	2	18.2	8	2	Q9258	Q9258 synecococc
45	2	18.2	8	2	Q56429	Q56429 thermus the
46	2	18.2	8	2	Q9R9E0	Q9r9e0 bacillus su
47	2	18.2	8	2	Q9SR0	Q9sr0 shigella dy
48	2	18.2	8	2	P72221	P72221 pseudomonas
49	2	18.2	8	2	Q9R5L7	Q9r5l7 clostridium
50	2	18.2	8	4	Q15900	Q15900 homo sapien
51	2	18.2	8	4	Q15901	Q15901 homo sapien
52	2	18.2	8	4	Q60773	Q60773 homo sapien
53	2	18.2	8	5	Q9TWH6	Q9twh6 perinerreis
54	2	18.2	8	5	Q8MUN6	Q8mun6 helicobac
55	2	18.2	8	5	Q94655	Q94655 physarum po
56	2	18.2	8	6	Q9BFA7	Q9bfa7 macroscelid
57	2	18.2	8	6	Q9BF82	Q9bf82 ursus arcto
58	2	18.2	8	6	Q9BEC2	Q9bec2 macropus eu
59	2	18.2	8	6	Q9HF90	Q9hf90 tragelaphus
60	2	18.2	8	6	Q9BFA1	Q9bfa1 echinops te
61	2	18.2	8	6	Q9BFA1	Q9bfa1 ateles fusc
62	2	18.2	8	6	Q9BF87	Q9bf87 tapirus ind
63	2	18.2	8	6	Q8WNS1	Q8wns1 bos taurus
64	2	18.2	8	6	Q9BF89	Q9bf89 euphractus
65	2	18.2	8	6	Q9BF88	Q9bf88 chaetophrac
66	2	18.2	8	6	Q9BFA8	Q9bfa8 loxodonta a
67	2	18.2	8	6	Q9BFA9	Q9bfa9 procavia ca
68	2	18.2	8	6	Q9BF82	Q9bf82 sorex arane
69	2	18.2	8	6	Q9BF85	Q9bf85 erinaceus c
70	2	18.2	8	6	Q9BF86	Q9bf86 myrmecophag
71	2	18.2	8	6	Q9BF83	Q9bf83 condylura c
72	2	18.2	8	6	Q9BF88	Q9bf88 equus cabal
73	2	18.2	8	6	Q9BF85	Q9bf85 roussetta l
74	2	18.2	8	6	Q9BF84	Q9bf84 panthera on
75	2	18.2	8	6	Q9BF83	Q9bf83 didelphis m
76	2	18.2	8	6	Q9BFA4	Q9bfa4 tupia mino
77	2	18.2	8	6	Q9BFA2	Q9bfa2 tarsius ban
78	2	18.2	8	6	Q9BF85	Q9bf85 leopardus p
79	2	18.2	8	6	Q9BF81	Q9bf81 chooleopus h
80	2	18.2	8	6	Q9BF89	Q9bf89 akapia john
81	2	18.2	8	6	Q9BF96	Q9bf96 pteropus gl
82	2	18.2	8	6	Q9BF80	Q9bf80 trichechus
83	2	18.2	8	6	Q9BF86	Q9bf86 felis silve
84	2	18.2	8	6	Q9BF92	Q9bf92 tursiops tr
85	2	18.2	8	6	Q9BF87	Q9bf87 hippopotamu
86	2	18.2	8	6	Q9BF91	Q9bf91 tamandua te
87	2	18.2	8	6	Q9BF84	Q9bf84 talpa alta
88	2	18.2	8	6	Q9BF80	Q9bf80 chooleopus d
89	2	18.2	8	6	Q9BF98	Q9bf98 callimico q

90	2	18.2	8	6	Q93A43	Q9B1A3	temar calta	163	2	18.2	9	8	Q9TKG1	Q9tkq1 calothamun
91	2	18.2	8	6	Q9B4B6	Q9B1A6	cryctelopis	164	2	18.2	9	8	Q316S3	Q316S3 anser caeru
92	2	18.2	8	6	Q9B4B6	Q9B1A6	canis famli	165	2	18.2	9	10	Q940K4	Q940K4 aradidopsis
93	2	18.2	8	6	Q9B4B6	Q9B1A6	artibeus ja	166	2	18.2	9	11	Q8R514	Q8R514 rattus norv
94	2	18.2	8	6	Q9B4B6	Q9B1A6	cyoccephalu	167	2	18.2	9	11	Q9QZ47	Q9qza7 mus musculu
95	2	18.2	8	6	Q9B4B6	Q9B1A6	nycterus te	168	2	18.2	9	11	Q9QVH9	Q9qv19 mus sp. sup
96	2	18.2	8	6	Q9B4B6	Q9B1A6	saccharomye	169	2	18.2	9	12	Q86545	Q86545 human herpe
97	2	18.2	8	6	Q9B4B6	Q9B1A6	alcedinara p	170	2	18.2	9	12	Q82622	Q82622 avian infec
98	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	171	2	18.2	9	12	Q95100	Q95100 herpes simp
99	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	172	2	18.2	9	13	Q92009	Q92009 gallus gall
100	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	173	2	18.2	10	2	Q9R791	Q9r791 borrelia af
101	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	174	2	18.2	10	2	Q9X8H3	Q9xbh3 bacillus ce
102	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	175	2	18.2	10	2	Q50032	Q50032 mycobacteri
103	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	176	2	18.2	10	2	Q8VN85	Q8vn85 helicobacte
104	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	177	2	18.2	10	2	Q52837	Q52837 rhizobium 1
105	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	178	2	18.2	10	2	Q60194	Q60194 spiroplasma
106	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	179	2	18.2	10	2	Q60192	Q60192 spiroplasma
107	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	180	2	18.2	10	2	Q48469	Q48469 klebsiella
108	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	181	2	18.2	10	2	Q51812	Q51812 escherichia
109	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	182	2	18.2	10	2	Q52762	Q52762 rhizobium s
110	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	183	2	18.2	10	2	Q9AE19	Q9ae19 streptococc
111	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	184	2	18.2	10	3	Q8J0C2	Q8j0c2 encephalito
112	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	185	2	18.2	10	4	Q96QA7	Q96qa7 homo sapien
113	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	186	2	18.2	10	4	Q8NER0	Q8ner0 homo sapien
114	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	187	2	18.2	10	4	Q00493	Q00493 homo sapien
115	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	188	2	18.2	10	4	Q9UMK9	Q9umk9 homo sapien
116	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	189	2	18.2	10	4	Q13318	Q13318 homo sapien
117	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	190	2	18.2	10	4	Q9UCS3	Q9ucs3 homo sapien
118	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	191	2	18.2	10	4	Q8NEY9	Q8ney9 homo sapien
119	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	192	2	18.2	10	4	Q9P229	Q9p229 homo sapien
120	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	193	2	18.2	10	4	Q9UCU6	Q9ucu6 homo sapien
121	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	194	2	18.2	10	4	Q8WXB5	Q8wxb5 homo sapien
122	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	195	2	18.2	10	5	Q8MUP1	Q8mup1 heliconiur
123	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	196	2	18.2	10	5	Q8WPL6	Q8wpl6 oikopleura
124	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	197	2	18.2	10	5	Q8MUN7	Q8mun7 heliconiur
125	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	198	2	18.2	10	5	Q82383	Q82383 drosophila
126	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	199	2	18.2	10	6	Q9TRU6	Q9trs3 sus scrofa
127	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	200	2	18.2	10	6	Q9TKF7	Q9tru6 bos taurus
128	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	201	2	18.2	10	8	Q9TKF7	Q9tkf7 agonis gran
129	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	202	2	18.2	10	8	Q9TKG2	Q9tkg2 callistemon
130	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	203	2	18.2	10	8	Q9TKF5	Q9tkf5 agonis spat
131	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	204	2	18.2	10	8	Q9TKF1	Q9tkf1 homalosperm
132	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	205	2	18.2	10	8	Q9TKF4	Q9tkf4 angasomyrtu
133	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	206	2	18.2	10	8	Q9TKF3	Q9tkf3 asteromyrtu
134	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	207	2	18.2	10	8	Q9TKF0	Q9tkf0 neofabricia
135	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	208	2	18.2	10	8	Q9TKF0	Q9tkf0 neofabricia
136	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	209	2	18.2	10	8	Q9TKF6	Q9tkf6 agonis obtu
137	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	210	2	18.2	10	8	Q9TKF7	Q9tkf7 leptospermu
138	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	211	2	18.2	10	8	Q9TKF2	Q9tkf2 leptospermu
139	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	212	2	18.2	10	8	Q9TKF3	Q9tkf3 leptospermu
140	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	213	2	18.2	10	8	Q9TKF7	Q9tkf7 kunzea pulc
141	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	214	2	18.2	10	8	Q9TKM6	Q9tkm6 leptospermu
142	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	215	2	18.2	10	8	Q9TKF6	Q9tkf6 leptospermu
143	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	216	2	18.2	10	8	Q9TKF6	Q9tkf6 leptospermu
144	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	217	2	18.2	10	8	Q9TKF9	Q9tkf9 kunzea eric
145	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	218	2	18.2	10	8	Q9TKF9	Q9tkf9 kunzea baxt
146	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	219	2	18.2	10	8	Q9TKF1	Q9tkf1 neofabricia
147	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	220	2	18.2	10	8	Q9TKF4	Q9tkf4 leptospermu
148	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	221	2	18.2	10	10	Q94119	Q94119 zea mays (m
149	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	222	2	18.2	10	10	Q8L7F5	Q8l7f5 hevea brasl
150	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	223	2	18.2	10	10	Q82938	Q82938 hordeum vul
151	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	224	2	18.2	10	11	Q08622	Q08622 rattus norv
152	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	225	2	18.2	10	11	Q9QVJ7	Q9qv17 mus sp. nep
153	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	226	2	18.2	10	11	Q91W23	Q91w23 rattus sp.
154	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	227	2	18.2	10	11	Q9QVF0	Q9qv10 mus sp. pro
155	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	228	2	18.2	10	11	Q9QVF1	Q9qv11 mus sp. pro
156	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	229	2	18.2	10	12	Q9Q0W9	Q9q0w9 polymaviru
157	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	230	2	18.2	10	12	Q8JW7C	Q8jw7c polymaviru
158	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	231	2	18.2	10	12	Q9Q0W1	Q9q0w1 polymaviru
159	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	232	2	18.2	10	12	Q8JW68	Q8jw68 polymaviru
160	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	233	2	18.2	10	12	Q9J1G8	Q9j1g8 tt virus. o
161	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	234	2	18.2	10	12	Q69347	Q69347 herpes simp
162	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	235	2	18.2	10	12	Q9Q0W9	Q9q0w9 polymaviru
	2	18.2	8	6	Q9B4B6	Q9B1A6	bacteriopho	235	2	18.2	10	12	Q6JV84	Q6jv84 polymaviru

236	2	18.2	10	12	Q930W7	Q930W7 polyomavirus	409	2	18.2	11	13	Q8UUP1	Q8UUP1 xenopus lae
237	2	18.2	10	12	Q8JCV6	Q8JCV6 polyomavirus	310	2	18.2	11	13	Q8JCV6	Q8JCV6 ticedula al
238	2	18.2	10	12	Q9QV7	Q9QV7 polyomavirus	311	2	18.2	11	13	Q9QV7	Q9QV7 gallus gall
239	2	18.2	10	12	Q8JW7	Q8JW7 polyomavirus	312	2	18.2	11	15	Q8YS3	Q8YS3 human immun
240	2	18.2	10	12	Q8JW7	Q8JW7 polyomavirus	313	2	18.2	11	15	P88018	P88018 human immun
241	2	18.2	10	12	Q8JW7	Q8JW7 polyomavirus	314	2	18.2	12	2	Q56442	Q56442 escherichia
242	2	18.2	10	12	Q8JW7	Q8JW7 polyomavirus	315	2	18.2	12	2	Q8KH47	Q8KH47 enterococcus
243	2	18.2	10	12	Q930X7	Q930X7 polyomavirus	316	2	18.2	12	2	Q50342	Q50342 mycoplasma
244	2	18.2	10	12	Q8JW7	Q8JW7 polyomavirus	317	2	18.2	12	2	Q93208	Q93208 acinetobact
245	2	18.2	10	12	Q9QW5	Q9QW5 polyomavirus	318	2	18.2	12	2	Q46712	Q46712 escherichia
246	2	18.2	10	12	Q9QX3	Q9QX3 polyomavirus	319	2	18.2	12	2	Q53183	Q53183 rhodococcus
247	2	18.2	10	12	Q9QX3	Q9QX3 polyomavirus	320	2	18.2	12	2	Q54226	Q54226 saccharopol
248	2	18.2	10	12	Q9QX3	Q9QX3 polyomavirus	321	2	18.2	12	2	Q8KT49	Q8KT49 fischerella
249	2	18.2	10	12	Q8JW7	Q8JW7 polyomavirus	322	2	18.2	12	2	Q8VIX8	Q8VIX8 thermus the
250	2	18.2	10	12	Q9QX1	Q9QX1 polyomavirus	323	2	18.2	12	2	Q8KH15	Q8KH15 campylobact
251	2	18.2	10	12	Q9QX3	Q9QX3 polyomavirus	324	2	18.2	12	2	Q9X6Y0	Q9X6Y0 aquifex pyr
252	2	18.2	10	12	Q8JW7	Q8JW7 polyomavirus	325	2	18.2	12	2	Q9K3H3	Q9K3H3 helicobacte
253	2	18.2	10	13	Q8JW7	Q8JW7 polyomavirus	326	2	18.2	12	2	Q52112	Q52112 acinetobact
254	2	18.2	10	15	Q8JW7	Q8JW7 polyomavirus	327	2	18.2	12	2	Q8GMV1	Q8GMV1 acinetobact
255	2	18.2	10	15	Q9QK10	Q9QK10 human immun	328	2	18.2	12	2	Q8GKT8	Q8GKT8 acinetobact
256	2	18.2	11	2	Q9R750	Q9R750 borrelia ga	329	2	18.2	12	2	Q8GML2	Q8GML2 acinetobact
257	2	18.2	11	2	Q924F7	Q924F7 bacillus ce	330	2	18.2	12	3	Q01275	Q01275 neurospora
258	2	18.2	11	2	Q9X956	Q9X956 streptomyce	331	2	18.2	12	4	Q9UMR0	Q9UMR0 homo sapien
259	2	18.2	11	2	Q9S618	Q9S618 prochlorococ	332	2	18.2	12	4	Q9H126	Q9H126 homo sapien
260	2	18.2	11	2	Q87882	Q87882 mycobacteri	333	2	18.2	12	4	Q9UC37	Q9UC37 homo sapien
261	2	18.2	11	2	Q8KTN1	Q8KTN1 candidatus	334	2	18.2	12	4	Q16452	Q16452 homo sapien
262	2	18.2	11	2	Q93MH7	Q93MH7 escherichia	335	2	18.2	12	4	Q9UMQ9	Q9UMQ9 homo sapien
263	2	18.2	11	2	Q9RF72	Q9RF72 mycoplasma	336	2	18.2	12	4	Q9UC29	Q9UC29 homo sapien
264	2	18.2	11	2	Q95518	Q95518 pasteurella	337	2	18.2	12	4	Q9H3W2	Q9H3W2 homo sapien
265	2	18.2	11	2	Q47420	Q47420 escherichia	338	2	18.2	12	4	Q96PK0	Q96PK0 homo sapien
266	2	18.2	11	2	Q44090	Q44090 acholeplasm	339	2	18.2	12	4	Q13865	Q13865 homo sapien
267	2	18.2	11	2	Q8GMU3	Q8GMU3 acinetobact	340	2	18.2	12	4	Q9UGS1	Q9UGS1 homo sapien
268	2	18.2	11	3	Q9UR95	Q9UR95 pichia anqu	341	2	18.2	12	4	Q9H4X3	Q9H4X3 homo sapien
269	2	18.2	11	3	Q9UR95	Q9UR95 neurospora	342	2	18.2	12	4	Q9NTQ2	Q9NTQ2 homo sapien
270	2	18.2	11	3	Q96V15	Q96V15 cryptorectu	343	2	18.2	12	4	Q9BR06	Q9BR06 homo sapien
271	2	18.2	11	4	Q14759	Q14759 homo sapien	344	2	18.2	12	5	Q8MUN4	Q8MUN4 heliconi
272	2	18.2	11	4	Q60761	Q60761 homo sapien	345	2	18.2	12	5	Q9U7R8	Q9U7R8 conus querc
273	2	18.2	11	4	Q75811	Q75811 homo sapien	346	2	18.2	12	5	Q8MUN9	Q8MUN9 heliconi
274	2	18.2	11	4	Q9H4H5	Q9H4H5 homo sapien	347	2	18.2	12	5	Q61574	Q61574 osteria
275	2	18.2	11	4	Q15997	Q15997 homo sapien	348	2	18.2	12	5	Q9TWY0	Q9TWY0 fasciola he
276	2	18.2	11	4	Q8NFN9	Q8NFN9 homo sapien	349	2	18.2	12	6	Q46664	Q46664 macropus ro
277	2	18.2	11	4	Q9UC45	Q9UC45 homo sapien	350	2	18.2	12	6	Q9N2B9	Q9N2B9 gorilla gor
278	2	18.2	11	4	Q9JCH1	Q9JCH1 homo sapien	351	2	18.2	12	6	Q9TQW3	Q9TQW3 bos taurus
279	2	18.2	11	4	Q4UH72	Q4UH72 homo sapien	352	2	18.2	12	6	Q9TRV6	Q9TRV6 bos taurus
280	2	18.2	11	5	Q26042	Q26042 pisaster oc	353	2	18.2	12	6	Q9N2C0	Q9N2C0 pan troglod
281	2	18.2	11	5	Q9TWX6	Q9TWX6 manduca sex	354	2	18.2	12	8	Q9G196	Q9G196 sargassum p
282	2	18.2	11	5	Q92432	Q92432 drosophila	355	2	18.2	12	8	P92454	P92454 cycas revol
283	2	18.2	11	5	Q95PX6	Q95PX6 caenorhabdi	356	2	18.2	12	8	P82164	P82164 spinacia ol
284	2	18.2	11	5	Q9TWH2	Q9TWH2 aplysia cal	357	2	18.2	12	8	Q8HB27	Q8HB27 picea glauc
285	2	18.2	11	5	Q6MWH8	Q6MWH8 helicobact	358	2	18.2	12	8	Q8HB26	Q8HB26 picea maria
286	2	18.2	11	5	Q9FW45	Q9FW45 bos taurus	359	2	18.2	12	8	Q8HB25	Q8HB25 picea ruben
287	2	18.2	11	6	Q91BX2	Q91BX2 bos taurus	360	2	18.2	12	10	Q8SAS2	Q8SAS2 pinus sylve
288	2	18.2	11	6	Q91Q59	Q91Q59 equus cabal	361	2	18.2	12	10	Q93X21	Q93X21 zea mays (m
289	2	18.2	11	7	Q77842	Q77842 oreochromis	362	2	18.2	12	10	Q41744	Q41744 zea mays (m
290	2	18.2	11	7	Q77860	Q77860 oreochromis	363	2	18.2	12	10	Q02320	Q02320 pinus sylve
291	2	18.2	11	7	Q77906	Q77906 oreochromis	364	2	18.2	12	10	Q9SQF8	Q9SQF8 pinus taeda
292	2	18.2	11	7	Q77893	Q77893 oreochromis	365	2	18.2	12	10	Q38715	Q38715 arachis hyp
293	2	18.2	11	8	Q77907	Q77907 oreochromis	366	2	18.2	12	10	Q02319	Q02319 pinus sylve
294	2	18.2	11	8	Q9G3Y0	Q9G3Y0 pseudotrape	367	2	18.2	12	10	P94011	P94011 arabidopsis
295	2	18.2	11	8	Q9G356	Q9G356 aquana atra	368	2	18.2	12	10	Q8H6E6	Q8H6E6 hordeum vul
296	2	18.2	11	9	Q38415	Q38415 bacterioph	369	2	18.2	12	11	Q35868	Q35868 mus musculu
297	2	18.2	11	9	Q37925	Q37925 bacterioph	370	2	18.2	12	11	Q64313	Q64313 rattus norv
298	2	18.2	11	10	Q37884	Q37884 gossypium h	371	2	18.2	12	11	Q9WUX1	Q9WUX1 rattus norv
299	2	18.2	11	10	Q8RUE7	Q8RUE7 zea mays (m	372	2	18.2	12	11	Q61331	Q61331 mus musculu
300	2	18.2	11	10	Q04131	Q04131 lycopersico	373	2	18.2	12	11	Q91YF5	Q91YF5 mus musculu
301	2	18.2	11	10	P82336	P82336 pisum sativ	374	2	18.2	12	11	Q8CJ30	Q8CJ30 mus musculu
302	2	18.2	11	11	Q9YN81	Q9YN81 mus musculu	375	2	18.2	12	12	Q91F00	Q91F00 human adeno
303	2	18.2	11	11	Q9R1N6	Q9R1N6 mus musculu	376	2	18.2	12	12	Q84268	Q84268 human papil
304	2	18.2	11	11	Q921H5	Q921H5 mus musculu	377	2	18.2	12	12	Q86570	Q86570 hepatitis d
305	2	18.2	11	11	P81075	P81075 mus musculu	378	2	18.2	12	12	Q91EZ9	Q91EZ9 human adeno
306	2	18.2	11	12	Q83083	Q83083 leucania se	379	2	18.2	12	13	Q9PVC2	Q9PVC2 gadus morhu
307	2	18.2	11	12	Q9J1G3	Q9J1G3 tt virus, o	380	2	18.2	12	13	Q9PVC3	Q9PVC3 lampris sp.
308	2	18.2	11	12	Q40974	Q40974 cauliflower	381	2	18.2	12	13	Q9PVC0	Q9PVC0 mugil cepha

382	2	18.2	12	13	Q9PVC1	Q9PVC1 lephus sp.	455	2	18.2	13	11	Q14804	Q14804 mus musculus
383	2	18.2	12	13	Q9PVB9	Q9PVB9 apizias lat	456	2	18.2	13	11	Q97944	Q97944 mus musculus
384	2	18.2	12	13	Q9PVC6	Q9PVC6 plecciossu	457	2	18.2	13	11	Q9CM04	Q9CM04 mus sp. pi
385	2	18.2	12	13	Q9PVB8	Q9PVB8 hemiraphus	458	2	18.2	13	11	Q8CJ33	Q8CJ33 mus musculus
386	2	18.2	12	13	Q9PVB8	Q9PVB8 nullus sp.	459	2	18.2	13	11	Q8CFN7	Q8CFN7 mus musculus
387	2	18.2	12	13	Q9PVC7	Q9PVC7 esox lucius	460	2	18.2	13	12	Q9PXB5	Q9PXB5 duck hepatic
388	2	18.2	12	13	Q9PVC4	Q9PVC4 harpadon sp.	461	2	18.2	13	12	Q83171	Q83171 cauliflower
389	2	18.2	12	13	Q9PVC7	Q9PVC7 gallus gali	462	2	18.2	13	12	Q83394	Q83394 pseudoflower
390	2	18.2	12	13	Q9PVC5	Q9PVC5 gallus gali	463	2	18.2	13	13	Q9PVA0	Q9PVA0 colisa lali
391	2	18.2	12	13	Q9PVC3	Q9PVC3 xenopus lae	464	2	18.2	13	13	Q9PVB1	Q9PVB1 dendrochiru
392	2	18.2	12	13	Q8A820	Q8A820 rana catesb	465	2	18.2	13	13	Q9PVC5	Q9PVC5 mola mola (
393	2	18.2	12	13	Q8A820	Q8A820 rana catesb	466	2	18.2	13	13	Q9PVC7	Q9PVC7 dissostichu
394	2	18.2	12	13	Q8AUP7	Q8AUP7 salmo salar	467	2	18.2	13	13	Q9PVB3	Q9PVB3 hippocampus
395	2	18.2	12	13	Q8AUP7	Q8AUP7 salmo salar	468	2	18.2	13	13	Q9PVB8	Q9PVB8 pettodes s
396	2	18.2	12	13	Q8AUP7	Q8AUP7 human immun	469	2	18.2	13	13	Q9PVC7	Q9PVC7 ballistes sp
397	2	18.2	12	13	Q8AUP7	Q8AUP7 avian carc	470	2	18.2	13	13	Q9PVB2	Q9PVB2 mastacembel
398	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	471	2	18.2	13	13	Q9PVA2	Q9PVA2 thunnus sp.
399	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	472	2	18.2	13	13	Q9PVB0	Q9PVB0 dicentrarch
400	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	473	2	18.2	13	13	Q9PVB4	Q9PVB4 zeus faber
401	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	474	2	18.2	13	13	Q9PVC9	Q9PVC9 channa sp.
402	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	475	2	18.2	13	13	Q9PVA5	Q9PVA5 cryptocentr
403	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	476	2	18.2	13	13	Q9PVA3	Q9PVA3 acanthurus
404	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	477	2	18.2	13	13	Q9PVA9	Q9PVA9 epinephelus
405	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	478	2	18.2	13	13	Q9PVC5	Q9PVC5 galaxias ma
406	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	479	2	18.2	13	13	Q8QG25	Q8QG25 fugu rubrip
407	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	480	2	18.2	13	13	Q9PVA4	Q9PVA4 siganus sp.
408	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	481	2	18.2	13	13	Q9PVA1	Q9PVA1 stromateus
409	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	482	2	18.2	13	13	Q9PVC6	Q9PVC6 ostracion s
410	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	483	2	18.2	13	13	Q9PVB5	Q9PVB5 sargocentro
411	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	484	2	18.2	13	13	Q9PVB7	Q9PVB7 fundulus he
412	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	485	2	18.2	13	13	Q9PVB6	Q9PVB6 poecilia la
413	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	486	2	18.2	13	13	Q9PVA6	Q9PVA6 salarias sp
414	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	487	2	18.2	13	13	Q82821	Q82821 rana catesb
415	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	488	2	18.2	13	13	Q82822	Q82822 rana catesb
416	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	489	2	18.2	13	13	Q82823	Q82823 rana catesb
417	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	490	2	18.2	13	13	Q82881	Q82881 rana clamit
418	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	491	2	18.2	13	13	Q82830	Q82830 rana luteiv
419	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	492	2	18.2	13	13	Q82848	Q82848 rana pipien
420	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	493	2	18.2	13	15	Q00789	Q00789 human immun
421	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	494	2	18.2	13	15	Q98YJ7	Q98YJ7 human immun
422	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	495	2	18.2	13	16	Q8X4F5	Q8X4F5 escherichia
423	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	496	2	18.2	14	2	Q9R8G3	Q9R8G3 chlamydia t
424	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	497	2	18.2	14	2	Q9R8F0	Q9R8F0 chlamydia t
425	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	498	2	18.2	14	2	Q93U00	Q93U00 escherichia
426	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	499	2	18.2	14	2	Q9E8H8	Q9E8H8 chlamydia t
427	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun	500	2	18.2	14	2	Q9R8G4	Q9R8G4 chlamydia t
428	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
429	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
430	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
431	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
432	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
433	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
434	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
435	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
436	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
437	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
438	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
439	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
440	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
441	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
442	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
443	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
444	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
445	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
446	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
447	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
448	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
449	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
450	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
451	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
452	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
453	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							
454	2	18.2	12	13	Q9PVC5	Q9PVC5 human immun							

## ALIGNMENTS

RESULT 1  
Q43960 PRELIMINARY: PRT: 9 AA.  
ID Q43960: AC Q43960: 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Hydrogenase-related protein (fragment).  
GN HUPA.  
OS Azotobacter chroococcum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Azotobacter.  
OX NCBI\_TaxID=353:  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MC01;  
RX MEDLINE=95055698; PubMed=7966281;  
RA Du L., Tabei L., K.H., Souza E.M., Garq R.P., Yates M.G.;  
RT "Sequences, organization and analysis of the hup2MNOQRTV genes from  
the Azotobacter chroococcum hydrogenase gene cluster.";  
RL J. Mol. Biol. 243:549-557(1994).  
DR EMBL; L25315; AAA64455.1; .

FT NON\_TER 9 9 1904 MW: EF42115045069411 CRC64;  
SQ SEQUENCE 9 AA: 27.3% Score 3; DB 2; Length 9;  
Query Match:  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
DB 7 AEG 9

RESULT 2  
P72149  
ID P72149 PRELIMINARY: PRI: 9 AA.  
AC P72149;  
DT 01-FEB-1997 (FEBMREL: 02, Created)  
DI 01-FEB-1997 (FEBMREL: 02, Last sequence update)  
DE Putative glucokinase (Fragment).  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OX NCBI\_TaxID-287;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA STRAIN-PA01;  
RC MELLING-96427344; PubMed:880079;  
RA Sage A.E., Proctor W.D., Phillips P.V. Jr.  
RT "A two-component response regulator, GltK, is located for glucose transport activity in Pseudomonas aeruginosa [Acl]."  
RT J. Bacteriol. 178:6064-6066(1996)  
DR EMBL: J50932; AAC44474.1;  
KW Kinase.  
FT NON\_TER 1 1  
SQ SEQUENCE 9 AA: 944 MW: C407163AA7200676 CRC64;

Query Match 27.3% Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3  
DB 7 AEG 9

RESULT 3  
Q9H4Y3  
ID Q9H4Y3 PRELIMINARY: PRI: 9 AA.  
AC Q9H4Y3;  
DT 01-MAR-2001 (FEBMREL: 16, Created)  
DI 01-MAR-2001 (FEBMREL: 16, Last sequence update)  
DE 10499811.1 (Novel protein with a similar structure to the  
DE inhibitor domain and WAP-type (Wey acid-binding domain) (near disulfide  
DE core) domains (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX NCBI\_TaxID-9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Lloyd D.;  
RC Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL: AL121778; CAB76844.1;  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA: 1036 MW: 254120.6412064 CRC64;

Query Match 27.3% Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 7 EGG 9

RESULT 4  
Q99MG3  
ID Q99MG3 PRELIMINARY: PRI: 9 AA.  
AC Q99MG3;  
DT 01-JUN-2001 (FEBMREL: 17, Created)  
DI 01-JUN-2001 (FEBMREL: 17, Last sequence update)  
DE NCAM protein (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX NCBI\_TaxID-10090;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA More M.L., Kirsch F.P., Rathjen F.G.;  
RT "Targeted ablation of NCAM and ankyrin-B results in disorganized lens  
RT fibres leading to cataract formation."  
RT Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL: AF146472; AAK25814.1;  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA: 1039 MW: 32FCH721E3333327 CRC64;

Query Match 27.3% Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
DB 3 KKK 9

RESULT 5  
Q9TS42  
ID Q9TS42 PRELIMINARY: PRI: 10 AA.  
AC Q9TS42;  
DT 01-MAY-2000 (FEBMREL: 13, Created)  
DI 01-MAY-2000 (FEBMREL: 13, Last sequence update)  
DE 01-JUN-2002 (FEBMREL: 21, Last annotation update)  
DE OESTRADIOL-RECEPTOR-P2 peptide (Fragment).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX NCBI\_TaxID-9823;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Thiele H.H., Jungblut P.W., Jakob F.;  
RT "The proteolysis-driven dissociation of oestradiol-receptor dimers as a  
RT preparative tool. Isolation of a 32 kDa fragment from porcine uteri  
RT and assignment of C-terminal origin by partial sequencing."  
RT Biochem. J. 276:709-714(1991).  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA: 992 MW: D95E047B1451B76D CRC64;

Query Match 27.3% Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
DB 7 EGG 9

RESULT 6  
Q97103  
ID Q97103 PRELIMINARY: PRI: 10 AA.

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AC Q17103;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 2.1 kDa protein.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Mitochondrion.
PC Bakaydai; Pudi; Ascomycota; Saccharomycotina; Basidiomycetes.
NC NCBITaxID:4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:WILD TYPE STRAIN A;
RX MEDLINE:85155510; PubMed:649436;
RA de Zambrano M., Faudon-Rodriguez G., Boudreau J., Goussard P.,
  Bernardi G.;
RT "The ori sequences of the Mitochondria, derived of a wild-type yeast
  RT strain: number, location, orientation and structure";
RL Gene 32,439-457(1984);
DR EMBL: K03305; AAA66858.1;
DR EMBL: K03296; AAA69852.1;
DR EMBL: K03297; AAA69853.1;
DR EMBL: K03300; AAA69854.1;
KW Hypothetical protein; Mitochondrion
SQ SEQUENCE 10 AA: 1141 MW: 11638.6369 kDa CRC64:

Query Match 27.3% Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KKR 9
DB 4 KKR 6

RESULT 7
Q8217 7
ID Q8217 PRELIMINARY; PRI; 11 AA.
AC Q8217;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DE 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
LE Bacteriophage HK5-T promoter P1 DNA (Fragment)
OS Lactococcus phage HK5-T.
OC Viruses; dsDNA viruses, no RNA stage; Bacteriophages; Siphoviridae.
NC NCBITaxID:11754;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE:90254170; PubMed:211177;
RA Lakshminarayana G., Davidson K.E., Brierley J.E.;
PT Molecular characterization of promoters of the Lactococcus lactis
PT subsp. cremoris temperate bacteriophage HK5-T: identification of a
RT phage gene implicated in the temperate lifestyle and activity";
RL Appl. Environ. Microbiol. 56:544-542(1990);
DR EMBL: M14490; AAA32241.1;
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1203 MW: 9725.9466 kDa CRC64:

Query Match 27.3% Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 KKR 10
DB 7 KKR 9

RESULT 8
P46574
ID P46574 PRELIMINARY; PRI; 11 AA.
AC P46574;
DT 01-MAY-1997 (TrEMBLrel. 01, Created)
DI 01-MAY-1997 (TrEMBLrel. 01, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 015 (Fragment);
OS Pseudorabies virus.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
NC NCBITaxID:10445;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:Rock;
RA Pederson N.E., Casey J.L., Il. Koslowski K.M.;
RT "Pseudorabies virus 015 and 017 sequence";
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U66824; AAA47266.1;
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 859 MW: 92424.1000 kDa CRC64:

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 3
DB 7 AEG 9

RESULT 9
Q8RKN1
ID Q8RKN1 PRELIMINARY; PRI; 11 AA.
AC Q8RKN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-lactamase CTX-M-9 (Fragment);
NC BLASTX MW 9;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NC NCBITaxID:552;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:743 B;
RA Sabete M., Navarro F., Miro E., Campoy S., Miralles B., Barbe J.,
RA Prats G.;
RT "A novel complex salivary integron in Escherichia coli carrying the
RT bla(CTX-M-9) gene";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY092038; AAM15718.1;
FT NON_TER 11 11
SQ SEQUENCE 11 AA: 1071 MW: 12684.1800 kDa CRC64:

Query Match 27.3% Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AEG 4
DB 8 AEG 10

RESULT 10
Q9SRZ8
ID Q9SRZ8 PRELIMINARY; PRI; 11 AA.
AC Q9SRZ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE W2 peptide (Fragment);
OS Psphocarpus tetrasolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids; Fabales; Papilionoideae; Phaseoleae;
OC Psphocarpus.
NC NCBITaxID:3591;

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RN (1)
RP SEQUENCE
RX MEDLINE-92232221; PubMed 1468037;
RI Hirano H., Kagawa H., Okubo K.;
RE Phytochemistry 31:731-735(1992).
RF NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1165 MW; 304275164384207 CIRCULAR;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSK 3
DB 5 AEG 10

RESULT 11
Q9PS22 PRELIMINARY; PRT; 11 AA.
AC Q9PS22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hydrix 1'; VASOTOCINYL-GLY-LYS
OS Xenopus laevis (African Clawed Frog);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesolestheria; Pipididae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID 8455;
RN 11
RP SEQUENCE
RX MEDLINE-93200145; PubMed-8452872.
RI Iwamuro S., Hayashi H., Kikuyama S.;
RE "An additional arginine-vasotocin related peptide, vasotocinyl-GLY-LYS, in Xenopus neurohypophysis."
RC Biochim. Biophys. Acta 1176:143-147(1994).
DR InterPro: IP000981; Neurohyp-Form.
DK Flute: IP00220; Hormone4; 1.
DR PROSITE: P50264; NEUROHYPOPHYS_HORM_1.
SQ SEQUENCE 11 AA; 1238 MW; 025857871718454 CIRCULAR;

Query Match 27.4%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 12
Q9HQJ1 PRELIMINARY; PRT; 12 AA.
AC Q9HQJ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE BA28309.2.2 (Novel protein (Isotom 3)) (Fragment);
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
OX NCBI_TaxID 9606;
RN 11
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL121582; CAC36069.1;
FT NON_TER 1
SQ SEQUENCE 12 AA; 1017 MW; 4784672188787577 CIRCULAR;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

RESULT 13
Q9N2B8 PRELIMINARY; PRT; 12 AA.
AC Q9N2B8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
OS Pongo pygmaeus (Orangutan);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
OX NCBI_TaxID 9600;
RN 11
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RE "Silver Project";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB041305; HAA94454.1;
KW Methyltransferase; Transferase.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CIRCULAR;

Query Match 27.3%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4
DB 2 EGG 4

RESULT 14
Q75729 PRELIMINARY; PRT; 12 AA.
AC Q75729;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Not.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID 11576;
RN 11
RP SEQUENCE FROM N.A.
RA Strain HP9411;
RA Martini R., Kirchhoff F., Greenough T.C., Sullivan J.L.,
RA Desrosiers R.C., Skowronski J.;
RT "High frequency of defective nef alleles in a long-term survivor with
RT nonprogressive HIV-1 infection.";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U61801; AA04720.1;
DR InterPro: IPR000583; GATase_2.
DR PROSITE: PS00443; GATASE_TYPE_11; 1.
SQ SEQUENCE 12 AA; 1238 MW; 2B921E1187B325A3 CIRCULAR;

Query Match 27.3%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSK 5
DB 9 GSK 11

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Db          2 GKK 4

RESULT 15
Q41611
ID Q41611 PRELIMINARY: PRT: 12 AA.
AC Q41611
DT 01-JAN-1998 (TRENBLrel: 05, Created)
DI 01-JAN-1998 (TRENBLrel: 05, Last sequence update)
DI 01-OCT-2002 (TRENBLrel: 22, Last annotation update)
DE Nei protein (Fragment).
GN NEI.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentiviruses
GX NCBI_TaxID:11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN:M02;
RX MEDLINE:98105804; PubMed:9445059;
RA Connor R.L., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA Walker R.D., Neumann A.U., Vornum S.R., Weststock J., Jackson S.,
RA Fendmore E., Cao Y., Gao F., Katsura S., Kunstman K.J., McDonald D.,
RA McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.,
RT "Immunological and virological analyses of persons infected by human
RT immunodeficiency virus type 1 while participating in trials of
RT recombinant gp120 subunit vaccines";
RL J. Virol. 72:1552-1576(1998).
DR EMBL: U84854; AAC58899.1;
FT NON_TER 12 12
SQ SEQUENCE 12 AA: 1222 MW: 28921E119; H: 545 CR 64;

Query Match 27.3%; Score 3; DB 16; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5
DB 2 GKK 4

RESULT 16
Q25179
ID Q25179 PRELIMINARY: PRT: 12 AA.
AC Q25179;
DT 01 JAN 1998 (TRENBLrel: 05, Created)
DI 01 JAN 1998 (TRENBLrel: 05, Last sequence update)
DI 01 MAR-2002 (TRENBLrel: 20, Last annotation update)
DE Hypothetical protein HP0429
GX NCBI_TaxID:210;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN:26695 / ATCC 700392.
RX MEDLINE:97394467; PubMed:9252184;
RA Lomb J.F., White O., Kerlavage A.R., Planton P.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klee H., Gill S., Goodberty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson J., Kaul R., Glodek A.,
RA McKenney K., Fitzgerald L.M., De N. Adams R.D., Hickey E.K.,
RA Goff D.E., Gorayne J.D., Uffordback J.B., Pedersen J.D., Kelley C.M.,
RA Cotton M.D., Weidman J.M., Ehalt C., Rasmussen L., Wootley M., Wallis E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.G., Fraser C.M.,
RA Venter J.S.;
RT "The complete genome sequence of the human pathogen Helicobacter
RT pylori";
RL Nature 388:539-547(1997).
DR EMBL: AF000559; AAD07512.1;
DR 11GR: HP0429;
KW Hypothetical protein; Complete proteome;
SQ SEQUENCE 12 AA: 1375 MW: 20959A84E211163 CR 64;

Query Match 27.3%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6
DB 5 GKK 7

RESULT 17
Q9NR93
ID Q9NR93 PRELIMINARY: PRT: 13 AA.
AC Q9NR93;
DT 01-OCT-2000 (TRENBLrel: 15, Created)
DI 01-OCT-2000 (TRENBLrel: 15, Last sequence update)
DI 01-OCT-2000 (TRENBLrel: 15, Last annotation update)
DE ULIP (Fragment).
GN ULIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:20287517; PubMed:10748015;
RA Matsuo T., Stauffer J.K., Walker R.L., Melizer P., Thiele C.J.;
RT "Structure and promoter analysis of the human unc-33-like
RT phosphoprotein gene, E-box required for maximal expression in
RT neuroblastoma and myoblasts";
RL J. Biol. Chem. 275:16560-16568(2000).
DR EMBL: AF246692; AAF76324.1;
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1536 MW: 517F5F2CE06D4333 CR 64;

Query Match 27.3%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKK 6
DB 5 GKK 7

RESULT 18
Q9T569
ID Q9T569 PRELIMINARY: PRT: 13 AA.
AC Q9T569;
DT 01-MAY-2000 (TRENBLrel: 13, Created)
DI 01-MAY-2000 (TRENBLrel: 13, Last sequence update)
DI 01 DEC-2001 (TRENBLrel: 19, Last annotation update)
DE Mitochondrial plasmid S 2 DNA, 5' end (fragment).
OS Zea mays (Maize).
GX NCBI_TaxID:4577;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Seed.
RA Traynor P.L., Levings C.S. III.;
RT "Transcription of the S-2 maize mitochondrial plasmid.";
RL Plant Mol. Biol. 7:255-263(1986).
DR EMBL: M16992; AAA70281.1;
KW Mitochondrion.
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1626 MW: 7B5E03673918A1F4 CR 64;

Query Match 27.3%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 KKK 7  
 III  
 DB 9 KKK 11

## RESULT 19

Q39480 Q39480 PRELIMINARY: PRT: 13 AA.  
 AC Q39480;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE IFA binding protein (Sp10) (Fragment).  
 DE Brassica oleracea (cauliflower).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Eukaryota; Magnoliophyta; eudicotyledons; core eudots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Brassica;  
 OX NCBI\_TaxID=3712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DOK; TISSUE=Curd surface;  
 RA Willis G.;  
 RI "An investigation of nuclear lamin homologies in plants: an apparently  
 KI non intermediate filament sequence that bind a polyclonal anti-lamin  
 KI antiserum";  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X97678; CAA66268.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA: 1413 MW; D1D4EA126B42772 CRC64;

Query Match 27.3% Score 4; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
 III  
 DB 9 EGG 11

## RESULT 20

Q62355 Q62355 PRELIMINARY: PRT: 13 AA.  
 AC Q62355;  
 DT 01-NOV-1995 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1995 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Trypsin (Fragment).  
 DE TRV4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Mammalia; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurophila; Muridae; Murinae; Mus;  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A2;  
 RA MEDLINE=67066713; PubMed=3641189;  
 RA Stevenson B.J., Hagenbuchle G., Weisiger R.K.;  
 RT "Sequence organisation and transcriptional regulation of the mouse  
 RT elastase II and trypsin genes";  
 RL Nucleic Acids Res. 14:8307-8330(1986)  
 DR EMBL: X04580; CAA28248.1;  
 DR MGI: 102757; Trv4.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA: 1346 MW; D0FF4200214D729 CRC64;

Query Match 27.3% Score 4; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MRA 11  
 III  
 DB 1 MRA 3

## RESULT 21

Q9NY40 Q9NY40 PRELIMINARY: PRT: 14 AA.  
 AC Q9NY40;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE CH13L1 protein (Fragment).  
 GN CH13L1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ammon C., Rehli M., Andreessen R., Krause S.W.;  
 RT "Alternative splicing of the human cartilage gp-39 gene generates  
 RT multiple mRNA transcripts encoding for at least four putative protein  
 RT isoforms with distinct carboxyl termini";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ251847; CAB76473.1;  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA: 1431 MW; 9EFAACDE1A14A7C5 CRC64;

Query Match 27.3% Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGG 4  
 III  
 DB 1 EGG 3

## RESULT 22

Q96050 Q96050 PRELIMINARY: PRT: 14 AA.  
 AC Q96050;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Mitochondrial ribosomal protein L33 (Fragment).  
 GN MRPL33.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE:21429115; PubMed=11543634;  
 RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.;  
 RA Watanabe K., Tanaka T.;  
 RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes  
 RT to the chromosomes and implications for human disorders";  
 RL Genomics 77:65-70(2001).  
 DR EMBL: AB051623; BAB54951.1;  
 KW Ribosomal protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 14 AA: 1744 MW; 64ED243E9AED663B CRC64;

Query Match 27.3% Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 III  
 DB 8 KKK 10

## RESULT 23

O15222 O15222 PRELIMINARY: PRT: 14 AA.  
 ID O15222  
 AC O15222;

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC	NCBI_TaxID=9823;
OC	[1]
RP	SEQUENCE
KX	MEDLINE=95132498; PubMed=7831203;
KX	Kawa I., Kito Y., Okada J.;
KL	Prep. Biochem. 24:203-223(1994).
SL	SEQUENCE 14 AA; 1441 MW; C1F10C81590001DD CRC64;
SO	Query Match 27.4%; Score 3; DB 6; Length 14;
	Best Local Similarity 100.0%; Pred. No. 8.5e+03;
	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	2 GSK 4
	1-1
Qb	4 GSK 5
RESULT 26	
Q8UT17	PRELIMINARY; PRT; 14 AA.
ID	Q8UT17;
AC	Q8UT17;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE	Gag protein.
OS	GAG.
ON	Human immunodeficiency virus 1.
OC	Viruses; Retroviruses; Retroviridae; Lentivirus.
OX	NCBI_TaxID=11674;
OC	[1]
RP	SEQUENCE FROM N.A.
RC	STRAINS=00BW2127-214;
KA	Novitsky V.A., Smith H.R., Gilbert P., McLane M.F., Chigwedere P.,
KA	Williamson C., Nung'u I., Klein I., Chang S.-Y., Peter T., Thior I.,
KA	Foley B.F., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,
KA	Marlink R., Lee I.-H., Essex M.;
RT	"HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS
RT	vaccine design."
KL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
EMBL	AF443195; AAL34832.1;
SR	SEQUENCE 14 AA; 1486 MW; 1F9F1F22AA03E20 CRC64;
SO	Query Match 27.3%; Score 3; DB 15; Length 14;
	Best Local Similarity 100.0%; Pred. No. 8.5e+03;
	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	3 GSK 5
	111
Qb	10 GSK 12
RESULT 27	
Q9UC7	PRELIMINARY; PRT; 15 AA.
ID	Q9UC7;
AC	Q9UC7;
DT	01-MAY-2000 (TrEMBLrel. 13, Created)
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Midline (Fragment).
DE	Midline (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC	NCBI_TaxID=9606;
OC	[1]
RP	SEQUENCE
KX	MEDLINE=94059921; PubMed=8241100;
KX	Novotny M.F., Matti T., Mehta R.L., Milner P.G.;
KA	"Identification of novel heparin-releasable proteins, as well as the
RT	cytokines midline and pleiotrophin, in human postheparin plasma.";
KL	Arterioscler. Thromb. 1:1798-1805(1993).
SL	SEQUENCE 15 AA; 1527 MW; C34B68978747AC CRC64;
SO	Query Match 15.0%; Score 3; DB 15; Length 15;
	Best Local Similarity 100.0%; Pred. No. 8.5e+03;
	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	3 GSK 5
	111
Qb	10 GSK 12



162431  
 ID P62431 PRELIMINARY: PRT: 15 AA.  
 AC P62431;  
 DT 01-JUN-2000 (TRENBLER: 14, Created)  
 DT 01-JUN-2000 (TRENBLER: 14, Last sequence update)  
 DT 01-JUN-2000 (TRENBLER: 14, Last annotation update)  
 DE 100 kDa cell wall protein (Fragment).  
 DE Truncated nei protein.  
 GN Nicotiana glauca (Common tobacco).  
 OS Eukaryota; Viridiplantae; Streptophyta; Erythrophytas; Tracheophyta.  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
 OC Asterales; Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID:4097;  
 RN [1]  
 RP SEQUENCE  
 RC STRAIN: CV. PELL HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Bacterisera D., Slates A.P.,  
 RA Wojtaszek P., Howell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture."  
 RL Planta 200:3-3(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall;  
 KW NUNTER;  
 FT  
 SQ SEQUENCE 15 AA: 1694 MW: 5F4B62E346187626 (52964)  
 Query Match 27.3% Score 3; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 4 KKK 6

RESULT 35  
 ID P62431 PRELIMINARY: PRT: 15 AA.  
 AC P62431;  
 DT 01-JUN-2000 (TRENBLER: 14, Created)  
 DT 01-JUN-2000 (TRENBLER: 14, Last sequence update)  
 DT 01-JUN-2000 (TRENBLER: 14, Last annotation update)  
 DE 100 kDa cell wall protein (Fragment).  
 DE Truncated nei protein.  
 GN Nicotiana glauca (Common tobacco).  
 OS Eukaryota; Viridiplantae; Streptophyta; Erythrophytas; Tracheophyta.  
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots;  
 OC Asterales; Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID:4097;  
 RN [1]  
 RP SEQUENCE  
 RC STRAIN: CV. PELL HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Bacterisera D., Slates A.P.,  
 RA Wojtaszek P., Howell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture."  
 RL Planta 200:3-3(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall;  
 KW NUNTER;  
 FT  
 SQ SEQUENCE 15 AA: 1694 MW: 5F4B62E346187626 (52964)  
 Query Match 27.3% Score 3; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7  
 DB 11 KKK 13

RESULT 34

Q8USK4  
 ID Q8USK4 PRELIMINARY: PRT: 15 AA.  
 AC Q8USK4;  
 DT 01-MAR-2002 (TRENBLER: 20, Created)  
 DT 01-MAR-2002 (TRENBLER: 20, Last sequence update)  
 DT 01-OCT-2002 (TRENBLER: 22, Last annotation update)  
 DE Truncated nei protein.  
 GN NEF.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: LTS 700;  
 RA Ashton D., Rhodes D., Solomon A., Deacon N., Satchell C., Carr A.,  
 RA Cooper D., Hill R., Stewart G., Kaldor J.;  
 RT "Viral diversity in the nef/LTR region of the HIV-1 genome:  
 RT associations with long-term nonprogression.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall;  
 KW NUNTER;  
 FT  
 SQ SEQUENCE 15 AA: 1648 MW: 65D594E957E4A19D (CRC64)  
 Query Match 27.3% Score 3; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5  
 DB 2 GKK 4

RESULT 35  
 ID Q8USK4 PRELIMINARY: PRT: 15 AA.  
 AC Q8USK4;  
 DT 01-MAR-2002 (TRENBLER: 20, Created)  
 DT 01-MAR-2002 (TRENBLER: 20, Last sequence update)  
 DT 01-OCT-2002 (TRENBLER: 22, Last annotation update)  
 DE Truncated nei protein.  
 GN NEF.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID:11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN: LTS 700; LTS 70a, LTS 70c, LTS 70d, and LTS 70e;  
 RA Ashton D., Rhodes D., Solomon A., Deacon N., Satchell C., Carr A.,  
 RA Cooper D., Hill R., Stewart G., Kaldor J.;  
 RT "Viral diversity in the nef/LTR region of the HIV-1 genome:  
 RT associations with long-term nonprogression.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 KW Cell wall;  
 KW NUNTER;  
 FT  
 SQ SEQUENCE 15 AA: 1717 MW: 65D594E957E4A02D (CRC64)  
 Query Match 27.3% Score 3; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9e-03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKK 5  
 DB 2 GKK 4

RESULT 34  
 ID Q8USK4 PRELIMINARY: PRT: 8 AA.  
 AC Q8USK4;  
 DT 01-MAY-2000 (TRENBLER: 13, Created)  
 DT 01-MAY-2000 (TRENBLER: 13, Last sequence update)

QY 5 KKK 7  
 DB 11 KKK 13

```

DT 01-MAY-2000 (TrEMBLrel. 13, last annotation update)
DE Putative 1530 transposase (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
ON NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=V295b;
RC MEDLINE=99194747; PubMed=10094716;
RA Kato A., Brumme-Smith J., Whitfield G.
RI "Conserved organization in the cps gene clusters for expression of
RI Escherichia coli group 1 K antigens: relationship to the colanic acid
RI biosynthesis locus and the cps genes from Klebsiella pneumoniae."
RL J. Bacteriol. 181:2337-2343(1999).
DR EMBL: AF118231; AAD30008.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 7 AE 8

RESULT 39
P72279 PRELIMINARY; PRI: 8 AA
AC P72279;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DI 01-FEB-1997 (TrEMBLrel. 02, last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Biphenyl dioxygenase (Fragment).
GN HPHB.
OS Rhodococcus globerulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus
ON NCBI_TaxID=13008;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asterias J.A., Diaz E., Timmis K.N.;
RI "Evolutionary relationship of the biphenyl dioxygenase of the gram-
RI positive bacterium Rhodococcus globerulus to multicompnent
RI dioxygenases of gram-negative bacteria."
RL Gene 156:111-18(1995).
DR EMBL: X80041; CAA56350.1; -.
KW Dioxygenase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 989 MW; FB2DCE1A9D1B41406 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 1 MR 2

RESULT 40
Q9R712 PRELIMINARY; PRI: 8 AA
AC Q9R712;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
GN YQF6.
OS Escherichia coli.

```

```

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
ON NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RC MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RI "A 718-kb DNA sequence of Escherichia coli K-12 Genome Corresponding
RI to the 12.7-28.0 min Region on the Linkage Map."
RL DNA Res. 3:147-155(1996).
DR EMBL: D90705; HAA95310.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 964 MW; DF133BLDD04B476A CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 5 AE 6

RESULT 39
Q9AGP4 PRELIMINARY; PRI: 8 AA
AC Q9AGP4;
DI 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Serine hydroxymethyltransferase (Fragment).
GN GUYA.
OS Arthrobacter sp. lin.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Micrococcaceae; Arthrobacter.
ON NCBI_TaxID=153502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=lin;
RA Meskys R., Harris R.J., Casalte V., Basran J., Scrutton N.S.;
RI "Genetic organization of the genes involved in dimethylglycine and
RI sarcosine degradation in Arthrobacter spp.: implications for glycine
RI betaine catabolism."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF329478; AAK16486.1; -.
KW Methyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 898 MW; 6B1870533372457 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 4 KK 5

RESULT 40
O68485 PRELIMINARY; PRI: 8 AA
AC O68485;
DI 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).

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GN AAPAL.
OS Klebsiella pneumoniae.
GC Plasmid pAQ1000.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
OC Enterobacteriaceae; Klebsiella.
CX NCBI_TaxID=573;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN-K-1;
RX MEDLINE=98287600; PubMed 9624504;
KA Cotton D., Roy P.H.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
RT abc(5')-1g from the integron of a natural multi-resistance plasmid.";
BL Antimicrob. Agents Chemother. 42:1506-1518(1998).
DR EMBL: AF047556; AAC25501.1;
KW Plasmid; Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA: 878 MW: 87065A23B155956 CRC64;

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AE 2
DB 11
3 AE 4

RESULT 41
ID QV3SK0 PRELIMINARY; PRT: 8 AA.
AC QV3SK0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-lactamase repressor Blal (Fragment).
GN BLAL.
OS Staphylococcus epidermidis.
GC Plasmid pST6.
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
CX NCBI_TaxID=1282;
RN [1];
RP SEQUENCE FROM N.A.
KA Sidhu M.S., Hair E., Sorum H., Holtek A.L.;
RT "Genetic linkage between quadruply ammonium compound and beta lactam
RT resistance in Staphylococci isolated from food.";
BL Submitted (MAR-2001) to the EMBL/GenBank/DBJ Databases.
DR EMBL: AY028779; AAK38453.1;
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA: 930 MW: 451250AA142307040;

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 7 KK 8

RESULT 42
ID Q44463 PRELIMINARY; PRT: 8 AA.
AC Q44463;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE Aerobacterium tumefaciens Ti plasmid 9113A and virB4 genes
DE (Fragment).
OS Rhizobiales (rhizobacteria).
GC Plasmid T1.

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OC Bacteria; Proteobacteria; Alphaproteobacteria.
CX NCBI_TaxID=356;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=8015611; PubMed=4658701;
RA Portner S.G., Yancofsky M.F., Nester E.W.;
RT "Molecular characterization of the virD operon from Agrobacterium
RT tumefaciens.";
RL Nucleic Acids Res. 15:7503-7517(1987).
DR EMBL: X06045; CAA29439.1;
KW Plasmid.
FT NON_TER 8
SQ SEQUENCE 8 AA: 857 MW: F8F2C325B33861A6 CRC64;

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CK 5
DB 3 CK 4

RESULT 43
ID Q32560 PRELIMINARY; PRT: 8 AA.
AC Q32560;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Propionate kinase (Fragment).
GN TKCD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=562;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN-W3110;
RX MEDLINE=99449059; PubMed=10520749;
RA Hesslering G., Sawers G.;
RT "The tdcE gene in Escherichia coli W3110 is separated from the rest of
RT the tdc operon by insertion of 155 elements.";
RL DNA Seq. 9:183-188(1998).
DR EMBL: AJ001620; CAA04875.1;
KW Kinase.
FT NON_TER 1
SQ SEQUENCE 6 AA: 1000 MW: 3A505EB04140DC4 CRC64;

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 RA 11
DB 1 RA 2

RESULT 44
ID Q09258 PRELIMINARY; PRT: 8 AA.
AC Q09258;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NifH (Fragment).
GN NIFH.
OS Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
CX NCBI_TaxID=41431;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN-RF-1;

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RX MEDLINE-99231861; PubMed-10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.:
RT "Organization and expression of nitrogen fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RT RF-1."
RL Microbiology 145:743-753(1999).
DR EMBL: AF001760; AAC33369.1;
FT NON_TER 8
SQ SEQUENCE 8 AA; 965 MW; F16B59D0B46C43676964;

Query Match
Best Local Similarity 100.0%; Score 2: 18 2; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MR 10
DB 1 MR 2

RESULT 45
Q56429 PRELIMINARY: PRT: 8 AA.
AC Q56429;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAPDH (Fragment).
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinetococcus; Thermobacteriales; Thermaceae;
CX Thermus.
GX NCBI_TaxId-274;
FN 1;
RP SEQUENCE FROM N.A.
SC STRAIN-Hs-8;
RX MEDLINE-99025722; PubMed-3052437;
RA Bowen D., Littlechild J.A., Forthofer J.E., Watson R.C., Hall L.:
RT "Nucleotide sequence of the phosphoenolpyruvate kinase gene from the
RT extreme thermophile, Thermus thermophilus L-8."
RL Biochem. J. 254:509-517(1989).
DR EMBL: X12464; CAA31005.1;
FT NON_TER 1
SQ SEQUENCE 8 AA; 885 MW; 33CB743A71272467664;

Query Match
Best Local Similarity 100.0%; Score 2: 18 2; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 1
5 KK 6

RESULT 46
Q9R9E0 PRELIMINARY: PRT: 8 AA.
AC Q9R9E0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Stage V sporulation protein E (Fragment).
GX SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
GX NCBI_TaxId-1423;
FN 1;
RP SEQUENCE FROM N.A.
SC STRAIN-168;
RX MEDLINE-94003529; PubMed-4391053;
RA Henriques A.O., de Lencastre H., Piquot J.:
RT "A Bacillus subtilis morphotype cluster that includes SPOVE is
RT homologous to the mra region of Escherichia coli."
RL Biochimie 74:735-748(1992).
DR EMBL: X64258; CAA45556.1;

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FT NON_TER 8
SQ SEQUENCE 8 AA; 893 MW; FE75A1A3321B1A6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2: 18 2; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 4 KK 5

RESULT 47
Q9R5R0 PRELIMINARY: PRT: 8 AA.
AC Q9R5R0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11,500 bp product of ORF4 (Fragment).
OS Shigella dysenteriae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
GX Enterobacteriaceae; Shigella.
GX NCBI_TaxId-622;
FN 1;
RP SEQUENCE.
RX MEDLINE-92085268; PubMed-1560923;
RA Polard P., Piore M.F., Chandler M., Fayet O.:
RT "Programmed translational frameshifting and initiation at an AUU codon
RT in gene expression of bacterial insertion sequence IS911."
RL J. Mol. Biol. 222:465-477(1991).
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; F4C5B9C45AE33336 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2: 18 2; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KK 6
DB 2 KK 3

RESULT 48
P72221 PRELIMINARY: PRT: 8 AA.
AC P72221;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Arginate lyase (Fragment).
GX ALY.
OS Pseudomonas sp. (strain OS-ALG-9).
OC Bacteria; Proteobacteria.
GX NCBI_TaxId-86038;
FN 1;
RP SEQUENCE FROM N.A.
SC STRAIN-OS-ALG-9;
RA Fujiyama K.:
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
FN 12;
RP SEQUENCE FROM N.A.
SC STRAIN-OS-ALG-9;
RX MEDLINE-93329366; PubMed-8336113;
RA Maki H., Mori A., Fujiyama K., Kinoshita S., Yoshida T.:
RT "Cloning, sequence analysis and expression in Escherichia coli of a
RT gene encoding an arginate lyase from Pseudomonas sp. OS-ALG-9."
RL J. Gen. Microbiol. 139:987-993(1993).
DR EMBL: D38469; BAA21704.1;
KW Lyase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 841 MW; 461DDC5A5B041BB CRC64;

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Db 6 RA 7

Search completed: September 30, 2003, 10:18:06  
Job time : 37.6667 secs

Query Match 18.28% Score 21 1P 21 Length 61  
Best Local Similarity 100.00% Pref. No. 8 0-95  
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AE 2  
DB 7 AE 8

RES011 49  
Q9R5U7  
ID Q9R5U7 PRELIMINARY: PR1 8 AA  
AC Q9R5U7  
BT 01 MAY 2000 (TRENBLER1, 14, Created)  
BT 01 MAY 2000 (TRENBLER1, 14, Last sequence update)  
BT 01 JUN 2000 (TRENBLER1, 14, Last annotation update)  
DE 1,4-beta D-glucan glucanohydrolase (EC 3.2.1.4) (Fragment)  
OS Clostridium thermocellum  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium  
CC NCBI\_TaxID:1516  
CX [1]  
RN [1]  
RP SEQUENCE  
RX MEDLINE:94211850; PubMed:1667839  
RA Kozakiec M.P., Fauth U., Kobayashi T., Buskessen N.S., Barker P.L.,  
RA Gaudin A.L.  
RT Purification and characterization of a new endoglucanase from  
RT Clostridium thermocellum.  
RG Biochem J 283:69-73(1992)  
SQ SEQUENCE 8 AA: 823 MW: 82146.00pI:5.96

Query Match 18.28% Score 21 1P 21 Length 61  
Best Local Similarity 100.00% Pref. No. 8 0-95  
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AE 2  
DB 7 AE 8

RES011 50  
Q159J2  
ID Q159J2 PRELIMINARY: PR1 8 AA  
AC Q159J2  
BT 01 NOV 1996 (TRENBLER1, 61, Created)  
BT 01 NOV 1996 (TRENBLER1, 61, Last sequence update)  
BT 01 DEC 2001 (TRENBLER1, 19, Last annotation update)  
DE Cloned XP3311A (Fragment)  
OS Homo sapiens (Human)  
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo  
CX NCBI\_TaxID:9606  
RN [1]  
RP SEQUENCE FR M N A  
RT TISSUE-Placenta  
RA Lee C., G. Vazdani A., Weinert M., Bercy J., Chirault G.A., Xu H.,  
RA Chirault M.L., Chirault G.A., Baidya A., Gaudin A.L., Gaudin A.L.,  
RA Caskey C.T.  
RT Isolation of chromosome-specific genes from a cell produced by  
RT arrayed cDNAs and cosmid libraries.  
RI Hum Mol Genet 14:100-105(1995)  
DR EMBL:U32579; AAA73890.1  
FT NON TER 1  
FT NON TER 8  
FT NON TER 8  
SQ SEQUENCE 8 AA: 931 MW: 95044.30pI:5.96

Query Match 18.28% Score 21 1P 21 Length 61  
Best Local Similarity 100.00% Pref. No. 8 0-95  
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 10 RA 11

GenCore version 5.1.6  
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OW protein protein search, using sw model

Run on: September 30, 2003, 10:07:00 : Search time 11.8333 seconds  
(without alignment)  
42.533 Million cell updates/sec

Title: US-09-787-443-19

Perfect score: 11

Sequence: 1 AEGKKKKMRA 11

Scoring table: 3.160

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 6

Total number of hits satisfying chosen parameters: 7859

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	6	54.5	9	3	US-08-135-9045-5	Sequence 5, Appl
2	6	54.5	9	3	US-08-135-9045-6	Sequence 6, Appl
3	6	54.5	9	3	US-08-135-9045-7	Sequence 7, Appl
4	6	54.5	9	3	US-08-135-9045-8	Sequence 8, Appl
5	6	54.5	9	3	US-08-135-9045-9	Sequence 9, Appl
6	6	54.5	9	3	US-08-135-9045-10	Sequence 10, Appl
7	6	54.5	9	3	US-08-135-9045-11	Sequence 11, Appl
8	6	54.5	9	3	US-08-135-9045-12	Sequence 12, Appl
9	6	54.5	9	3	US-08-135-9045-13	Sequence 13, Appl
10	6	54.5	9	3	US-08-135-9045-14	Sequence 14, Appl
11	6	54.5	9	3	US-08-135-9045-15	Sequence 15, Appl
12	6	54.5	9	3	US-08-135-9045-16	Sequence 16, Appl
13	6	54.5	9	3	US-08-135-9045-17	Sequence 17, Appl
14	6	54.5	9	3	US-08-135-9045-18	Sequence 18, Appl
15	6	54.5	9	3	US-08-135-9045-19	Sequence 19, Appl
16	6	54.5	9	3	US-08-135-9045-20	Sequence 20, Appl
17	6	54.5	9	3	US-08-135-9045-21	Sequence 21, Appl
18	6	54.5	9	3	US-08-135-9045-22	Sequence 22, Appl
19	6	54.5	9	3	US-08-135-9045-23	Sequence 23, Appl
20	6	54.5	9	3	US-08-135-9045-24	Sequence 24, Appl
21	6	54.5	9	3	US-08-135-9045-25	Sequence 25, Appl
22	6	54.5	9	3	US-08-135-9045-26	Sequence 26, Appl
23	6	54.5	9	3	US-08-135-9045-27	Sequence 27, Appl
24	6	54.5	9	3	US-08-135-9045-28	Sequence 28, Appl
25	6	54.5	9	3	US-08-135-9045-29	Sequence 29, Appl
26	6	54.5	9	3	US-08-135-9045-30	Sequence 30, Appl
27	6	54.5	9	3	US-08-135-9045-31	Sequence 31, Appl

101	4	36.4	10	3	US-08-159-439A-1164	Sequence 1164, App	174	4	36.4	15	2	US-08-841-483-23	Sequence 23, Appl
102	4	36.4	10	3	US-07-978-674B-49	Sequence 49, Appl	175	4	36.4	15	3	US-08-369-643-76	Sequence 76, Appl
103	4	36.4	10	3	US-07-978-674B-49	Sequence 49, Appl	176	4	36.4	15	3	US-08-479-744A-19	Sequence 19, Appl
104	4	36.4	10	3	US-09-208-145A-54	Sequence 54, Appl	177	4	36.4	15	3	US-08-469-141A-6	Sequence 6, Appl
105	4	36.4	10	3	US-09-208-366-45	Sequence 45, Appl	178	4	36.4	15	3	US-08-280-757B-19	Sequence 19, Appl
106	4	36.4	10	4	US-09-556-011-54	Sequence 54, Appl	179	4	36.4	15	3	US-09-382-911-23	Sequence 23, Appl
107	4	36.4	10	4	US-08-594-043A-42	Sequence 42, Appl	180	4	36.4	15	4	US-09-230-405-6	Sequence 6, Appl
108	4	36.4	10	4	US-08-584-043A-42	Sequence 42, Appl	181	4	36.4	15	4	US-09-459-956-16	Sequence 16, Appl
109	4	36.4	10	4	US-08-584-043A-42	Sequence 42, Appl	182	4	36.4	15	4	US-08-584-043A-42	Sequence 9, Appl
110	4	36.4	10	4	US-09-019-434A-58	Sequence 58, Appl	183	4	36.4	15	4	US-08-584-043A-42	Sequence 47, Appl
111	4	36.4	10	4	US-09-019-434A-58	Sequence 58, Appl	184	4	36.4	15	4	US-08-584-043A-42	Sequence 103, App
112	4	36.4	10	4	US-09-019-434A-58	Sequence 58, Appl	185	4	36.4	15	4	US-09-120-653D-30	Sequence 30, Appl
113	4	36.4	10	4	US-09-019-434A-58	Sequence 58, Appl	186	4	36.4	15	4	US-09-050-811-6	Sequence 6, Appl
114	4	36.4	10	5	PCT-US95-02431-B	Sequence 8, Appl	187	4	36.4	15	4	US-09-050-811-6	Sequence 11, Appl
115	4	36.4	10	5	PCT-US95-02431-B	Sequence 8, Appl	188	4	36.4	15	4	US-09-101-751A-4	Sequence 4, Appl
116	4	36.4	10	6	5196404-28	Patent No. 5,196404	189	4	36.4	15	4	US-09-082-358B-24	Sequence 24, Appl
117	4	36.4	10	6	5240848-2	Patent No. 5,240848	190	4	36.4	15	4	US-09-082-358B-24	Sequence 62, Appl
118	4	36.4	10	6	5433940-25	Patent No. 5,433940	191	4	36.4	15	4	US-09-129-192C-63	Sequence 63, Appl
119	4	36.4	10	6	5514565-10	Patent No. 5,514565	192	4	36.4	15	4	US-09-574-749B-54	Sequence 54, Appl
120	4	36.4	11	1	US-07-694-983-15	Sequence 15, Appl	193	4	36.4	15	4	US-09-434-354-30	Sequence 30, Appl
121	4	36.4	11	3	US-08-592-500-9	Sequence 9, Appl	194	4	36.4	15	5	PCT-US95-00147-76	Sequence 76, Appl
122	4	36.4	11	3	US-08-970-833-8	Sequence 8, Appl	195	4	36.4	15	5	PCT-US95-13794-6	Sequence 6, Appl
123	4	36.4	11	4	US-08-193-006-34	Sequence 34, Appl	196	3	27.3	8	1	US-07-872-644-2	Sequence 2, Appl
124	4	36.4	11	4	US-08-584-043A-5	Sequence 5, Appl	197	3	27.3	8	1	US-07-931-931A-5	Sequence 5, Appl
125	4	36.4	11	4	US-08-584-043A-43	Sequence 43, Appl	198	3	27.3	8	1	US-08-212-433A-20	Sequence 20, Appl
126	4	36.4	11	4	US-08-584-043A-99	Sequence 99, Appl	199	3	27.3	8	1	US-08-424-567-4	Sequence 4, Appl
127	4	36.4	11	4	US-09-382-358B-1	Sequence 1, Appl	200	3	27.3	8	1	US-08-002-466-10	Sequence 10, Appl
128	4	36.4	11	4	US-09-574-749B-54	Sequence 54, Appl	201	3	27.3	8	1	US-08-297-494-2	Sequence 2, Appl
129	4	36.4	11	5	PCT-US94-07644A-59	Sequence 49, Appl	202	3	27.3	8	1	US-08-146-152-7	Sequence 7, Appl
130	4	36.4	11	6	5219749-40	Patent No. 5,219749	203	3	27.3	8	1	US-08-146-152-9	Sequence 9, Appl
131	4	36.4	12	1	US-08-413-681A-29	Sequence 29, App	204	3	27.3	8	1	US-08-146-152-9	Sequence 10, Appl
132	4	36.4	12	3	US-08-742-243-4	Sequence 4, Appl	205	3	27.3	8	1	US-08-297-510-2	Sequence 2, Appl
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1  REFERENCE/DOCKET NUMBER: ABIC-001/020S
2  TELECOMMUNICATION INFORMATION:
3  TELEPHONE: (415)843-5000
4  TELEFAX: (415)857-0663
5  TELEFAX: (415)857-0663
6  INFORMATION FOR SEQ ID NO: 5:
7  SEQUENCE CHARACTERISTICS:
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11  MOLECULE TYPE: peptide
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49  Sequence 6; Application US/08105904B
50  Patent No. 6001364
51  GENERAL INFORMATION:
52  APPLICANT: Rose, Keith
53  TITLE OF INVENTION: HETERO-POLYXIME COMPOUNDS AND THEIR
54  PREPARATION BY PARALLEL ASSEMBLY
55  NUMBER OF SEQUENCES: 24
56  CORRESPONDENCE ADDRESS:
57  ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
58  STREET: 5 Palo Alto Square, 4000 El Camino Real
59  CITY: Palo Alto
60  STATE: California
61  COUNTRY: U.S.A.
62  ZIP: 94306
63  COMPUTER READABLE FORM:
64  MEDIUM TYPE: Floppy disk
65  OPERATING SYSTEM: IBM PC compatible
66  SOFTWARE: PatentIn Release #1.0, Version #1.0
67  CURRENT APPLICATION DATA:
68  APPLICATION NUMBER: US/08/105-904B
69  FILING DATE: 31-AUG-1993
70  CLASSIFICATION: 424

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1  PRIOR APPLICATION DATA:
2  APPLICATION NUMBER: US 08/057,594
3  FILING DATE: 05-MAY-1993
4  CLASSIFICATION: 424
5  ATTORNEY/AGENT INFORMATION:
6  NAME: Neeley, Richard L.
7  REGISTRATION NUMBER: 30,042
8  REFERENCE/DOCKET NUMBER: ABIC-001/020S
9  TELECOMMUNICATION INFORMATION:
10  TELEPHONE: (415)843-5000
11  TELEFAX: (415)857-0663
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13  INFORMATION FOR SEQ ID NO: 6:
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56  Sequence 8; Application US/08105904B
57  Patent No. 6001364
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59  APPLICANT: Rose, Keith
60  TITLE OF INVENTION: HETERO-POLYXIME COMPOUNDS AND THEIR
61  PREPARATION BY PARALLEL ASSEMBLY
62  NUMBER OF SEQUENCES: 24
63  CORRESPONDENCE ADDRESS:
64  ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
65  STREET: 5 Palo Alto Square, 4000 El Camino Real
66  CITY: Palo Alto
67  STATE: California
68  COUNTRY: U.S.A.
69  ZIP: 94306
70  COMPUTER READABLE FORM:
71  MEDIUM TYPE: Floppy disk

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1  COMPUTER: IBM PC compatible
2  OPERATING SYSTEM: PC-DOS/MS-DOS
3  SOFTWARE: Patent Release #1.0, Version #1.25
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: US/08/105-904B
6  FILING DATE: 31-AUG-1993
7  CLASSIFICATION: 424
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 08/057,544
10 FILING DATE: 05-MAY-1994
11 CLASSIFICATION: 424
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Neeley, Richard L.
14 REGISTRATION NUMBER: 30,092
15 REFERENCE/DOCKET NUMBER: ABIC-001/020S
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (415)843-5000
18 TELEFAX: (415)857-0663
19 TELEX: 380816 Coolvypa
20 INFORMATION FOR SEQ ID NO: 1:
21 LENGTH: 9 amino acids
22 TYPE: amino acid
23 TOPOLOGY: linear
24 MOLECULE TYPE: peptide
25 HYPOTHETICAL: NO
26 FEATURE:
27 NAME/KEY: Modified-site
28 LOCATION: 1
29 OTHER INFORMATION: Bronchodilator, Gly
30 FEATURE:
31 NAME/KEY: Modified-site
32 LOCATION: 4
33 OTHER INFORMATION: Lys-Gly
34 FEATURE:
35 NAME/KEY: Modified-site
36 LOCATION: 5
37 OTHER INFORMATION: Lys-Gly
38 FEATURE:
39 NAME/KEY: Modified-site
40 LOCATION: 6
41 OTHER INFORMATION: Lys-Gly
42 FEATURE:
43 NAME/KEY: Modified-site
44 LOCATION: 7
45 OTHER INFORMATION: Lys-Gly
46 FEATURE:
47 NAME/KEY: Modified-site
48 LOCATION: 8
49 OTHER INFORMATION: Lys-Gly
50 US-08-105-904B-8

```

```

Query Match: 54.5% Score 6; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GCKKKK 8
11111
DB 2 GCKKKK 7

```

```

RESULT: 4
US-08-105-904B-20
Sequence 20, Application US/08/05904B
Patent No. 6001364
GENERAL INFORMATION:
APPLICANT: Rose, Keith
APPLICANT: Offord, Robin
TITLE OF INVENTION: HETERO-POLYMER COMPOUNDS AND THEIR
PREPARATION BY PASSENGER ASSEMBLY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Ricks & S. P.C.

```

```

1  STREET: 5 Palo Alto Square, 3000 El Camino Real
2  CITY: Palo Alto
3  STATE: California
4  COUNTRY: U.S.A.
5  ZIP: 94306
6  COMPUTER READABLE FORM:
7  MEDIUM TYPE: Floppy disk
8  COMPUTER: IBM PC compatible
9  OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent Release #1.0, Version #1.25
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/105-904B
13 FILING DATE: 31-AUG-1993
14 CLASSIFICATION: 424
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/057,544
17 FILING DATE: 05-MAY-1994
18 CLASSIFICATION: 424
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Neeley, Richard L.
21 REGISTRATION NUMBER: 30,092
22 REFERENCE/DOCKET NUMBER: ABIC-001/020S
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (415)843-5000
25 TELEFAX: (415)857-0663
26 TELEX: 380816 Coolvypa
27 INFORMATION FOR SEQ ID NO: 20:
28 LENGTH: 9 amino acids
29 TYPE: amino acid
30 TOPOLOGY: linear
31 MOLECULE TYPE: peptide
32 HYPOTHETICAL: NO
33 FEATURE:
34 NAME/KEY: Modified-site
35 LOCATION: 4
36 OTHER INFORMATION: Lys-BAC
37 FEATURE:
38 NAME/KEY: Modified-site
39 LOCATION: 5
40 OTHER INFORMATION: Lys-BAC
41 FEATURE:
42 NAME/KEY: Modified-site
43 LOCATION: 6
44 OTHER INFORMATION: Lys-BAC
45 FEATURE:
46 NAME/KEY: Modified-site
47 LOCATION: 7
48 OTHER INFORMATION: Lys-BAC
49 FEATURE:
50 NAME/KEY: Modified-site
51 LOCATION: 8
52 OTHER INFORMATION: Lys-BAC
53 FEATURE:
54 NAME/KEY: Modified-site
55 LOCATION: 9
56 OTHER INFORMATION: Gly-PAM
57 US-08-105-904B-20

```

```

Query Match: 54.5% Score 6; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GCKKKK 8
11111
DB 2 GCKKKK 7

```

```

RESULT: 5
US-08-105-904B-22
Sequence 22, Application US/08105904B
Patent No. 6001364
GENERAL INFORMATION:

```



```

: APPLICANT: Rose, Keith
: APPLICANT: Offord, Robin
: TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square, 3000 El Camino Real
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/105,904B
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,042
: REFERENCE/DOCKET NUMBER: ABIC 001/0205
: TELEPHONE: (415)843-5000
: TELEFAX: (415)857-0663
: TELEX: 380816 CooleyPA
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Lys-Boc-Ser(benzyl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: Lys-Boc-Ser(benzyl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6
: OTHER INFORMATION: Lys-Boc-Ser(benzyl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7
: OTHER INFORMATION: Lys-Boc-Ser(benzyl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys-Boc-Ser(benzyl)
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 9
: OTHER INFORMATION: Gly-PAM
: US-08 105-904B-22

```

```

Query Match 54.5% Score 6: 0b 4: Length 9:
Best Local Similarity 100.0% Prod No. 2.5e+05
Matches 6: Conservative 0: Mismatches 0: Indels 0:

```

```

QY 3 GKKKK 8
DB 2 GKKKK 7

```

```

: RESULT 6
: US-08-105-904B-23
: Sequence 23, Application US/08105904B
: Patent No. 6001304
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: APPLICANT: Offord, Robin
: TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square, 3000 El Camino Real
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/105,904B
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: ABIC-001/0205
: TELEPHONE: (415)843-5000
: TELEFAX: (415)857-0663
: TELEX: 380816 CooleyPA
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: bromoacetyl-Gly
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified site
: LOCATION: 6
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7
: OTHER INFORMATION: Lys-Boc-Ser
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys-Boc-Ser
: US-08-105-904B-23

```

```

Query Match      54.5%; Score 6; Db 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCKKKK 8
Db 2 GCKKKK 7

RESULT 7
US-08-114-877A-5
: Sequence 5, Application US/08114877A
: Patent No. 6174530
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: APPLICANT: Offord, Robin
: TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/114,877A
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Neeley, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: ABIC 0.1/01US
: TELEPHONE: (415) 843 5070
: TELEFAX: (415) 857-0663
: TELEFAX: 380816 Coolcypa
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEetical: NO
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: ACA-Gly
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Lys-AcA
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: Lys-ACA
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6
: OTHER INFORMATION: Lys-AcA
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7

```

```

: OTHER INFORMATION: Lys-AcA
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys AOA
US-08-114-877A-5
Query Match      54.5%; Score 6; Db 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCKKKK 8
Db 2 GCKKKK 7

RESULT 6
US-08-114-877A 6
: Sequence 6, Application US/08114877A
: Patent No. 6174530
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: APPLICANT: Offord, Robin
: TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
: TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/114,877A
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Neeley, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: ABIC-G01/01US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 843 5070
: TELEFAX: (415) 857 0663
: TELEFAX: 380816 Coolcypa
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEtical: NO
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: GXL-Gly
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Lys-GXL
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: Lys-GXL

```

```

FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: Lys-GXL
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: Lys-GXL
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: Lys-GXL
US-08-114-877A-6

```

```

Query Match: 54.5% Score 6: DB 6: Length 9:
Best Local Similarity 100.0% Pred. No. 2.5e+05
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

```

QY 3 GKKKK 8
    IIIII
DB 2 GKKKK 7

```

```

RESULT 9
US-08-114-877A-8
: Sequence 8, Application US/08114877A
: Patent No. 6174530
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,092
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 843 5070
: TELEFAX: (415) 857-0663
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Lys-GXL
: FEATURE:

```

```

: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: Lys-GXL
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 6
: OTHER INFORMATION: Lys-GXL
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7
: OTHER INFORMATION: Lys-GXL
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys-GXL
US-08-114-877A-8
Query Match: 54.5% Score 6: DB 3: Length 9:
Best Local Similarity 100.0% Pred. No. 2.5e+05:
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 GKKKK 8
    IIIII
DB 2 GKKKK 7
RESULT 10
US-08-114-877A-13
: Sequence 13, Application US/08114877A
: Patent No. 6174530
: GENERAL INFORMATION:
: APPLICANT: Rose, Keith
: TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
: PREPARATION BY PARALLEL ASSEMBLY
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
: STREET: 5 Palo Alto Square
: CITY: Palo Alto
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 94036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/114,877A
: FILING DATE: 31-AUG-1993
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/057,594
: FILING DATE: 05-MAY-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Nealey, Richard L.
: REGISTRATION NUMBER: 30,092
: REFERENCE/DOCKET NUMBER: ABIC-001/0105
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 843 5070
: TELEFAX: (415) 857-0663
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: Modified-site

```

```

1 LOCATION: 4
2 OTHER INFORMATION: Lys-Boc
3 FEATURE:
4 NAME/KEY: Modified-site
5 LOCATION: 5
6 OTHER INFORMATION: Lys-Boc
7 FEATURE:
8 NAME/KEY: Modified-site
9 LOCATION: 6
10 OTHER INFORMATION: Lys-Boc
11 FEATURE:
12 NAME/KEY: Modified-site
13 LOCATION: 7
14 OTHER INFORMATION: Lys-Boc
15 FEATURE:
16 NAME/KEY: Modified-site
17 LOCATION: 8
18 OTHER INFORMATION: Lys-Boc
19 FEATURE:
20 NAME/KEY: Modified-site
21 LOCATION: 9
22 OTHER INFORMATION: Gly-PAM
23 US-08-114-877A-15

```

```

Query Match 54.5% Score 6; DB 3; Length 9;
Best Local Similarity 100.0%; Prod No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GKKKKK 8
DB 2 GKKKKK 7

```

## RESULT 11

```

US-08-114-877A-15
Sequence 15, Application US/08:114877A
Patent No. 6174530
GENERAL INFORMATION:

```

```

APPLICANT: Rose, Keith
TITLE OF INVENTION: HOMOGENEOUS POLY(AMINE) COMPOSITIONS AND THEIR
PREPARATION BY PARALLEL ASSEMBLY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94306

```

## COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,877A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 424

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,594
FILING DATE: 05-MAY-1993
CLASSIFICATION: 424

```

## ATTORNEY/AGENT INFORMATION:

```

NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: ABIC 001/01/05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843 5070
TELEFAX: (415) 857-0663
TELEX: 480816 CooleyPA
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: Lys-Boc-Set (benzyl)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: Lys-Boc-Set (benzyl)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: Lys-Boc-Set (benzyl)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: Lys-Boc-Set (benzyl)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: Lys-Boc-Set (benzyl)
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: Gly-ORZ PAM
US-08-114-877A-15

```

```

Query Match 54.5% Score 6; DB 3; Length 9;
Best Local Similarity 100.0%; Prod No. 2.5e-05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GKKKKK 8
DB 2 GKKKKK 7

```

## RESULT 12

```

US-08-105-904B-7
Sequence 7, Application US/08:105904B
Patent No. 6001464
GENERAL INFORMATION:

```

```

APPLICANT: Rose, Keith
TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR
PREPARATION BY PARALLEL ASSEMBLY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square, 1000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94306

```

## COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,904B
FILING DATE: 31-AUG-1993
CLASSIFICATION: 424

```

## PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: US 08/057,594
FILING DATE: 05-MAY-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092

```

1 REFERENCE/DOCKET NUMBER: ABIC 001/0205  
 2 TELECOMMUNICATION INFORMATION:  
 3 TELEPHONE: (415)843-5000  
 4 TELEFAX: (415)857-0663  
 5 TELE: 380816 CooleyPA  
 6 INFORMATION FOR SEQ ID NO: 7:  
 7 SEQUENCE CHARACTERISTICS:  
 8 LENGTH: 10 amino acids  
 9 TYPE: amino acid  
 10 TOPOLOGY: linear  
 11 MOLECULE TYPE: peptide  
 12 HYPOTHETICAL: NO  
 13 FEATURE:  
 14 NAME/KEY: Modified site  
 15 LOCATION: 5  
 16 OTHER INFORMATION: Lys-Serine  
 17 FEATURE:  
 18 NAME/KEY: Modified-site  
 19 LOCATION: 6  
 20 OTHER INFORMATION: Lys-Serine  
 21 FEATURE:  
 22 NAME/KEY: Modified site  
 23 LOCATION: 7  
 24 OTHER INFORMATION: Lys-Serine  
 25 FEATURE:  
 26 NAME/KEY: Modified site  
 27 LOCATION: 8  
 28 OTHER INFORMATION: Lys-Serine  
 29 FEATURE:  
 30 NAME/KEY: Modified-site  
 31 LOCATION: 9  
 32 OTHER INFORMATION: Lys-Serine  
 33 US 08-105-904B-7

Query Match 54.5%; Score 6; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 8  
 1111  
 DB 3 GKKKK 8

RESULT 14  
 US-08-114-877A-7  
 ? Sequence 7, Application US/08114877A  
 ? Patent No. 6174530  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Rose, Keith  
 ? TITLE OF INVENTION: HOMOCENES POLYMERIZATION BY PARALLEL ASSEMBLY  
 ? NUMBER OF SEQUENCES: 15  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 ? STREET: 5 Palo Alto Square  
 ? CITY: Palo Alto  
 ? STATE: California  
 ? COUNTRY: U.S.A.  
 ? ZIP: 94306  
 ? COMPUTER READABLE FORM:  
 ? MEDIUM TYPE: Floppy disk  
 ? COMPUTER: IBM PC compatible  
 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 ? SOFTWARE: PatentIn Release #1.0, Version #1.2  
 ? CURRENT APPLICATION DATA:  
 ? APPLICATION NUMBER: US/08/114,877A  
 ? FILING DATE: 31-AUG-1993  
 ? CLASSIFICATION: 424  
 ? PRIOR APPLICATION DATA:  
 ? APPLICATION NUMBER: US 08/057,154  
 ? FILING DATE: 05-MAY-1993  
 ? CLASSIFICATION: 424

1 ATTORNEY/AGENT INFORMATION:  
 2 NAME: Neeley, Richard L.  
 3 REGISTRATION NUMBER: 30,092  
 4 REFERENCE/DOCKET NUMBER: ABIC-001/0105  
 5 TELECOMMUNICATION INFORMATION:  
 6 TELEPHONE: (415) 843 5070  
 7 TELEFAX: (415) 857-0663  
 8 TELE: 380816 CooleyPA  
 9 INFORMATION FOR SEQ ID NO: 7:  
 10 SEQUENCE CHARACTERISTICS:  
 11 LENGTH: 10 amino acids  
 12 TYPE: amino acid  
 13 TOPOLOGY: linear  
 14 MOLECULE TYPE: peptide  
 15 HYPOTHETICAL: NO  
 16 FEATURE:  
 17 NAME/KEY: Modified site  
 18 LOCATION: 5  
 19 OTHER INFORMATION: Lys-Serine  
 20 FEATURE:  
 21 NAME/KEY: Modified site  
 22 LOCATION: 6  
 23 OTHER INFORMATION: Lys-Serine  
 24 FEATURE:  
 25 NAME/KEY: Modified-site  
 26 LOCATION: 7  
 27 OTHER INFORMATION: Lys-Serine  
 28 FEATURE:  
 29 NAME/KEY: Modified-site  
 30 LOCATION: 8  
 31 OTHER INFORMATION: Lys-Serine  
 32 FEATURE:  
 33 NAME/KEY: Modified site  
 34 LOCATION: 9  
 35 OTHER INFORMATION: Lys-Serine  
 36 US-08-114-877A-7  
 37 Query Match 54.5%; Score 6; DB 3; Length 10;  
 38 Best Local Similarity 100.0%; Pred. No. 2.8;  
 39 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 40 QY 3 GKKKK 8  
 41 1111  
 42 DB 3 GKKKK 8  
 43 RESULT 14  
 44 US-08-105-904B-9  
 45 ? Sequence 9, Application US/08105904B  
 46 ? Patent No. 6001364  
 47 ? GENERAL INFORMATION:  
 48 ? APPLICANT: Rose, Keith  
 49 ? TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR  
 50 ? PREPARATION BY PARALLEL ASSEMBLY  
 51 ? NUMBER OF SEQUENCES: 24  
 52 ? CORRESPONDENCE ADDRESS:  
 53 ? ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 54 ? STREET: 5 Palo Alto Square, 3000 El Camino Real  
 55 ? CITY: Palo Alto  
 56 ? STATE: California  
 57 ? COUNTRY: U.S.A.  
 58 ? ZIP: 94306  
 59 ? COMPUTER READABLE FORM:  
 60 ? MEDIUM TYPE: Floppy disk  
 61 ? COMPUTER: IBM PC compatible  
 62 ? OPERATING SYSTEM: PC-DOS/MS-DOS  
 63 ? SOFTWARE: PatentIn Release #1.0, Version #1.25  
 64 ? CURRENT APPLICATION DATA:  
 65 ? APPLICATION NUMBER: US/08/105,904B  
 66 ? FILING DATE: 31-AUG-1993  
 67 ? CLASSIFICATION: 424  
 68 ? PRIOR APPLICATION DATA:



Db 2 GSKKKK 7

RESULT 16

US-08-114-877A-9

Sequence 9, Application US/08114877A

Patent No. 6174530

GENERAL INFORMATION:

APPLICANT: Rose, Keith

APPLICANT: Offord, Robin

TITLE OF INVENTION: HOMOGENOUS POLYYOXIME COMPOSITIONS AND THEIR

PREPARATION BY PARALLEL ASSEMBLY

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: California

COUNTRY: U.S.A.

ZIP: 94036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/114-877A

FILING DATE: 31-AUG-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/057,594

FILING DATE: 05-MAY-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Neeley, Richard L.

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: ABIC-061/010US

TELEPHONE: (415) 843 5070

TELEFAX: (415) 857-0663

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: GLX Gly

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: Lys-GLX

FEATURE:

NAME/KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: Lys-GLX

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6

OTHER INFORMATION: Lys-GLX

FEATURE:

NAME/KEY: Modified-site

LOCATION: 7

OTHER INFORMATION: Lys-GLX

FEATURE:

NAME/KEY: Modified-site

LOCATION: 8

OTHER INFORMATION: Lys-GLX

FEATURE:

NAME/KEY: Modified-site

LOCATION: 9

OTHER INFORMATION: Lys-GLX

FEATURE:

NAME/KEY: Modified-site

LOCATION: 10

OTHER INFORMATION: Lys-GLX

US-08-114-877A-9

Query Match 54.5% Score 6; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GSKKKK 8

Db 2 GSKKKK 7

RESULT 17

US-08-114-877A 14

Sequence 14, Application US/08114877A

Patent No. 6174530

GENERAL INFORMATION:

APPLICANT: Rose, Keith

APPLICANT: Offord, Robin

TITLE OF INVENTION: HOMOGENOUS POLYYOXIME COMPOSITIONS AND THEIR

PREPARATION BY PARALLEL ASSEMBLY

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooley Godward Castro Huddleson & Tatum

STREET: 5 Palo Alto Square

CITY: Palo Alto

STATE: California

COUNTRY: U.S.A.

ZIP: 94036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/114-877A

FILING DATE: 31-AUG-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/057,594

FILING DATE: 05-MAY-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Neeley, Richard L.

REGISTRATION NUMBER: 30,092

REFERENCE/DOCKET NUMBER: ABIC-061/010US

TELEPHONE: (415) 843 5070

TELEFAX: (415) 857-0663

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Modified-site

LOCATION: 4

OTHER INFORMATION: Lys-BOC

FEATURE:

NAME/KEY: Modified-site

LOCATION: 5

OTHER INFORMATION: Lys-B-C

FEATURE:

NAME/KEY: Modified-site

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: LOCATION: 6
: OTHER INFORMATION: Lys-Boc
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 7
: OTHER INFORMATION: Lys-Boc
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: Lys-Boc
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 9
: OTHER INFORMATION: Lys-Boc
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 10
: OTHER INFORMATION: Lys-Boc
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 11
: OTHER INFORMATION: Gly-PAM
US 08-114-877A-14

Query Match          54.5%; Score 6; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 8
Db 2 GKKKK 7

RESULT 18
US 08-615-181-67
: Sequence 67, Application US/08615181
: Patent No. 5756666
: GENERAL INFORMATION:
: APPLICANT: MASAFUMI, TAKIUCHI
: TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE
: TITLE OF INVENTION: RESPONSE TO HIV AND AID1 AGENT FOR PREVENTING AND
: NUMBER OF SEQUENCES: 115
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: OBLOM, SPIVAK, MOULLELAND, MAIER & NEUSTALT,
: STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
: CITY: ARLINGTON
: STATE: VA
: COUNTRY: USA
: ZIP: 22202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.00
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/615-181
: FILING DATE: 04-APR-1996
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP94/01756
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 261302/1993
: FILING DATE: 19-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: OBLOM, NORMAN F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DOCKET NUMBER: 10-756-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-413-3000

```

```

: TELEFAX: 703-413-2220
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
: US-08-615-181-67

Query Match          45.5%; Score 5; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7
Db 3 GKKKK 7

RESULT 19
US-09-389-390-7
: Sequence 7, Application US/09389390
: Patent No. 6558961
: GENERAL INFORMATION:
: APPLICANT: SAKPHIE
: TITLE OF INVENTION: IMMUNODIAGNOSTICS USING PARTICLE DELIVERY METHODS
: FIFE REFERENCE: OPF1620
: CURRENT APPLICATION NUMBER: US/09/389,390
: PRIOR FILING DATE: 1999-09-03
: PRIOR APPLICATION NUMBER: 60/099,261
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 60/139,045
: PRIOR FILING DATE: 1999-06-10
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 8
: TYPE: PPT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-389-390-7

Query Match          45.5%; Score 5; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7
Db 1 GKKKK 5

RESULT 20
US-08-159-339A-1163
: Sequence 1163, Application US/08159339A
: Patent No. 6037135
: GENERAL INFORMATION:
: APPLICANT: Kubo, Ralph T.
: APPLICANT: Grey, Howard M.
: APPLICANT: Settle, Alessandro
: APPLICANT: Celis, Esteban
: TITLE OF INVENTION: HLA Binding peptides and Their
: TITLE OF INVENTION: Uses
: NUMBER OF SEQUENCES: 1254
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA

```



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1 ZIP: 94111-3834
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Diskette
4 COMPUTER: IBM Compatible
5 OPERATING SYSTEM: DOS
6 SOFTWARE: FastSeq for Windows Version: 2.0
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/08/159,444A
9 FILING DATE: 29-NOV-1993
10 CLASSIFICATION: 424
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/926,596
13 FILING DATE: 07-AUG-1992
14 APPLICATION NUMBER: US 08/027,746
15 FILING DATE: 05-MAR-1993
16 APPLICATION NUMBER: US 08/03,396
17 FILING DATE: 06-AUG-1993
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Weber, Ellen Lauver
20 REGISTRATION NUMBER: 32,762
21 REFERENCE/DOCKET NUMBER: 018623-00500005
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (415) 576-0200
24 TELEFAX: (415) 576-0300
25 TELEX:
26 INFORMATION FOR SEQ ID NO: 1:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 9 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32 MOLECULE TYPE: peptide
33 US-08-159-339A-1163
34
35 Query Match: 45.5%; Score 5; DB 3; Length 9;
36 Best Local Similarity: 100.0%; Pred. No. 2.5e+05;
37 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
38
39 QY 5 GKKKK 7
40 DB 5 GKKKK 9
41
42 RESULT 2:
43 US-08-197-484-30
44 Sequence 30, Application US/08/197484
45 Patent No. 6419931
46 GENERAL INFORMATION:
47 APPLICANT: VITIELLO, Maria A.
48 APPLICANT: CHESTNUT, Robert W.
49 APPLICANT: SETTE, Alessandro D.
50 APPLICANT: CELIS, Esteban
51 APPLICANT: GRAY, Howard
52 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
53 NUMBER OF SEQUENCES: 153
54 CORRESPONDENCE ADDRESS:
55 ADDRESSEE: Townsend and Townsend Koorntje and Crew
56 STREET: Stewart Street Tower, One Market Plaza
57 CITY: San Francisco
58 STATE: California
59 COUNTRY: US
60 ZIP: 94105-1493
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Floppy disk
63 COMPUTER: IBM PC compatible
64 OPERATING SYSTEM: PC-DOS/MS-DOS
65 SOFTWARE: PatentIn Release #1.0, Version #1.25
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/08/197,484
68 FILING DATE: 16-FEB-1994
69 CLASSIFICATION: 424
70 PRIOR APPLICATION DATA:

```

```

1 APPLICATION NUMBER: US 07/935,811
2 FILING DATE: 26-AUG-1992
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 07/874,491
5 FILING DATE: 27-APR-1992
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 07/827,682
8 FILING DATE: 29-JAN-1992
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/749,568
11 FILING DATE: 26-AUG-1991
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Parmelee, Steven W.
14 REGISTRATION NUMBER: 31,990
15 REFERENCE/DOCKET NUMBER: 14137-26-4
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (206) 467-9600
18 TELEFAX: (206) 623-6794
19 INFORMATION FOR SEQ ID NO: 30:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 9 amino acids
22 TYPE: amino acid
23 STRANDEDNESS: unknown
24 TOPOLOGY: unknown
25 MOLECULE TYPE: peptide
26 US-08-197-484-30
27
28 Query Match: 45.5%; Score 5; DB 4; Length 9;
29 Best Local Similarity: 100.0%; Pred. No. 2.5e+05;
30 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
31
32 QY 3 GKKKK 7
33 DB 1 GKKKK 5
34
35 RESULT 22:
36 PCT US95-02121-30
37 Sequence 30, Application PC/TUS9502121
38 GENERAL INFORMATION:
39 APPLICANT:
40 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
41 NUMBER OF SEQUENCES: 153
42 COMPUTER READABLE FORM:
43 MEDIUM TYPE: Floppy disk
44 COMPUTER: IBM PC Compatible
45 OPERATING SYSTEM: PC-DOS/MS-DOS
46 SOFTWARE: PatentIn Release #1.0, Version #1.25
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: PCT/US95/02121
49 FILING DATE: 16-FEB-1995
50 CLASSIFICATION:
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: US 08/197,484
53 FILING DATE: 16-FEB-1994
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: US 07/935,811
56 FILING DATE: 26-AUG-1992
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US 07/874,491
59 FILING DATE: 27-APR-1992
60 PRIOR APPLICATION DATA:
61 APPLICATION NUMBER: US 07/827,682
62 FILING DATE: 29-JAN-1992
63 PRIOR APPLICATION DATA:
64 APPLICATION NUMBER: US 07/749,568
65 FILING DATE: 26-AUG-1991
66 ATTORNEY/AGENT INFORMATION:
67 NAME: Parmelee, Steven W.
68 REGISTRATION NUMBER: 31,990
69 REFERENCE/DOCKET NUMBER: 14137-26-4PC
70 TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (206) 467-9609  
 TELEFAX: (415) 543-5043  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 ECT-US95-02121-10

Query Match 45.5%, Score 5, ID 2, Length 9  
 Best Local Similarity 100.0%, Pred. No. 2, Gaps 0  
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 3 GKKK 7  
 DB 1111  
 6 KKKK 5

RESULT 24  
 US 08-928-958 16  
 Sequence 16, Application US/08928-958  
 Patent No. 5877282  
 GENERAL INFORMATION:  
 APPLICANT: NADLER, STEVEN S.  
 APPLICANT: CLEVELAND, JEFFREY S.  
 APPLICANT: BLAKE, JAMES K.  
 APPLICANT: HAEFAR, OMAR K.  
 TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
 TITLE OF INVENTION: TRANSLATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
 TITLE OF INVENTION: METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ROBINS & ASSOCIATES  
 STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
 CITY: MENLO PARK  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94025  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/928-958  
 FILING DATE: 12-SEP-1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/928-958  
 FILING DATE: 20-SEP-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: F. HENS, ROBERTA L.  
 REGISTRATION NUMBER: 33,248  
 REFERENCE/DECKET NUMBER: 5948-0019  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 325-7812  
 TELEFAX: (650) 325-7823  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US 08-928-958 16

Query Match 45.5%, Score 5, ID 2, Length 12  
 Best Local Similarity 100.0%, Pred. No. 2  
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 5 KKKK 9

DB 1111  
 6 KKKK 10  
 RESULT 24  
 US-09-072-429-16  
 Sequence 16, Application US/09072429  
 Patent No. 5962415  
 GENERAL INFORMATION:  
 APPLICANT: NADLER, STEVEN S.  
 TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
 TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLATION AND AN  
 TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BRISTOL MYERS Squibb Company  
 STREET: P.O. Box 4000  
 CITY: Princeton  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 08543-4000  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/072-429  
 FILING DATE: 04 MAY-1998  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Klein, Christopher A.  
 REGISTRATION NUMBER: 34,364  
 REFERENCE/DECKET NUMBER: 0901410  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (609) 252-3714  
 TELEFAX: (609) 252-4526  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 12 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-072-429-16

Query Match 45.5%, Score 5, ID 2, Length 12  
 Best Local Similarity 100.0%, Pred. No. 31  
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 5 KKKK 9  
 DB 1111  
 6 KKKK 10

RESULT 25  
 US-08-970-833 9  
 Sequence 9, Application US/08970833  
 Patent No. 6522859  
 GENERAL INFORMATION:  
 APPLICANT: Kresling, Linda L.  
 APPLICANT: Murphy, Robert M.  
 TITLE OF INVENTION: INHIBITORS OF BETA AMYLOID TOXICITY  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Quarles & Brady  
 STREET: 411 East Wisconsin Avenue  
 CITY: Milwaukee  
 STATE: Wisconsin  
 COUNTRY: U.S.A.  
 ZIP: 53202-4307  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,008
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: OBION, NO. 5700469man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DCKET NUMBER: 3077-003-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 413-3000
: TELEFAX: (703) 413-2220
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-474-008-11
: Query Match 45.5% Score 5: DB 1: Length 15:
: Best Local Similarity 100.0% Pred. No. 37:
: Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 4 GKKKK 8
: DE 6 GKKKK 10
:
: RESULT 26
: US-07-854-629-11
: Sequence 11: Application US/07854629
: Patent No. 5480967
: GENERAL INFORMATION:
: APPLICANT: MCMICHAEL, ANDREW J.
: APPLICANT: NIXON, DOUGLAS F.
: APPLICANT: TOWNSEND, ALAIN R. M.
: APPLICANT: GUTCH, FRANCES M.
: TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: P.C.
: STREET: 1755 S. Jefferson Davis Highway, Suite 400
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/854,629
: FILING DATE: 05-JAN-1990
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9004577.5
: FILING DATE: 16-FEB-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: OBION, NO. 5480967man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DCKET NUMBER: 3077-003-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 413-3000
: TELEFAX: (703) 413-2220
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-07-854-629-11
: Query Match 45.5% Score 5: DB 1: Length 12:
: Best Local Similarity 100.0% Pred. No. 37:
: Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 4 GKKKK 8
: DE 6 GKKKK 10
:
: RESULT 27
: US-08-474-008-11
: Sequence 11: Application US/08474008
: Patent No. 5700469
: GENERAL INFORMATION:
: APPLICANT: MCMICHAEL, ANDREW J.
: APPLICANT: NIXON, DOUGLAS F.
: APPLICANT: TOWNSEND, ALAIN R. M.
: APPLICANT: GUTCH, FRANCES M.
: TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: P.C.
: STREET: 1755 S. Jefferson Davis Highway, Suite 400
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,008
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/854,629
: FILING DATE: 06-JUL-1992
: APPLICATION NUMBER: GB 9000287.4
: FILING DATE: 05-JAN-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9003577.5
: FILING DATE: 16-FEB-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: OBION, NO. 5700469man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DCKET NUMBER: 3077-003-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 413-3000
: TELEFAX: (703) 413-2220
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Human immunodeficiency virus
: US-08-474-008-11

```

```

: TELEX: 248855 OPAT UR
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Human immunodeficiency virus
: US-07-854-629-11
: Query Match 45.5% Score 5: DB 1: Length 15:
: Best Local Similarity 100.0% Pred. No. 37:
: Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
:
: QY 3 GKKKK 7
: DE 4 GKKKK 5
:
: RESULT 27
: US-08-474-008-11
: Sequence 11: Application US/08474008
: Patent No. 5700469
: GENERAL INFORMATION:
: APPLICANT: MCMICHAEL, ANDREW J.
: APPLICANT: NIXON, DOUGLAS F.
: APPLICANT: TOWNSEND, ALAIN R. M.
: APPLICANT: GUTCH, FRANCES M.
: TITLE OF INVENTION: HIV-1 CORE PROTEIN FRAGMENTS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: P.C.
: STREET: 1755 S. Jefferson Davis Highway, Suite 400
: CITY: Arlington
: STATE: Virginia
: COUNTRY: U.S.A.
: ZIP: 22202
: COMPUTER READABLE FORM:
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/474,008
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/854,629
: FILING DATE: 06-JUL-1992
: APPLICATION NUMBER: GB 9000287.4
: FILING DATE: 05-JAN-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 9003577.5
: FILING DATE: 16-FEB-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: OBION, NO. 5700469man F.
: REGISTRATION NUMBER: 24,618
: REFERENCE/DCKET NUMBER: 3077-003-0 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 413-3000
: TELEFAX: (703) 413-2220
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Human immunodeficiency virus
: US-08-474-008-11

```

```

Query Match          45.5%  Score 5:  56 37  Length 15:
Best Local Similarity 100.0%  Pred. No. 477
Matches 5:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY  4 GKKKK 7
DB  4 GKKKK 8

RESULT 28
US-08-985-124A-1
: Sequence 1, Application US/08985147A
: Patent No. 5972599
: GENERAL INFORMATION:
: APPLICANT: Ciscatone, Terrence M.
: APPLICANT: desolms, S. Jane
: TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN
: TITLE OF INVENTION: TRANSFERASE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O. Box 2000, 126 E. Lincoln Ave.
: CITY: Rahway
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/985,147A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/042,578
: FILING DATE: 05-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Mulhard, David A.
: REGISTRATION NUMBER: 35,297
: REFERENCE/DOCKET NUMBER: 19833Y
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 908-594-3903
: TELEFAX: 908-594-4720
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-985-124A-1

Query Match          45.5%  Score 5:  56 37  Length 15:
Best Local Similarity 100.0%  Pred. No. 477
Matches 5:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY  4 GKKKK 8
DB  4 GKKKK 5

RESULT 30
US-08-985-126A-1
: Sequence 1, Application US/8985120A
: Patent No. 5971134
: GENERAL INFORMATION:
: APPLICANT: Ciscatone, Terrence M.
: APPLICANT: Halczenko, Wasyli
: APPLICANT: Hutchinson, John H.
: APPLICANT: Lamma, Jr., William C.
: APPLICANT: Stokker, Gerald E.
: APPLICANT: Stump, Craig A.
: APPLICANT: Williams, Theresa M.
: TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
: TITLE OF INVENTION: TRANSFERASE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O. Box 2000, 126 E. Lincoln Ave.
: CITY: Rahway
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065-0900
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0

```

1 CURRENT APPLICATION DATA:  
2 APPLICATION NUMBER: US/08/985,320A  
3 FILING DATE:  
4 CLASSIFICATION: 514  
5 PRIOR APPLICATION DATA:  
6 APPLICATION NUMBER: 60/032,579  
7 FILING DATE: 05-DEC-1996  
8 ATTORNEY/AGENT INFORMATION:  
9 NAME: Muthard, David A.  
10 REGISTRATION NUMBER: 35,297  
11 REFERENCE/DOCKET NUMBER: 19850Y  
12 TELECOMMUNICATION INFORMATION:  
13 TELEPHONE: 908-594-3903  
14 TELEFAX: 908-594-4720  
15 TELEX:

16 INFORMATION FOR SEQ ID NO: 1:

17 SEQUENCE CHARACTERISTICS:

18 LENGTH: 15 amino acids

19 TYPE: amino acid

20 STRANDEDNESS: single

21 TOPOLOGY: linear

22 MOLECULE TYPE: protein

23 US 08-985-320A-1

24 Query Match 45.5% Score 5; DB 3; Length 15;

25 Best Local Similarity 100.0%; Pred. No. 37;

26 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 QY 4 GKKKK 8

28 Db 1 GKKKK 5

29 RESULT 3:

30 US-08-984,732A-1

31 Sequence 1, Application US/08484732A

32 Patent No. 6015417

33 GENERAL INFORMATION:

34 APPLICANT: Halczenko, Wasyi

35 APPLICANT: Slump, Craig A.

36 TITLE OF INVENTION: INHIBITORS OF FARNESYL PROTEIN

37 TITLE OF INVENTION: TRANSFERASE

38 NUMBER OF SEQUENCES: 14

39 CORRESPONDENCE ADDRESS:

40 ADDRESSEE: Merck & Co., Inc.

41 STREET: P.O. Box 2000, 126 E. Lincoln Ave.

42 CITY: Rahway

43 STATE: NJ

44 COUNTRY: USA

45 ZIP: 07065-0900

46 COMPUTER READABLE FORM:

47 MEDIUM TYPE: Diskette

48 COMPUTER: IBM Compatible

49 OPERATING SYSTEM: DOS

50 SOFTWARE: FastSeq for Windows Version 2.0

51 CURRENT APPLICATION DATA:

52 APPLICATION NUMBER: US/08/984,732A

53 FILING DATE:

54 CLASSIFICATION: 514

55 PRIOR APPLICATION DATA:

56 APPLICATION NUMBER: 60/032,126

57 FILING DATE: 05-DEC-1996

58 ATTORNEY/AGENT INFORMATION:

59 NAME: Muthard, David A.

60 REGISTRATION NUMBER: 35,297

61 REFERENCE/DOCKET NUMBER: 19849Y

62 TELECOMMUNICATION INFORMATION:

63 TELEPHONE: 908-594-3903

64 TELEFAX: 908-594-4720

65 TELEX:

66 INFORMATION FOR SEQ ID NO: 1:

67 SEQUENCE CHARACTERISTICS:

68 LENGTH: 15 amino acids

1 TYPE: amino acid  
2 STRANDEDNESS: single  
3 TOPOLOGY: linear  
4 MOLECULE TYPE: protein  
5 US-08-984-732A-1

6 Query Match 45.5% Score 5; DB 3; Length 15;

7 Best Local Similarity 100.0%; Pred. No. 37;

8 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

9 QY 4 GKKKK 8

10 Db 1 GKKKK 5

11 RESULT 32

12 US-09-195-578-13

13 Sequence 13, Application US/09195578

14 Patent No. 6054466

15 GENERAL INFORMATION:

16 APPLICANT: Ciccarone, Terrence M.

17 APPLICANT: deSolms, Jane S. J.

18 APPLICANT: Merck & Co., Inc.

19 TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN

20 TITLE OF INVENTION: TRANSFERASE

21 FILE REFERENCE: 20121Y

22 CURRENT APPLICATION NUMBER: US/09/195,578

23 CURRENT FILING DATE: 1998-11-18

24 EARLIER APPLICATION NUMBER: 60/067,552

25 EARLIER FILING DATE: 1997-12-04

26 NUMBER OF SEQ ID NOS: 26

27 SOFTWARE: FastSeq for Windows Version 3.0

28 SEQ ID NO 13

29 LENGTH: 15

30 TYPE: PRT

31 ORGANISM: Homosapien

32 US-09-195-578-13

33 Query Match 45.5% Score 5; DB 3; Length 15;

34 Best Local Similarity 100.0%; Pred. No. 37;

35 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

36 QY 4 GKKKK 8

37 Db 1 GKKKK 5

38 RESULT 33

39 US-09-140-557-13

40 Sequence 13, Application US/09140557A

41 Patent No. 6103487

42 GENERAL INFORMATION:

43 APPLICANT: Merck & Co., Inc.

44 APPLICANT: Barnett, Stanley F.

45 APPLICANT: Heimbrook, David C.

46 APPLICANT: Huber, Hans E.

47 APPLICANT: Patrick, Denis R.

48 TITLE OF INVENTION: A METHOD OF TREATING CANCER

49 FILE REFERENCE: 20034Y

50 CURRENT APPLICATION NUMBER: US/09/140,557A

51 CURRENT FILING DATE: 1998-08-26

52 EARLIER APPLICATION NUMBER: 60/057,340

53 EARLIER FILING DATE: 1997-08-27

54 NUMBER OF SEQ ID NOS: 15

55 SOFTWARE: FastSeq for Windows Version 3.0

56 SEQ ID NO 13

57 LENGTH: 15

58 TYPE: PRT

59 ORGANISM: Artificial Sequence

60 FEATURE:

61 OTHER INFORMATION: synthesized peptide substrate for

62 OTHER INFORMATION: geranylgeranyl-protein transferase type I

63 US-09-140-557-13

Query Match 45.5% Score 5; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 DB 1 GKKKK 5

## RESULT 14

US-09-170-951-13

Sequence 13, Application US/05170951

Patent No. 6104723

GENERAL INFORMATION:

APPLICANT: Bergman, Jeffrey M.

APPLICANT: Dismore, Christopher J.

APPLICANT: Graham, Samuel L.

APPLICANT: Merck & Co., Inc.

TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN

FILE REFERENCE: 19867Y

CURRENT APPLICATION NUMBER: US/09/170-951

CURRENT FILING DATE: 1998-10-13

EARLIER APPLICATION NUMBER: 60/364,342

EARLIER FILING DATE: 1997-10-17

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRT

ORGANISM: Homosapien

US-09-170-951-13

## Query Match

45.5% Score 5; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 DB 1 GKKKK 5

## RESULT 15

US-09-164-482-13

Sequence 13, Application US/09164442A

Patent No. 6127490

GENERAL INFORMATION:

APPLICANT: Merck & Co., Inc.

APPLICANT: deSoums, S. Jane

APPLICANT: Lema, William P.

APPLICANT: Shaw, Anthony W.

APPLICANT: Susko, John T.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

FILE REFERENCE: 20025Y

CURRENT APPLICATION NUMBER: US/09/164-482A

CURRENT FILING DATE: 1998-10-01

EARLIER APPLICATION NUMBER: 60/660,871

EARLIER FILING DATE: 1997-10-02

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: synthesized peptide substrate for

OTHER INFORMATION: geranylgeranyl-protein transferase type 1

US-09-164-482-13

## Query Match

45.5% Score 5; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;

US-09-164-482-13

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GKKKK 8  
 DB 1 GKKKK 5

## RESULT 36

US-09-332-769-2

Sequence 2, Application US/09332769

Patent No. 6172076

GENERAL INFORMATION:

APPLICANT: Embrey, Mark W.

APPLICANT: Perlow, Debra S.

APPLICANT: Wai, Colin S.

APPLICANT: Hoffman, Jacob M.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN

FILE REFERENCE: 19982Y

CURRENT APPLICATION NUMBER: US/09/332,769

CURRENT FILING DATE: 1999-06-14

EARLIER APPLICATION NUMBER: US 60/089,311

EARLIER FILING DATE: 1998-06-15

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRT

ORGANISM: Homosapien

US-09-332-769-2

## Query Match

45.5% Score 5; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 DB 1 GKKKK 5

## RESULT 37

US-09-456-153-2

Sequence 2, Application US/09456153

Patent No. 6284755

GENERAL INFORMATION:

APPLICANT: deSoums, S. Jane

APPLICANT: Shaw, Anthony W.

APPLICANT: Ciccarone, Terrence M.

APPLICANT: Stokker, Gerald E.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN

FILE REFERENCE: 20312Y

CURRENT APPLICATION NUMBER: US/09/456,153

CURRENT FILING DATE: 1999-12-07

EARLIER APPLICATION NUMBER: US 60/111,416

EARLIER FILING DATE: 1998-12-08

EARLIER APPLICATION NUMBER: US 60/129,282

EARLIER FILING DATE: 1999-04-14

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRT

ORGANISM: Homosapien

US-09-456-153-2

## Query Match

45.5% Score 5; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 DB 1 GKKKK 5

db 1 GKKKK 5

# RESULT 38

US 09-157-180 14

Sequence 13, Application US/09157180

Patent No. 6297239

GENERAL INFORMATION:

APPLICANT: DeSolms, S. Jane

APPLICANT: Hutchinsch, John H.

APPLICANT: Shaw, Anthony W.

APPLICANT: Graham, Samuel L.

APPLICANT: Citicorone, Terrence M.

APPLICANT: Merck & Co., Inc.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

FILE REFERENCE: 19928Y

CURRENT APPLICATION NUMBER: US/09157180

CURRENT FILING DATE: 1998-10-06

EARLIER APPLICATION NUMBER: 09/062,546

EARLIER FILING DATE: 1997-10-08

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 13

LENGTH: 15

TYPE: PRI

ORGANISM: Homosapien

US 09-167-180-14

## Query Match

Best Local Similarity 45.5%; Score 5; DB 1; Length 15;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8

||||

DB 1 GKKKK 5

# RESULT 39

US-09-455-627-2

Sequence 2, Application US/09455627

Patent No. 6316416

GENERAL INFORMATION:

APPLICANT: deSolms, S. Jane

APPLICANT: Shaw, Anthony W.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN

TITLE OF INVENTION: TRANSFERASE

FILE REFERENCE: 20325

CURRENT APPLICATION NUMBER: US/09455627

CURRENT FILING DATE: 1999-12-07

EARLIER APPLICATION NUMBER: US 09/11,062

EARLIER FILING DATE: 1998-12-08

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRI

ORGANISM: Homosapien

US 09-455-627-2

## Query Match

Best Local Similarity 45.5%; Score 5; DB 4; Length 15;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8

||||

DB 1 GKKKK 5

# RESULT 40

US 09-426-533-2

Sequence 2, Application US/09426533

Patent No. 6353476

GENERAL INFORMATION:

APPLICANT: Merck & Co., Inc.

APPLICANT: Lema, William G. Jr.

APPLICANT: Smith, Anthony M.

APPLICANT: Sisko, John T.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

FILE REFERENCE: 20335Y

CURRENT APPLICATION NUMBER: US/09426533

CURRENT FILING DATE: 2000-03-01

EARLIER APPLICATION NUMBER: 60/122,976

EARLIER FILING DATE: 1998-03-03

APPLICANT: Bergman, Jeffrey M.

TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase

FILE REFERENCE: 2028Y

CURRENT APPLICATION NUMBER: US/09/426,533

CURRENT FILING DATE: 1999-10-26

EARLIER APPLICATION NUMBER: 60/101,177

EARLIER FILING DATE: 1998-10-29

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRI

ORGANISM: Homosapien

US 09-426-533-2

## Query Match

Best Local Similarity 45.5%; Score 5; DB 4; Length 15;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8

||||

DB 1 GKKKK 5

# RESULT 41

US-09-609-205-2

Sequence 2, Application US/09609205

Patent No. 6333325

GENERAL INFORMATION:

APPLICANT: Merck & Co., Inc.

APPLICANT: Dinsmore, Christopher J.

APPLICANT: Graham, Samuel L.

APPLICANT: Williams, Theresa M.

TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS

FILE REFERENCE: 20488

CURRENT APPLICATION NUMBER: US/09/609,205

CURRENT FILING DATE: 2000-05-30

PRIOR APPLICATION NUMBER: 60/145,331

PRIOR FILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRI

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: completely synthetic sequence

US 09-609-205-2

## Query Match

Best Local Similarity 45.5%; Score 5; DB 4; Length 15;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8

||||

DB 1 GKKKK 5

# RESULT 42

US 09-516-945-2

Sequence 2, Application US/09516945

Patent No. 6355345

GENERAL INFORMATION:

APPLICANT: Merck & Co., Inc.

APPLICANT: Lema, William G. Jr.

APPLICANT: Smith, Anthony M.

APPLICANT: Sisko, John T.

TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

FILE REFERENCE: 20435Y

CURRENT APPLICATION NUMBER: US/09/516,945

CURRENT FILING DATE: 2000-03-01

EARLIER APPLICATION NUMBER: 60/122,976

EARLIER FILING DATE: 1998-03-03

: EARLIER APPLICATION NUMBER: 60/127,259  
 : EARLIER FILING DATE: 1999-03-31  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: completely synthetic sequence  
 US-09-516-945-2

Query Match 45.5% Score 5: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 37:  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 III  
 DB 1 GKKKK 5

RESULT 44  
 US-09-757-218-3  
 : Sequence 2: Application US/0957218  
 : Patent No. 6350755  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Luzzo, William C. Jr.  
 : APPLICANT: Sisk, John T.  
 : APPLICANT: Smith, Anthony M.  
 : APPLICANT: Tucker, Thomas J.  
 : APPLICANT: Dinsmore, Christopher J.  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20399Y  
 : CURRENT APPLICATION NUMBER: US/09/757,218  
 : PRIOR APPLICATION NUMBER: 60/175,333  
 : PRIOR FILING DATE: 2000-01-12  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 3  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely synthetic sequence  
 US-09-757-218-3

Query Match 45.5% Score 5: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 37:  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 III  
 DB 1 GKKKK 5

RESULT 44  
 US-09-516-757-2  
 : Sequence 2: Application US/09516757  
 : Patent No. 635643  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Luzzo, William C. Jr.  
 : APPLICANT: Sisk, John T.  
 : APPLICANT: Smith, Anthony M.  
 : APPLICANT: Tucker, Thomas J.  
 : APPLICANT: Dinsmore, Christopher J.  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20399Y  
 : CURRENT APPLICATION NUMBER: US/09/516,757  
 : PRIOR APPLICATION NUMBER: 60/127,259  
 : PRIOR FILING DATE: 1999-03-31  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: completely synthetic sequence  
 US-09-516-750-2

: EARLIER FILING DATE: 1999-03-31  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: completely synthetic sequence  
 US-09-516-757-2

Query Match 45.5% Score 5: DB 4: Length 15:  
 Best Local Similarity 100.0% Pred. No. 37:  
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 GKKKK 8  
 III  
 DB 1 GKKKK 5

RESULT 45  
 US-09-516-750-2  
 : Sequence 2: Application US/09516750  
 : Patent No. 6358956  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Hartman, George R. Jr.  
 : APPLICANT: Luzzo, William C. Jr.  
 : APPLICANT: Sisk, John T.  
 : APPLICANT: Smith, Anthony M.  
 : APPLICANT: Tucker, Gerald J.  
 : APPLICANT: Tucker, Thomas J.  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 20399Y  
 : CURRENT APPLICATION NUMBER: US/09/516,750  
 : PRIOR APPLICATION NUMBER: 60/127,768  
 : PRIOR FILING DATE: 1998-04-03  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRI  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: completely synthetic sequence  
 US-09-516-750-2

Query Match 45.5% Score 5: DB 4: Length 15:  
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QY 4 GKKKK 8  
 III  
 DB 1 GKKKK 5

RESULT 45  
 US-09-516-577-4  
 : Sequence 3: Application US/0942577  
 : Patent No. 6358965  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Anthony, Neville J.  
 : APPLICANT: Bell, Ian M.  
 : APPLICANT: Beshore, Douglas C.  
 : APPLICANT: Ciccatone, Terrence M.  
 : APPLICANT: Desolms, S. Jane  
 : APPLICANT: Dinsmore, Christopher J.  
 : APPLICANT: Stokker, Gerald E.  
 : TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN



; TITLE OF INVENTION: TRANSFERASE  
 ; FILE REFERENCE: 202751  
 ; CURRENT APPLICATION NUMBER: US/09/342,577  
 ; CURRENT FILING DATE: 1999-06-29  
 ; PRIOR APPLICATION NUMBER: 60/291,513  
 ; EARLIER FILING DATE: 1998-07-02  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 15  
 ; TYPE: PRI  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: completely synthetic sequence  
 US-09-342-577-3

Query Match 45.5% Score 5; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 IIII  
 DB 1 GKKKK 5

RESULT 47  
 US-09-516-756-2  
 ; Sequence 2; Application US/09516756  
 ; Patent No. 6475496  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Battman, George D.  
 ; APPLICANT: Lamma, William C. Jr.  
 ; APPLICANT: Smith, Anthony M.  
 ; APPLICANT: Tucker, Thomas J.  
 ; APPLICANT: Refamag, Jeffrey M.  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 ; FILE REFERENCE: 20288Y  
 ; CURRENT APPLICATION NUMBER: US/09/516,756  
 ; CURRENT FILING DATE: 2000-03-01  
 ; EARLIER APPLICATION NUMBER: 60/122,478  
 ; EARLIER FILING DATE: 1998-03-03  
 ; EARLIER APPLICATION NUMBER: 60/227,142  
 ; EARLIER FILING DATE: 1999-03-31  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 15  
 ; TYPE: PRI  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: completely synthetic sequence  
 US-09-516-756-2

Query Match 45.5% Score 5; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 IIII  
 DB 1 GKKKK 5

RESULT 48  
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 ; Sequence 3; Application US/09828061A  
 ; Patent No. 6480228  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Craig A. Stump  
 ; APPLICANT: Theresa M. Williams  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE

; FILE REFERENCE: 20635Y  
 ; CURRENT APPLICATION NUMBER: US/09/828,061A  
 ; CURRENT FILING DATE: 2001-04-06  
 ; PRIOR APPLICATION NUMBER: 60/196,231  
 ; PRIOR FILING DATE: 2000-04-10  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 15  
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 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely Synthetic Amino Acid  
 US-09-828-061A-3

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 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 IIII  
 DB 1 GKKKK 5

RESULT 49  
 US-09-463-917-2  
 ; Sequence 2; Application US/09463917  
 ; Patent No. 6387904  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Dinsmore, Christopher J.  
 ; APPLICANT: Hutchinson, John H.  
 ; APPLICANT: Williams, Theresa M.  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 ; FILE REFERENCE: 20040YP  
 ; CURRENT APPLICATION NUMBER: US/09/463,917  
 ; CURRENT FILING DATE: 2000-02-01  
 ; PRIOR APPLICATION NUMBER: 60/057,080  
 ; PRIOR FILING DATE: 1997-06-27  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 15  
 ; TYPE: PRI  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthesized peptide substrate for  
 ; OTHER INFORMATION: qcracylquanyl-prtoein transferase type I  
 US-09-463-917-2

Query Match 45.5% Score 5; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
 IIII  
 DB 1 GKKKK 5

RESULT 50  
 US-09-347-673-3  
 ; Sequence 3; Application US/09347673  
 ; Patent No. 6410544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Dinsmore, Christopher J.  
 ; APPLICANT: Reil, Ian M.  
 ; APPLICANT: Reshore, Douglas C.  
 ; APPLICANT: Williams, Theresa M.  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 ; FILE REFERENCE: 20236Y  
 ; CURRENT APPLICATION NUMBER: US/09/347,673  
 ; CURRENT FILING DATE: 1999-06-29

: EARLIER APPLICATION NUMBER: 60/091,596
: EARLIER FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 15
: TYPE: PKI
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: completely synthetic sequence
US 09-347-673-3

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			0	Gaps 0
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DB	1	GKKKK	5	

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OLM protein - protein search, using sw model

Run on: September 30, 2003, 10:13:03 : Search time 21.5 Seconds

(without alignments)  
77,413 Million cpi updates/sec

Title: US-09-787-443-19

Perfect score: 11

Sequence: 1 AEGCKKKMRA 11

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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 65387

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

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#### SUMMARIES

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4	5	45.5	8	14	US-10-024-918-10
5	5	45.5	9	7	US-08-844-824-35
6	5	45.5	9	9	US-09-898-461-5
7	5	45.5	9	12	US-10-206-156-13
8	5	45.5	9	15	US-10-128-713-30
9	5	45.5	11	11	US-09-876-904A-312
10	5	45.5	11	11	US-09-876-904A-363
11	5	45.5	12	11	US-09-876-904A-454
12	5	45.5	12	11	US-10-315-920-13
13	5	45.5	12	15	US-10-156-670A-12
14	5	45.5	15	9	US-09-770-967-2
15	5	45.5	15	9	US-09-858-369-2

16	45.5	15	9	US-09-819-522-2	Sequence 2, Appl
17	45.5	15	9	US-09-757-251-3	Sequence 3, Appl
18	45.5	15	9	US-09-784-897A-2	Sequence 2, Appl
19	45.5	15	9	US-09-770-983-2	Sequence 2, Appl
20	45.5	15	9	US-09-828-325A-3	Sequence 3, Appl
21	45.5	15	9	US-09-757-217A-3	Sequence 3, Appl
22	45.5	15	10	US-09-828-259A-3	Sequence 3, Appl
23	45.5	15	10	US-09-945-249-84	Sequence 84, Appl
24	45.5	15	10	US-09-784-818-2	Sequence 84, Appl
25	45.5	15	12	US-09-756-248-2	Sequence 2, Appl
26	45.5	8	9	US-09-813-653-5	Sequence 5, Appl
27	36.4	8	10	US-09-997-579-46	Sequence 46, Appl
28	36.4	8	10	US-09-380-323-1	Sequence 1, Appl
29	36.4	8	10	US-09-380-323-4	Sequence 4, Appl
30	36.4	8	10	US-09-813-448-2	Sequence 2, Appl
31	36.4	8	10	US-09-142-043-2	Sequence 2, Appl
32	36.4	8	10	US-09-843-676-223	Sequence 223, Appl
33	36.4	8	10	US-09-945-249-82	Sequence 82, Appl
34	36.4	8	10	US-09-805-301-2	Sequence 2, Appl
35	36.4	8	10	US-09-805-301-40	Sequence 40, Appl
36	36.4	8	10	US-09-805-301-96	Sequence 96, Appl
37	36.4	8	10	US-09-813-214A-2	Sequence 2, Appl
38	36.4	8	11	US-09-438-486-223	Sequence 223, Appl
39	36.4	8	11	US-09-999-724-1	Sequence 1, Appl
40	36.4	8	11	US-09-882-291-63	Sequence 63, Appl
41	36.4	8	11	US-09-882-291-73	Sequence 73, Appl
42	36.4	8	11	US-09-911-569-3	Sequence 3, Appl
43	36.4	8	11	US-09-876-904A-53	Sequence 53, Appl
44	36.4	8	11	US-09-876-904A-394	Sequence 394, Appl
45	36.4	8	11	US-09-876-904A-405	Sequence 405, Appl
46	36.4	8	11	US-09-876-904A-485	Sequence 485, Appl
47	36.4	8	12	US-09-791-524-139	Sequence 139, Appl
48	36.4	8	12	US-10-073-333A-26	Sequence 26, Appl
49	36.4	8	12	US-10-200-879-3	Sequence 3, Appl
50	36.4	8	12	US-10-014-322A-62	Sequence 62, Appl
51	36.4	8	12	US-10-061-607A-34	Sequence 34, Appl
52	36.4	8	15	US-10-053-758-223	Sequence 223, Appl
53	36.4	8	15	US-10-054-295-223	Sequence 223, Appl
54	36.4	8	15	US-10-054-611-223	Sequence 223, Appl
55	36.4	8	15	US-10-140-164-27	Sequence 27, Appl
56	36.4	8	15	US-10-140-164-56	Sequence 56, Appl
57	36.4	8	15	US-10-133-210-172	Sequence 172, Appl
58	36.4	8	15	US-10-131-210-173	Sequence 173, Appl
59	36.4	8	15	US-10-075-869-94	Sequence 94, Appl
60	36.4	9	9	US-09-884-681-8	Sequence 8, Appl
61	36.4	9	10	US-09-805-301-3	Sequence 3, Appl
62	36.4	9	10	US-09-805-301-41	Sequence 41, Appl
63	36.4	9	10	US-09-805-301-97	Sequence 97, Appl
64	36.4	9	11	US-09-882-291-61	Sequence 61, Appl
65	36.4	9	11	US-09-882-291-72	Sequence 72, Appl
66	36.4	9	11	US-09-876-904A-271	Sequence 271, Appl
67	36.4	9	11	US-09-876-904A-444	Sequence 444, Appl
68	36.4	9	11	US-09-876-904A-480	Sequence 480, Appl
69	36.4	9	11	US-09-876-904A-487	Sequence 487, Appl
70	36.4	9	12	US-09-791-524-135	Sequence 135, Appl
71	36.4	9	12	US-10-338-348-2	Sequence 2, Appl
72	36.4	9	12	US-10-077-106-16	Sequence 16, Appl
73	36.4	9	12	US-10-293-580-8	Sequence 8, Appl
74	36.4	9	15	US-10-211-207-16	Sequence 16, Appl
75	36.4	9	15	US-10-062-710-3	Sequence 3, Appl
76	36.4	9	15	US-10-133-210-189	Sequence 189, Appl
77	36.4	9	15	US-10-211-088-148	Sequence 148, Appl
78	36.4	9	15	US-10-211-088-190	Sequence 190, Appl
79	36.4	9	15	US-10-211-088-284	Sequence 284, Appl
80	36.4	10	9	US-09-124-280A-1	Sequence 1, Appl
81	36.4	10	9	US-09-124-280A-12	Sequence 12, Appl
82	36.4	10	9	US-09-124-280A-19	Sequence 19, Appl
83	36.4	10	9	US-09-124-280A-42	Sequence 42, Appl
84	36.4	10	10	US-09-952-432A-13	Sequence 13, Appl
85	36.4	10	10	US-09-846-350-1	Sequence 1, Appl
86	36.4	10	10	US-09-805-301-4	Sequence 4, Appl
87	36.4	10	10	US-09-805-301-42	Sequence 42, Appl
88	36.4	10	10	US-09-805-301-98	Sequence 98, Appl

89	4	35.4	10	11	US-09-134-7943-3	Sequence 3, Appl	162	4	36.4	13	15	US-10-106-698-8327	Sequence 8327, Ap
90	4	36.4	10	11	US-09-882-291-65	Sequence 65, Appl	163	4	36.4	14	8	US-08-910-386A-53	Sequence 53, Appl
91	4	36.4	10	11	US-09-882-291-66	Sequence 66, Appl	164	4	36.4	14	8	US-08-981-824-18	Sequence 18, Appl
92	4	36.4	10	11	US-09-882-291-71	Sequence 71, Appl	165	4	36.4	14	10	US-09-922-261-183	Sequence 183, Appl
93	4	36.4	10	11	US-09-882-291-75	Sequence 45, Appl	166	4	36.4	14	10	US-09-984-056-87	Sequence 87, Appl
94	4	36.4	10	11	US-09-876-904A-90	Sequence 90, Appl	167	4	36.4	14	10	US-09-775-840B-1	Sequence 1, Appl
95	4	36.4	10	11	US-09-876-904A-424	Sequence 484, Appl	168	4	36.4	14	10	US-09-775-840B-2	Sequence 2, Appl
96	4	36.4	10	11	US-09-572-404B-39,3	Sequence 3917, Ap	169	4	36.4	14	10	US-09-775-840B-8	Sequence 8, Appl
97	4	36.4	10	12	US-09-572-270A-242	Sequence 202, App	170	4	36.4	14	10	US-09-983-067-1	Sequence 1, Appl
98	4	36.4	10	12	US-09-572-270A-761	Sequence 761, App	171	4	36.4	14	10	US-09-984-057-87	Sequence 87, Appl
99	4	36.4	10	12	US-10-108-844-6	Sequence 5, Appl	172	4	36.4	14	10	US-09-805-301-8	Sequence 8, Appl
100	4	36.4	10	14	US-10-053-405-6	Sequence 6, Appl	173	4	36.4	14	10	US-09-805-301-46	Sequence 46, Appl
101	4	36.4	10	15	US-10-267-847-41	Sequence 41, Appl	174	4	36.4	14	10	US-09-805-301-102	Sequence 102, Appl
102	4	36.4	10	15	US-10-133-230-21	Sequence 21, Appl	175	4	36.4	14	11	US-09-876-904A-91	Sequence 91, Appl
103	4	36.4	10	15	US-10-075-869-45	Sequence 55, Appl	176	4	36.4	14	11	US-09-876-904A-330	Sequence 330, Appl
104	4	36.4	11	10	US-09-846-442-1	Sequence 1, Appl	177	4	36.4	14	12	US-10-133-973-51	Sequence 51, Appl
105	4	36.4	11	10	US-09-835-301-5	Sequence 5, Appl	178	4	36.4	14	12	US-10-264-672-13	Sequence 13, Appl
106	4	36.4	11	10	US-09-835-301-43	Sequence 43, Appl	179	4	36.4	14	12	US-10-226-629A-280	Sequence 280, Appl
107	4	36.4	11	10	US-09-835-301-99	Sequence 99, Appl	180	4	36.4	14	15	US-10-215-759-13	Sequence 13, Appl
108	4	36.4	11	11	US-09-882-291-55	Sequence 55, Appl	181	4	36.4	14	15	US-10-139-146-34	Sequence 34, Appl
109	4	36.4	11	11	US-09-882-291-64	Sequence 64, Appl	182	4	36.4	14	15	US-10-206-699-174	Sequence 174, Appl
110	4	36.4	11	12	US-09-876-904A-442	Sequence 464, App	183	4	36.4	14	15	US-10-211-088-197	Sequence 197, Appl
111	4	36.4	11	12	US-09-791-524-15	Sequence 15, Appl	184	4	36.4	15	9	US-09-811-094-30	Sequence 30, Appl
112	4	36.4	11	12	US-10-212-499-39	Sequence 39, Appl	185	4	36.4	15	9	US-09-810-644-30	Sequence 30, Appl
113	4	36.4	11	12	US-10-450-254-7	Sequence 7, Appl	186	4	36.4	15	10	US-09-927-709-1	Sequence 1, Appl
114	4	36.4	11	12	US-10-355-975-33	Sequence 33, Appl	187	4	36.4	15	10	US-09-927-436-10	Sequence 10, Appl
115	4	36.4	12	10	US-09-845-725-1	Sequence 1, Appl	188	4	36.4	15	10	US-09-845-719A-1	Sequence 1, Appl
116	4	36.4	12	10	US-09-805-301-6	Sequence 6, Appl	189	4	36.4	15	10	US-09-967-772-16	Sequence 16, Appl
117	4	36.4	12	10	US-09-805-301-44	Sequence 44, Appl	190	4	36.4	15	10	US-09-945-249-80	Sequence 80, Appl
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122	4	36.4	12	11	US-09-882-291-42	Sequence 42, Appl	195	4	36.4	15	10	US-09-805-301-47	Sequence 47, Appl
123	4	36.4	12	11	US-09-882-291-50	Sequence 50, Appl	196	4	36.4	15	10	US-09-805-301-103	Sequence 103, Appl
124	4	36.4	12	11	US-09-882-291-51	Sequence 51, Appl	197	4	36.4	15	10	US-09-185-904A-30	Sequence 30, Appl
125	4	36.4	12	11	US-09-882-291-52	Sequence 52, Appl	198	4	36.4	15	11	US-09-999-724-4	Sequence 4, Appl
126	4	36.4	12	11	US-09-882-291-53	Sequence 53, Appl	199	4	36.4	15	12	US-09-791-524-132	Sequence 132, Appl
127	4	36.4	12	12	US-09-882-291-54	Sequence 54, Appl	200	4	36.4	15	12	US-09-791-524-138	Sequence 138, Appl
128	4	36.4	12	12	US-09-882-291-57	Sequence 57, Appl	201	4	36.4	15	12	US-10-226-629A-281	Sequence 281, Appl
129	4	36.4	12	13	US-09-882-291-58	Sequence 58, Appl	202	4	36.4	15	12	US-10-226-629A-287	Sequence 287, Appl
130	4	36.4	12	13	US-09-882-291-59	Sequence 59, Appl	203	4	36.4	15	12	US-10-108-844-6	Sequence 6, Appl
131	4	36.4	12	11	US-09-876-904A-78	Sequence 78, Appl	204	4	36.4	15	12	US-10-108-844-11	Sequence 11, Appl
132	4	36.4	12	11	US-09-876-904A-148	Sequence 148, Appl	205	4	36.4	15	12	US-10-293-580-63	Sequence 63, Appl
133	4	36.4	12	12	US-10-361-607A-1	Sequence 619, Appl	206	4	36.4	15	14	US-10-020-436A-19	Sequence 19, Appl
134	4	36.4	12	15	US-10-267-847-41	Sequence 47, Appl	207	4	36.4	15	14	US-10-074-257-3	Sequence 3, Appl
135	4	36.4	12	15	US-10-267-847-42	Sequence 1210, Ap	208	4	36.4	15	15	US-10-174-105A-191	Sequence 191, Appl
136	4	36.4	13	15	US-10-267-847-43	Sequence 39, Appl	209	4	36.4	15	15	US-10-161-097-54	Sequence 54, Appl
137	4	36.4	13	10	US-09-775-840A-7	Sequence 7, Appl	210	4	36.4	15	15	US-10-206-699-102	Sequence 102, Appl
138	4	36.4	13	10	US-09-775-840A-9	Sequence 9, Appl	211	4	36.4	15	15	US-10-225-567A-1419	Sequence 1419, Ap
139	4	36.4	13	10	US-09-775-840A-9	Sequence 9, Appl	212	4	27.3	8	8	US-08-866-279A-9	Sequence 9, Appl
140	4	36.4	13	10	US-09-746-176-5	Sequence 1, Appl	213	3	27.3	8	9	US-09-756-594-45	Sequence 45, Appl
141	4	36.4	13	10	US-09-746-176-5	Sequence 40, Appl	214	3	27.3	8	9	US-09-765-527-237	Sequence 237, Appl
142	4	36.4	13	10	US-09-805-301-7	Sequence 7, Appl	215	3	27.3	8	9	US-09-796-264-6	Sequence 6, Appl
143	4	36.4	13	10	US-09-805-301-47	Sequence 45, Appl	216	3	27.3	8	9	US-09-796-264-9	Sequence 9, Appl
144	4	36.4	13	10	US-09-805-301-11	Sequence 101, App	217	3	27.3	8	9	US-09-949-780-7	Sequence 7, Appl
145	4	36.4	13	11	US-09-882-291-55	Sequence 56, Appl	218	3	27.3	8	9	US-09-847-712-3	Sequence 3, Appl
146	4	36.4	13	11	US-09-876-904A-38	Sequence 88, Appl	219	3	27.3	8	9	US-09-898-461-1	Sequence 1, Appl
147	4	36.4	13	11	US-09-876-904A-58	Sequence 89, Appl	220	3	27.3	8	10	US-09-845-226-6	Sequence 6, Appl
148	4	36.4	13	11	US-09-876-904A-58	Sequence 585, App	221	3	27.3	8	10	US-09-845-226-9	Sequence 9, Appl
149	4	36.4	13	11	US-09-876-904A-60	Sequence 600, App	222	3	27.3	8	10	US-09-984-056-69	Sequence 69, Appl
150	4	36.4	13	11	US-09-922-877-420	Sequence 420, App	223	3	27.3	8	10	US-09-984-056-79	Sequence 79, Appl
151	4	36.4	13	11	US-09-913-077A-6	Sequence 6, Appl	224	3	27.3	8	10	US-09-864-866-30	Sequence 30, Appl
152	4	36.4	13	11	US-09-922-666-23	Sequence 27, Appl	225	3	27.3	8	10	US-09-985-157-10	Sequence 10, Appl
153	4	36.4	13	11	US-09-948-783-422	Sequence 422, App	226	3	27.3	8	10	US-09-883-825-2	Sequence 2, Appl
154	4	36.4	13	12	US-09-791-524-24	Sequence 24, Appl	227	3	27.3	8	10	US-09-969-192-1	Sequence 1, Appl
155	4	36.4	13	12	US-09-791-524-136	Sequence 136, Appl	228	3	27.3	8	10	US-09-984-057-69	Sequence 69, Appl
156	4	36.4	13	12	US-10-153-244-75	Sequence 75, Appl	229	3	27.3	8	10	US-09-984-057-79	Sequence 79, Appl
157	4	36.4	13	12	US-10-153-244-75	Sequence 138, Appl	230	3	27.3	8	10	US-09-967-772-8	Sequence 8, Appl
158	4	36.4	13	12	US-10-153-244-185	Sequence 188, App	231	3	27.3	8	10	US-09-795-903A-6	Sequence 6, Appl
159	4	36.4	13	12	US-10-153-244-248	Sequence 248, App	232	3	27.3	8	10	US-09-795-903A-9	Sequence 9, Appl
160	4	36.4	13	12	US-10-153-244-248	Sequence 3, Appl	233	3	27.3	8	10	US-09-840-277-3	Sequence 3, Appl
161	4	36.4	13	15	US-10-267-847-45	Sequence 45, Appl	234	3	27.3	8	11	US-09-999-724-74	Sequence 74, Appl

235	8	11	US-09-599-724-34	Sequence 94, Appl	308	3	27.3	4	9	US-09-879-936-24	Sequence 24, Appl
236	8	11	US-09-547-249A-3	Sequence 3, Appl1	309	3	27.3	9	10	US-09-916-109-9	Sequence 9, Appl1
237	8	11	US-09-843-221A-6	Sequence 6, Appl1	310	3	27.3	9	10	US-09-850-351A-95	Sequence 95, Appl
238	8	11	US-09-840-669B-3	Sequence 3, Appl1	311	3	27.3	9	10	US-09-780-053-56	Sequence 56, Appl1
239	8	11	US-09-840-748-314Z	Sequence 414Z, Ap	312	3	27.3	9	10	US-09-780-053-255	Sequence 255, App
240	8	11	US-09-876-924A-84	Sequence 83, Appl	313	3	27.3	9	10	US-09-780-053-260	Sequence 260, App
241	8	11	US-09-876-904A-28	Sequence 28, Appl	314	3	27.3	9	10	US-09-780-053-333	Sequence 333, App
242	8	11	US-09-876-904A-28	Sequence 28, Appl	315	3	27.3	9	10	US-09-780-053-334	Sequence 334, App
243	8	11	US-09-876-904A-28	Sequence 456, App	316	3	27.3	9	10	US-09-894-018-224	Sequence 224, Appl
244	8	11	US-09-876-904A-28	Sequence 456, App	317	3	27.3	9	10	US-09-971-067-1	Sequence 1, Appl1
245	8	11	US-09-876-904A-28	Sequence 456, App	318	3	27.3	9	10	US-09-888-721-30	Sequence 30, Appl
246	8	11	US-09-876-904A-28	Sequence 456, App	319	3	27.3	9	10	US-09-883-649A-16	Sequence 16, Appl
247	8	11	US-09-876-904A-28	Sequence 456, App	320	3	27.3	9	10	US-09-753-831-10	Sequence 10, Appl
248	8	11	US-09-876-904A-28	Sequence 456, App	321	3	27.3	9	10	US-09-753-831-11	Sequence 11, Appl
249	8	11	US-09-876-904A-28	Sequence 456, App	322	3	27.3	9	10	US-09-753-831-27	Sequence 27, Appl
250	8	11	US-09-876-904A-28	Sequence 506, App	323	3	27.3	9	10	US-09-753-831-28	Sequence 28, Appl
251	8	11	US-09-876-904A-28	Sequence 506, App	324	3	27.3	9	10	US-09-753-831-33	Sequence 33, Appl
252	8	11	US-09-876-904A-28	Sequence 674, App	325	3	27.3	9	10	US-09-749-068-5	Sequence 5, Appl1
253	8	11	US-09-876-904A-28	Sequence 612, App	326	3	27.3	9	10	US-09-791-378-125	Sequence 125, App
254	8	11	US-09-932-613-13	Sequence 13, Appl	327	3	27.3	9	10	US-09-780-668A-24	Sequence 24, Appl
255	8	11	US-09-865-548A-54	Sequence 54, Appl	328	3	27.3	9	10	US-09-920-174-26	Sequence 26, Appl
256	8	12	US-10-073-133A-21	Sequence 21, Appl	329	3	27.3	9	10	US-09-919-048-95	Sequence 95, Appl
257	8	12	US-10-158-825-146	Sequence 146, App	330	3	27.3	9	10	US-09-919-048-173	Sequence 173, App
258	8	12	US-10-348-504-60	Sequence 60, Appl	331	3	27.3	9	10	US-09-779-308-210	Sequence 210, App
259	8	12	US-10-348-504-64	Sequence 64, Appl	332	3	27.3	9	10	US-09-779-308-378	Sequence 378, App
260	8	12	US-10-348-504-72	Sequence 72, Appl	333	3	27.3	9	10	US-09-779-308-594	Sequence 594, App
261	8	12	US-10-348-504-72	Sequence 72, Appl	334	3	27.3	9	10	US-09-779-308-674	Sequence 674, App
262	8	12	US-09-315-455-12	Sequence 42, Appl	335	3	27.3	9	10	US-09-017-743C-112	Sequence 112, App
263	8	12	US-10-244-672-10	Sequence 10, Appl	336	3	27.3	9	11	US-09-799-250-558	Sequence 558, App
264	8	12	US-10-257-050-13	Sequence 13, Appl	337	3	27.3	9	11	US-09-799-250-630	Sequence 630, App
265	8	12	US-10-272-497-84	Sequence 84, Appl	338	3	27.3	9	11	US-09-791-393-52	Sequence 52, Appl
266	8	12	US-10-274-317A-96	Sequence 96, Appl	339	3	27.3	9	11	US-09-791-389-52	Sequence 52, Appl
267	8	12	US-10-249-317A-224	Sequence 224, App	340	3	27.3	9	11	US-09-809-391-626	Sequence 626, App
268	8	12	US-10-249-317A-224	Sequence 675, App	341	3	27.3	9	11	US-09-880-748-3137	Sequence 3137, App
269	8	14	US-10-524-935-19	Sequence 19, Appl	342	3	27.3	9	11	US-09-876-904A-260	Sequence 260, App
270	8	14	US-10-527-761-6	Sequence 6, Appl1	343	3	27.3	9	11	US-09-876-904A-336	Sequence 336, App
271	8	14	US-10-527-761-13	Sequence 13, Appl	344	3	27.3	9	11	US-09-876-904A-543	Sequence 543, App
272	8	14	US-10-527-761-14	Sequence 14, Appl	345	3	27.3	9	11	US-09-876-904A-570	Sequence 570, App
273	8	14	US-10-527-761-15	Sequence 15, Appl	346	3	27.3	9	11	US-09-876-904A-588	Sequence 588, App
274	8	14	US-10-527-761-16	Sequence 16, Appl	347	3	27.3	9	11	US-09-876-904A-615	Sequence 615, App
275	8	14	US-10-527-761-17	Sequence 17, Appl	348	3	27.3	9	11	US-09-865-548A-715	Sequence 715, Appl
276	8	14	US-10-527-761-18	Sequence 18, Appl	349	3	27.3	9	11	US-09-978-309A-35	Sequence 35, Appl
277	8	14	US-10-527-761-19	Sequence 19, App	350	3	27.3	9	12	US-09-932-165-72	Sequence 72, Appl
278	8	14	US-10-527-761-22	Sequence 22, App	351	3	27.3	9	12	US-09-932-165-1201	Sequence 1201, Ap
279	8	14	US-10-527-761-25	Sequence 25, App	352	3	27.3	9	12	US-10-104-385-8	Sequence 8, Appl1
280	8	14	US-10-527-761-26	Sequence 26, Appl	353	3	27.3	9	12	US-10-291-250-13	Sequence 13, Appl
281	8	14	US-10-527-761-27	Sequence 27, Appl	354	3	27.3	9	12	US-10-291-250-16	Sequence 16, Appl
282	8	14	US-10-527-761-28	Sequence 28, Appl	355	3	27.3	9	12	US-10-292-418-13	Sequence 13, Appl
283	8	14	US-10-527-761-29	Sequence 29, App	356	3	27.3	9	12	US-10-190-082-529	Sequence 529, App
284	8	14	US-10-527-761-31	Sequence 30, Appl	357	3	27.3	9	12	US-10-251-805-2	Sequence 2, Appl1
285	8	14	US-10-527-761-32	Sequence 31, Appl	358	3	27.3	9	12	US-10-375-992-177	Sequence 177, App
286	8	14	US-10-527-761-33	Sequence 32, Appl	359	3	27.3	9	12	US-09-908-100-2	Sequence 2, Appl1
287	8	14	US-10-527-761-34	Sequence 33, Appl	360	3	27.3	9	12	US-09-935-384-112	Sequence 112, App
288	8	14	US-10-540-572-1	Sequence 8, Appl-1	361	3	27.3	9	12	US-09-935-384-140	Sequence 140, App
289	8	15	US-10-540-572-1	Sequence 10, Appl	362	3	27.3	9	12	US-09-935-384-207	Sequence 207, App
290	8	15	US-10-540-572-1	Sequence 22, Appl	363	3	27.3	9	12	US-09-935-384-312	Sequence 312, App
291	8	15	US-10-540-572-1	Sequence 51, Appl	364	3	27.3	9	12	US-09-935-384-550	Sequence 550, App
292	8	15	US-10-540-572-1	Sequence 12, Appl	365	3	27.3	9	12	US-09-935-384-642	Sequence 642, App
293	8	15	US-10-540-572-1	Sequence 74, Appl	366	3	27.3	9	12	US-09-935-384-643	Sequence 643, App
294	8	15	US-10-158-807-146	Sequence 146, App	367	3	27.3	9	12	US-10-062-109A-274	Sequence 274, App
295	8	15	US-10-512-819-1	Sequence 9, Appl1	368	3	27.3	9	12	US-10-062-109A-365	Sequence 365, App
296	8	15	US-10-512-819-1	Sequence 11, Appl	369	3	27.3	9	12	US-10-062-109A-559	Sequence 559, App
297	8	15	US-10-133-213-120	Sequence 179, App	370	3	27.3	9	12	US-10-062-109A-658	Sequence 658, App
298	8	15	US-10-156-573A-5	Sequence 5, Appl1	371	3	27.3	9	12	US-10-077-106-15	Sequence 15, Appl
299	8	15	US-10-156-573A-5	Sequence 11, Appl	372	3	27.3	9	12	US-10-077-106-15	Sequence 15, Appl
300	8	8	US-08-452-843A-19	Sequence 19, Appl	373	3	27.3	9	12	US-10-077-106-18	Sequence 18, Appl
301	8	9	US-08-455-811-7	Sequence 17, Appl	374	3	27.3	9	12	US-09-882-1751-626	Sequence 626, App
302	9	9	US-09-113-424-6	Sequence 6, Appl1	375	3	27.3	9	12	US-09-920-195A-26	Sequence 26, Appl
303	9	9	US-09-760-539-59	Sequence 39, Appl	376	3	27.3	9	12	US-10-138-434A-5	Sequence 5, Appl1
304	9	9	US-09-760-539-41	Sequence 45, Appl	377	3	27.3	9	12	US-10-239-313A-540	Sequence 540, App
305	9	9	US-09-765-286-77	Sequence 177, App	378	3	27.3	9	12	US-10-239-313A-544	Sequence 544, App
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307	9	9	US-09-849-946-13	Sequence 13, App	380	3	27.3	9	12	US-10-353-929-135	Sequence 145, App

381	3	27.3	9	12	US-10-353-929-149	Sequence 149, App	454	3	27.3	10	11	US-09-572-404B-72	Sequence 72, Appl
382	3	27.3	9	12	US-10-353-929-149	Sequence 168, App	455	3	27.3	10	11	US-09-572-404B-74	Sequence 74, Appl
383	3	27.3	9	14	US-10-613-323-4	Sequence 4, Appl	456	3	27.3	10	11	US-09-572-404B-122	Sequence 122, App
384	3	27.3	9	14	US-10-613-323-4	Sequence 15, App	457	3	27.3	10	11	US-09-572-404B-136	Sequence 136, App
385	3	27.3	9	15	US-10-062-257-15	Sequence 13, App	458	3	27.3	10	11	US-09-572-404B-227	Sequence 227, App
386	3	27.3	9	15	US-10-211-207-15	Sequence 15, Appl	459	3	27.3	10	11	US-09-572-404B-412	Sequence 412, App
387	3	27.3	9	15	US-10-211-207-15	Sequence 18, App	460	3	27.3	10	11	US-09-572-404B-626	Sequence 626, App
388	3	27.3	9	15	US-10-352-283-45	Sequence 95, Appl	461	3	27.3	10	11	US-09-572-404B-633	Sequence 633, App
389	3	27.3	9	15	US-10-394-283-45	Sequence 174, App	462	3	27.3	10	11	US-09-572-404B-636	Sequence 636, App
390	3	27.3	9	15	US-10-091-155-11	Sequence 11, Appl	463	3	27.3	10	11	US-09-572-404B-682	Sequence 682, App
391	3	27.3	9	15	US-10-097-555-546	Sequence 646, App	464	3	27.3	10	11	US-09-572-404B-770	Sequence 770, App
392	3	27.3	9	15	US-10-135-795-95	Sequence 95, Appl	465	3	27.3	10	11	US-09-572-404B-772	Sequence 772, App
393	3	27.3	9	15	US-10-135-795-173	Sequence 173, App	466	3	27.3	10	11	US-09-572-404B-774	Sequence 774, App
394	3	27.3	9	15	US-10-211-412A-9	Sequence 9, Appl	467	3	27.3	10	11	US-09-572-404B-787	Sequence 787, App
395	3	27.3	9	15	US-10-043-862-842	Sequence 9842, App	468	3	27.3	10	11	US-09-572-404B-842	Sequence 842, App
396	3	27.3	9	15	US-10-043-862-840	Sequence 9890, App	469	3	27.3	10	11	US-09-572-404B-990	Sequence 990, App
397	3	27.3	9	15	US-10-043-862-840	Sequence 9904, App	470	3	27.3	10	11	US-09-572-404B-992	Sequence 992, App
398	3	27.3	9	15	US-10-040-862-10089	Sequence 10089, A	471	3	27.3	10	11	US-09-572-404B-1078	Sequence 1078, App
399	3	27.3	9	15	US-10-040-862-10115	Sequence 10116, A	472	3	27.3	10	11	US-09-572-404B-1094	Sequence 1094, App
400	3	27.3	9	15	US-10-040-862-10131	Sequence 10130, A	473	3	27.3	10	11	US-09-572-404B-1120	Sequence 1120, App
401	3	27.3	9	15	US-10-040-862-10214	Sequence 10214, A	474	3	27.3	10	11	US-09-572-404B-1142	Sequence 1142, App
402	3	27.3	9	15	US-10-040-862-10294	Sequence 10299, A	475	3	27.3	10	11	US-09-572-404B-1158	Sequence 1158, App
403	3	27.3	9	15	US-10-040-862-10424	Sequence 10424, A	476	3	27.3	10	11	US-09-572-404B-1162	Sequence 1162, App
404	3	27.3	9	15	US-10-236-745-11	Sequence 11, App	477	3	27.3	10	11	US-09-572-404B-1237	Sequence 1237, App
405	3	27.3	9	15	US-10-133-213-74	Sequence 74, App	478	3	27.3	10	11	US-09-572-404B-1511	Sequence 1511, App
406	3	27.3	9	15	US-10-133-213-81	Sequence 81, App	479	3	27.3	10	11	US-09-572-404B-1619	Sequence 1619, App
407	3	27.3	9	15	US-10-213-888-291	Sequence 191, App	480	3	27.3	10	11	US-09-572-404B-1629	Sequence 1629, App
408	3	27.3	9	15	US-10-213-888-291	Sequence 271, App	481	3	27.3	10	11	US-09-572-404B-1632	Sequence 1632, App
409	3	27.3	9	15	US-10-091-724-5	Sequence 50, Appl	482	3	27.3	10	11	US-09-572-404B-1635	Sequence 1635, App
410	3	27.3	9	15	US-10-264-374-177	Sequence 177, App	483	3	27.3	10	11	US-09-572-404B-1640	Sequence 1640, App
411	3	27.3	10	9	US-09-765-935-34	Sequence 33, Appl	484	3	27.3	10	11	US-09-572-404B-1694	Sequence 1694, App
412	3	27.3	10	9	US-09-765-927-404	Sequence 204, App	485	3	27.3	10	11	US-09-572-404B-1696	Sequence 1696, App
413	3	27.3	10	9	US-09-765-927-405	Sequence 205, App	486	3	27.3	10	11	US-09-572-404B-1891	Sequence 1891, App
414	3	27.3	10	9	US-09-765-927-416	Sequence 216, App	487	3	27.3	10	11	US-09-572-404B-1896	Sequence 1896, App
415	3	27.3	10	9	US-09-731-221-6	Sequence 6, Appl	488	3	27.3	10	11	US-09-572-404B-1898	Sequence 1898, App
416	3	27.3	10	9	US-09-819-308-26	Sequence 26, Appl	489	3	27.3	10	11	US-09-572-404B-1947	Sequence 1947, App
417	3	27.3	10	9	US-09-753-9478-4	Sequence 4, Appl	490	3	27.3	10	11	US-09-572-404B-2016	Sequence 2016, App
418	3	27.3	10	9	US-09-753-9478-4	Sequence 12, Appl	491	3	27.3	10	11	US-09-572-404B-2066	Sequence 2066, App
419	3	27.3	10	9	US-09-845-663-18	Sequence 18, Appl	492	3	27.3	10	11	US-09-572-404B-2146	Sequence 2146, App
420	3	27.3	10	9	US-09-845-663-18	Sequence 1, Appl	493	3	27.3	10	11	US-09-572-404B-2149	Sequence 2149, App
421	3	27.3	10	9	US-09-790-662A	Sequence 1, Appl	494	3	27.3	10	11	US-09-572-404B-2481	Sequence 2481, App
422	3	27.3	10	9	US-09-841-433-179	Sequence 179, App	495	3	27.3	10	11	US-09-572-404B-2491	Sequence 2491, App
423	3	27.3	10	9	US-09-841-433-180	Sequence 180, App	496	3	27.3	10	11	US-09-572-404B-2534	Sequence 2534, App
424	3	27.3	10	10	US-09-780-053-267	Sequence 287, App	497	3	27.3	10	11	US-09-572-404B-2535	Sequence 2535, App
425	3	27.3	10	10	US-09-780-053-293	Sequence 294, App	498	3	27.3	10	11	US-09-572-404B-2547	Sequence 2547, App
426	3	27.3	10	10	US-09-780-053-325	Sequence 375, App	499	3	27.3	10	11	US-09-572-404B-2648	Sequence 2648, App
427	3	27.3	10	10	US-09-780-053-339	Sequence 379, App	500	3	27.3	10	11	US-09-572-404B-2706	Sequence 2706, App
428	3	27.3	10	10	US-09-984-358-66	Sequence 85, Appl							
429	3	27.3	10	10	US-09-920-508-1	Sequence 2, Appl							
430	3	27.3	10	10	US-09-920-508-1	Sequence 7, Appl							
431	3	27.3	10	10	US-09-739-066-19	Sequence 19, Appl							
432	3	27.3	10	10	US-09-739-066-19	Sequence 24, Appl							
433	3	27.3	10	10	US-09-739-066-24	Sequence 37, Appl							
434	3	27.3	10	10	US-09-739-066-24	Sequence 260, App							
435	3	27.3	10	10	US-09-739-066-24	Sequence 343, App							
436	3	27.3	10	10	US-09-739-066-32	Sequence 524, App							
437	3	27.3	10	10	US-09-739-066-32	Sequence 529, App							
438	3	27.3	10	10	US-09-739-066-32	Sequence 528, App							
439	3	27.3	10	10	US-09-739-066-32	Sequence 534, App							
440	3	27.3	10	10	US-09-739-066-32	Sequence 85, Appl							
441	3	27.3	10	10	US-09-554-965-15	Sequence 55, App							
442	3	27.3	10	10	US-09-554-965-15	Sequence 15, App							
443	3	27.3	10	11	US-09-778-026-23	Sequence 23, App							
444	3	27.3	10	11	US-09-799-250-23	Sequence 295, App							
445	3	27.3	10	11	US-09-799-250-23	Sequence 384, App							
446	3	27.3	10	11	US-09-799-250-23	Sequence 87, Appl							
447	3	27.3	10	11	US-09-876-904A-245	Sequence 245, App							
448	3	27.3	10	11	US-09-876-904A-245	Sequence 546, App							
449	3	27.3	10	11	US-09-876-904A-245	Sequence 611, App							
450	3	27.3	10	11	US-09-876-904A-245	Sequence 15, Appl							
451	3	27.3	10	11	US-09-876-904A-245	Sequence 15, Appl							
452	3	27.3	10	11	US-09-876-904A-245	Sequence 15, Appl							
453	3	27.3	10	11	US-09-876-904A-245	Sequence 15, Appl							

ALIGNMENTS

RESULT 1

US 09-876-904A-212

Sequence 262, Application NO US09876904A

Publication NO US20030072734A1

GENERAL INFORMATION:

APPLICANT: BODILIKAS, IENI

TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

FILE REFERENCE: TB 2002-00

CURRENT APPLICATION NUMBER: US/09/876,904A

PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/210,925

PRIOR FILING DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 629

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 262

LENGTH: 13

TYPE: PRT

ORGANISM: Bos sp.

FEATURE:

## ALIGNMENTS

## RESULT 1

US-09-876-904A-212  
 : Sequence 262, Application US/09876904A  
 : Publication No. US20030072734A1  
 : GENERAL INFORMATION:  
 : APPLICANT: BIOULIKAS, IENI  
 : TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
 : TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
 : FILE REFERENCE: TB 2002-00  
 : CURRENT FILING DATE: 2001-06-08  
 : PRIOR FILING DATE: 2000-06-09  
 : NUMBER OF SEQ ID NOS: 629  
 : SOFTWARE: Patent in Ver. 2.1  
 : SEQ ID NO 262  
 : LENGTH: 13  
 : TYPE: PRT  
 : ORGANISM: Bos sp.  
 : FEATURE:

OTHER INFORMATION: Calf thymus HMG 1  
US-09-876-904A-262

Query Match 63.6%; Score 7; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGKKKK 8  
DB 3 EGKKKK 9

## RESULT 2

US-09-876-904A-617  
Sequence 617, Application US/09876904A  
Publication No. US20030072794A1

GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMA DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INIC TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 617  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Bos sp.  
FEATURE:  
OTHER INFORMATION: Calf thymus HMG 2 (256 aa);  
US-09-876-904A-517

Query Match 63.6%; Score 7; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGKKKK 8  
DB 3 EGKKKK 9

## RESULT 3

US-09-876-904A-620  
Sequence 620, Application US/09876904A  
Publication No. US20030072794A1

GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMA DNA (LIPIDGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
TITLE OF INVENTION: CONJUGATES INIC TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
PRIOR FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 620  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Bos sp.  
FEATURE:  
OTHER INFORMATION: Calf thymus HMG 2 (256 aa);  
US-09-876-904A-620

Query Match 54.5%; Score 6; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 8  
DB 6 GKKKK 11

## RESULT 4

US-10-024-918-10  
Sequence 10, Application US/10024918  
Publication No. US20020168710A1  
GENERAL INFORMATION:  
APPLICANT: Hubbell, Jeffrey  
APPLICANT: Schense, Jason  
APPLICANT: Zisch, Andreas  
APPLICANT: Hall, Heike  
TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING  
FILE REFERENCE: CIT 2606 CIP  
CURRENT APPLICATION NUMBER: US/10/024,918  
CURRENT FILING DATE: 2001-12-18  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 8  
TYPE: PRT  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: random coupling polylysine peptide attached to active peptic  
NAME/KEY: MOD\_RES  
LOCATION: (1)-(11)  
OTHER INFORMATION: dansylated leucine  
US-10-024-918-10

Query Match 45.5%; Score 5; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5; le-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
DB 3 GKKKK 7

## RESULT 5

US-08-344-824-35  
Sequence 35, Application US/0844824  
Publication No. US20030152580A1  
GENERAL INFORMATION:  
APPLICANT: SEITE, Alessandro  
APPLICANT: SIDNEY, John  
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
NUMBER OF SEQUENCES: 399  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower, 20th  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 543-9600  
 TELEFAX: (415) 543-5043  
 INFORMATION FOR SEQ ID NO: 35:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-344 824-35

Query Match 45.5% Score 5; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5; le-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 III I  
 DB 1 GGKKK 5

RESULT 5  
 US-09-898 461-5  
 Sequence 5; Application US/09898461  
 Patent No. US2002090709A1  
 GENERAL INFORMATION:  
 APPLICANT: Bequet, Richard HJ  
 APPLICANT: Chester, Kerry  
 APPLICANT: Milton, Nigel P  
 APPLICANT: Rees, Anthony K  
 APPLICANT: Sharma, Surinder K  
 APPLICANT: Spencer, Daniel IR  
 TITLE OF INVENTION: Modified carboxypeptidase enzymes and their use  
 FILE REFERENCE: 620-150  
 CURRENT APPLICATION NUMBER: US/09/898 461  
 CURRENT FILING DATE: 2001-07-05  
 PRIOR APPLICATION NUMBER: US 60/226,689  
 PRIOR FILING DATE: 2000-07-07  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: Patent In Ver. 2.1  
 SEQ ID NO 5  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: Pseudomonas sp.  
 US-09-898 461-5

Query Match 45.5% Score 5; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5; le-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FGGKK 6  
 III I  
 DB 1 FGGKK 5

RESULT 7  
 US-10-206-155-13  
 Sequence 13; Application US/10206155  
 Publication No. US20030157135A1  
 GENERAL INFORMATION:  
 APPLICANT: Tsuji, Moriya  
 APPLICANT: Gonzalez-Asequinolaza, Gloria  
 APPLICANT: Nussenzweig, Ruth S.  
 APPLICANT: Kozuka, Yasuhiko  
 TITLE OF INVENTION: USE OF GLYCOSYLCEFAZOLIDES AS ADJUVANTS  
 FILE REFERENCE: 5986/1H9580S1  
 CURRENT APPLICATION NUMBER: US/10/206.155  
 CURRENT FILING DATE: 2002-07-25  
 PRIOR APPLICATION NUMBER: 60/308,056  
 PRIOR FILING DATE: 2001-07-25  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: FastSPQ for Windows Version 3.0

SEQ ID NO 13  
 LENGTH: 9  
 TYPE: PRT  
 ORGANISM: HIV-1  
 US-10-206-155-13

Query Match 45.5% Score 5; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 5; le-05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGKKK 7  
 III I  
 DB 5 GGKKK 9

RESULT 6  
 US-10-128-711-43  
 Sequence 30; Application US/10128711  
 Publication No. US20030099644A1  
 GENERAL INFORMATION:  
 APPLICANT: Vitello, Maria A.  
 APPLICANT: Chestnut, Robert W.  
 APPLICANT: Sette, Alessandro D.  
 APPLICANT: Celis, Esteban  
 APPLICANT: Gray, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING  
 CTL IMMUNITY  
 NUMBER OF SEQUENCES: 153  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend Kourie and Crew  
 STREET: Stewart Street Tower, One Market Plaza  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: US  
 ZIP: 94105-1493  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/128,711  
 FILING DATE: 22-Apr-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/197,484  
 FILING DATE: 15-FEB-1994  
 APPLICATION NUMBER: US 07/935,811  
 FILING DATE: 26-AUG-1992  
 APPLICATION NUMBER: US 07/874,491  
 FILING DATE: 27-APR-1992  
 APPLICATION NUMBER: US 07/827,682  
 FILING DATE: 29-JAN-1992  
 APPLICATION NUMBER: US 07/749,568  
 FILING DATE: 26-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parmelee, Steven W.  
 REGISTRATION NUMBER: 31,990  
 REFERENCE/DOCKET NUMBER: 14137-26-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 467-9600  
 TELEFAX: (206) 623-6793  
 INFORMATION FOR SEQ ID NO: 30:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
 US-10-128-711-30

Query Match 45.5% Score 5; DB 15; Length 9;



Best Local Similarity 100.0%; Pred. No. 5; Ie-05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKKKK 7  
IIII  
Db 1 GKKKK 5

## RESULT 9

US-09-876-904A-362  
; Sequence 362, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 362  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Murine DEF-1.  
US-09-876-904A-362

Query Match 45.5%; Score 5; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
IIII  
Db 1 GKKKK 5

## RESULT 10

US-09-876-904A-363  
; Sequence 363, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 363  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Human TGF-1 alpha.  
US-09-876-904A-363

Query Match 45.5%; Score 5; DB 11; Length 11;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKKK 8  
IIII  
Db 1 GKKKK 5

## RESULT 11

US-09-876-904A-51  
; Sequence 51, Application US/09876904A  
; Publication No. US20030072794A1  
; GENERAL INFORMATION:  
; APPLICANT: BOULIKAS, TENI  
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE  
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
; FILE REFERENCE: TB-2002.00  
; CURRENT APPLICATION NUMBER: US/09/876,904A  
; CURRENT FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: US 60/210,925  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 629  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 51  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Murine c-abl (  
US-09-876-904A-51

Query Match 45.5%; Score 5; DB 11; Length 12;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKK 9  
IIII  
Db 6 KKKKK 10

## RESULT 12

US-10-315-920-13  
; Sequence 13, Application US/10315920  
; Publication No. US20030175809A1  
; GENERAL INFORMATION:  
; APPLICANT: FIADKOV, Aleksey  
; TITLE OF INVENTION: FLUORESCENT TUMOR PROTEINS AND METHODS  
; TITLE OF INVENTION: FOR THEIR USE  
; FILE REFERENCE: CIGN-077C:P  
; CURRENT APPLICATION NUMBER: US/10/315,920  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: 60/211,607  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: PCT/US01/10097  
; PRIOR FILING DATE: 2001-06-13  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: nuclear localization signal  
US-10-315-920-13

Query Match 45.5%; Score 5; DB 12; Length 12;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKKK 9  
IIII  
Db 6 KKKKK 10

## RESULT 13

US-10-156-570A-12  
; Sequence 12, Application US/10156570A

```

1 Publication No. US20001012524A1
2 GENERAL INFORMATION:
3 APPLICANT: ROSENBERG, JOSEPH
4 APPLICANT: RITTER, WOLFGANG
5 APPLICANT: KUDOLPH, CARSTEN MAKIIN
6 APPLICANT: PLANK, CHRISTIAN
7 TITLE OF INVENTION: POLYPEPTIDES IMPROVING MULTIDRUG RESISTANCE OF TUMORS
8 TITLE OF INVENTION: LOCALIZATION SIGNALS OF A PROTEIN TRANSDUCTION DOMAIN
9 TITLE OF INVENTION: AND THEIR USE FOR TRANSFERING NUCLEIC ACID MOLECULES
10 TITLE OF INVENTION: INTO CELLS
11 FILE REFERENCE: WO-95-15
12 CURRENT APPLICATION NUMBER: US/09/156,522
13 PRIOR FILING DATE: 2000-05-24
14 PRIOR APPLICATION NUMBER: PCT/EP/01/00001
15 NUMBER OF SEQ ID NOS: 32
16 SOFTWARE: Patent In Ver. 2.1
17 SEQ ID NO 12
18 LENGTH: 12
19 TYPE: PPT
20 ORGANISM: Artificial Sequence
21 FEATURE:
22 OTHER INFORMATION: Description of Artificial Sequences and/or Chab 1V
23 OTHER INFORMATION: nuclear localization sequence
24 US 10-155-570A 12

Query Match 45.5% Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 5 KKKKK 9
DB 5 KKKKK 10

RESULT 14
US 09-770-467-2
1 Sequence 2, Application US/09770-067
2 Patent No. US20020310184A1
3 GENERAL INFORMATION:
4 APPLICANT: MERCK & CO., Inc.
5 APPLICANT: Edsmore, Christopher J.
6 APPLICANT: Benjamin, Jeffrey M.
7 TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferrase
8 FILE REFERENCE: 20495
9 CURRENT APPLICATION NUMBER: US/09/770-067
10 PRIOR FILING DATE: 2001-01-26
11 PRIOR APPLICATION NUMBER: 65/183,441
12 NUMBER OF SEQ ID NOS: 21
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 2
15 LENGTH: 15
16 TYPE: PPT
17 ORGANISM: Homosapien
18 US 09-770-467-2

Query Match 45.5% Score 6; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 GKRRK H
DB 1 GKRRK 5

RESULT 15
US 09-858-369-2
1 Sequence 2, Application US/09858-369
2 Patent No. US2002022634A1
3 GENERAL INFORMATION:
4 APPLICANT: Merck & Co., Inc.
5 APPLICANT: S. Jane deSolms
6 APPLICANT: Suzukawa, C. M.
7 APPLICANT: Anthony W. Shaw
8 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
9 FILE REFERENCE: 20001
10 CURRENT APPLICATION NUMBER: US/09/858-369
11 PRIOR FILING DATE: 2000-02-18
12 NUMBER OF SEQ ID NOS: 21
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 2
15 LENGTH: 15
16 TYPE: PPT
17 ORGANISM: Homosapien
18 US 09-858-369-2

Query Match 45.5% Score 5; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 GKRRK 8
DB 1 GKRRK 5

RESULT 16
US 09-819-522-2
1 Sequence 2, Application US/09819-522
2 Patent No. US2002037889A1
3 GENERAL INFORMATION:
4 APPLICANT: deSolms, S. Jane
5 APPLICANT: Graham, Samuel L.
6 APPLICANT: Shaw, Anthony W.
7 APPLICANT: Ciccarone, Terence M.
8 APPLICANT: Storker, Gerald E.
9 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
10 FILE REFERENCE: 20312Y
11 CURRENT APPLICATION NUMBER: US/09/819-522
12 PRIOR FILING DATE: 2001-03-28
13 PRIOR APPLICATION NUMBER: 09/456,153
14 PRIOR FILING DATE: 1999-12-07
15 PRIOR APPLICATION NUMBER: US 60/111,416
16 PRIOR FILING DATE: 1998-12-08
17 PRIOR APPLICATION NUMBER: US 60/129,282
18 PRIOR FILING DATE: 1999-04-14
19 NUMBER OF SEQ ID NOS: 21
20 SOFTWARE: FastSeq for Windows Version 4.0
21 SEQ ID NO 2
22 LENGTH: 15
23 TYPE: PPT
24 ORGANISM: Homosapien
25 US 09-819-522-2

Query Match 45.5% Score 5; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 GKRRK 8
DB 1 GKRRK 5

RESULT 17
US 09-757-251-3
1 Sequence 3, Application US/09757-251
2 Patent No. US2002004217A1
3 GENERAL INFORMATION:
4 APPLICANT: Merck & Co., Inc.
5 APPLICANT: S. Jane deSolms
6 APPLICANT: Suzukawa, C. M.
7 APPLICANT: Anthony W. Shaw
8 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
9 FILE REFERENCE: 20001
10 CURRENT APPLICATION NUMBER: US/09/757-251
11 PRIOR FILING DATE: 2000-02-18
12 NUMBER OF SEQ ID NOS: 21
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 2
15 LENGTH: 15
16 TYPE: PPT
17 ORGANISM: Homosapien
18 US 09-757-251-3

```

1 CURRENT APPLICATION NUMBER: US/09/757,251  
2 CURRENT FILING DATE: 2001-01-09  
3 PRIOR APPLICATION NUMBER: 60/175,784  
4 PRIOR FILING DATE: 2000-01-12  
5 NUMBER OF SEQ ID NOS: 25  
6 SOFTWARE: FastSeq for Windows Version 4.0  
7 SEQ ID NO 3  
8 LENGTH: 15  
9 TYPE: PRT  
10 ORGANISM: Artificial Sequence  
11 FEATURE:  
12 OTHER INFORMATION: Completely Synthetic Amino Acid  
13 US-09-757-251-3

Query Match 45.5% Score 5; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 GKKKK 8  
III I  
DB 1 GKKKK 5

## RESULT 14

US-09-784-897A-2

1 Sequence 2: Application US/09/784,897A  
2 Patent No. US20020052363A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Merck & Co., Inc.  
5 APPLICANT: Dinsmore, Christopher J.  
6 APPLICANT: Bergman, Jeffrey M.  
7 TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS  
8 FILE REFERENCE: 20497  
9 CURRENT APPLICATION NUMBER: US/09/784,897A  
10 CURRENT FILING DATE: 2001-06-20  
11 PRIOR APPLICATION NUMBER: 60/283,449  
12 PRIOR FILING DATE: 2000-02-18  
13 NUMBER OF SEQ ID NOS: 21  
14 SOFTWARE: FastSeq for Windows Version 4.0  
15 SEQ ID NO 2  
16 LENGTH: 15  
17 TYPE: PRT  
18 ORGANISM: Artificial Sequence  
19 FEATURE:  
20 OTHER INFORMATION: Completely Synthetic Amino Acid Sequence  
21 US-09-784-897A-2

Query Match 45.5% Score 5; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 GKKKK 8  
III I  
DB 1 GKKKK 5

## RESULT 19

US-09-770-983-2

1 Sequence 2: Application US/09/770,983  
2 Patent No. US20020052380A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Merck & Co., Inc.  
5 APPLICANT: Dinsmore, Christopher J.  
6 APPLICANT: Bergman, Jeffrey M.  
7 TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase  
8 FILE REFERENCE: 20309  
9 CURRENT APPLICATION NUMBER: US/09/770,983  
10 CURRENT FILING DATE: 2001-01-26  
11 PRIOR APPLICATION NUMBER: 60/183,658  
12 PRIOR FILING DATE: 2000-02-18  
13 NUMBER OF SEQ ID NOS: 21  
14 SOFTWARE: FastSeq for Windows Version 4.0  
15 SEQ ID NO 2

1 LENGTH: 15  
2 TYPE: PRT  
3 ORGANISM: Homosapien  
4 US-09-770-983-2

Query Match 45.5% Score 5; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 GKKKK 8  
III I  
DB 1 GKKKK 5

## RESULT 20

US-09-828-325A-3  
1 Sequence 3: Application US/09/828,325A  
2 Patent No. US20020068747A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Merck & Co., Inc.  
5 APPLICANT: Craig A. Stump  
6 APPLICANT: Theresa M. Williams  
7 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
8 FILE REFERENCE: 20646Y  
9 CURRENT APPLICATION NUMBER: US/09/828,325A  
10 CURRENT FILING DATE: 2001-08-17  
11 PRIOR APPLICATION NUMBER: 60/196,244  
12 PRIOR FILING DATE: 2000-04-10  
13 NUMBER OF SEQ ID NOS: 25  
14 SOFTWARE: FastSeq for Windows Version 4.0  
15 SEQ ID NO 3  
16 LENGTH: 15  
17 TYPE: PRT  
18 ORGANISM: Artificial Sequence  
19 FEATURE:  
20 OTHER INFORMATION: Completely Synthetic Amino Acid Sequence  
21 US-09-828-325A-3

Query Match 45.5% Score 5; DB 9; Length 15;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4 GKKKK 8  
III I  
DB 1 GKKKK 5

## RESULT 21

US-09-757-217A-4  
1 Sequence 3: Application US/09/757,217A  
2 Patent No. US20020049037A1  
3 GENERAL INFORMATION:  
4 APPLICANT: Merck & Co., Inc.  
5 APPLICANT: S. Jang deSouza  
6 APPLICANT: Gerald F. Stokker  
7 APPLICANT: Anthony W. Shaw  
8 TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
9 FILE REFERENCE: 20603Y  
10 CURRENT APPLICATION NUMBER: US/09/757,217A  
11 CURRENT FILING DATE: 2001-06-25  
12 PRIOR APPLICATION NUMBER: 60/175,801  
13 PRIOR FILING DATE: 2000-01-12  
14 NUMBER OF SEQ ID NOS: 25  
15 SOFTWARE: FastSeq for Windows Version 4.0  
16 SEQ ID NO 3  
17 LENGTH: 15  
18 TYPE: PRT  
19 ORGANISM: Artificial Sequence  
20 FEATURE:  
21 OTHER INFORMATION: Completely Synthetic Amino Acid  
22 US-09-757-217A-3

Query Match 45.5% Score 5; DB 9; Length 15;

Query Match 45.5% Score 5; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8  
 DB 1 GKXXX 5

RESULT 22  
 US-09-828-259A 4  
 : Sequence 1: Application US/09828259A  
 : Patent No. US2002013497A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Genom N. Nguyen  
 : APPLICANT: Gracia A. Stamp  
 : APPLICANT: Theresa M. Williams  
 : TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 : FILE REFERENCE: 26637Y  
 : CURRENT APPLICATION NUMBER: US/09/828-259A  
 : CURRENT FILING DATE: 2001-04-09  
 : PRIOR APPLICATION NUMBER: 60/719,951  
 : PRIOR FILING DATE: 2000-04-10  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 3  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Completely Synthetic Amino Acid  
 US-09-828-259A-3

Query Match 45.5% Score 5; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8  
 DB 1 GKXXX 5

RESULT 23  
 US-09-945-249-84  
 : Sequence 84: Application US/09945249  
 : Patent No. US20020168748A1  
 : GENERAL INFORMATION:  
 : APPLICANT: BERLIN, VIVIAN  
 : APPLICANT: RAMASREZ, VERENIQUE  
 : APPLICANT: SMITH, SUSAN E.  
 : TITLE OF INVENTION: ASSAYS AND REAGENTS FOR MEASURING AND PREDICTING AGENTS.  
 : FILE REFERENCE: MIV-074.06  
 : CURRENT APPLICATION NUMBER: US/09/945-249  
 : CURRENT FILING DATE: 2001-06-31  
 : PRIOR APPLICATION NUMBER: 09/041,993  
 : PRIOR FILING DATE: 2001-01-13  
 : PRIOR APPLICATION NUMBER: 08/771,212  
 : PRIOR FILING DATE: 1996-12-26  
 : PRIOR APPLICATION NUMBER: 08/631,311  
 : PRIOR FILING DATE: 1996-04-11  
 : NUMBER OF SEQ ID NOS: 89  
 : SOFTWARE: Patentig Ver. 2.1  
 : SEQ ID NO 84  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: Description of Artificial Sequence: Peptide that  
 : OTHER INFORMATION: corresponds to the C-terminus of Phase of Outase  
 : OTHER INFORMATION: substrates  
 US-09-945-249-84

Query Match 45.5% Score 5; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8  
 DB 1 GKXXX 5

RESULT 24  
 US-09-784-818-2  
 : Sequence 2: Application US/09784818  
 : Publication No. US20020193283A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Bismoro, Christopher J.  
 : APPLICANT: Bergman, Jeffrey M.  
 : TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS  
 : FILE REFERENCE: 20496  
 : CURRENT APPLICATION NUMBER: US/09/784-818  
 : CURRENT FILING DATE: 2001-02-16  
 : PRIOR APPLICATION NUMBER: 60/183,451  
 : PRIOR FILING DATE: 2000-02-18  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Artificial Sequence  
 : FEATURE:  
 : OTHER INFORMATION: completely synthetic sequence  
 US-09-784-818-2

Query Match 45.5% Score 5; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8  
 DB 1 GKXXX 5

RESULT 25  
 US-09-756-248-2  
 : Sequence 2: Application US/09756248  
 : Publication No. US20020144660A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Merck & Co., Inc.  
 : APPLICANT: Bismoro, Christopher J.  
 : TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase  
 : FILE REFERENCE: 26341  
 : CURRENT APPLICATION NUMBER: US/09/756,248  
 : CURRENT FILING DATE: 2001-01-08  
 : PRIOR APPLICATION NUMBER: 60/175,706  
 : PRIOR FILING DATE: 2000-01-12  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 2  
 : LENGTH: 15  
 : TYPE: PRT  
 : ORGANISM: Homosapien  
 US-09-756-248-2

Query Match 45.5% Score 5; DB 12; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKXXX 8  
 DB 1 GKXXX 5

RESULT 26

```
US-09-813-653-5
: Sequence 5, Application US/09813653
: Patent No. US20020064770A1
: GENERAL INFORMATION:
: APPLICANT: Nestor, John
: APPLICANT: Wilson, Carol
: APPLICANT: See, Raymond
: APPLICANT: Tan Heair, Christina
: TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
: FILE REFERENCE: CNS-005
: CURRENT APPLICATION NUMBER: US/09/813,653
: PRIOR FILING DATE: 2000-03-20
: PRIOR APPLICATION NUMBER: US 60/190,446
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/190,996
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/191,299
: PRIOR FILING DATE: 2000-03-21
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 5
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: preferred peptide for pdz binding domain
US-09-813-653-5
Query Match          36.4%; Score 4; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 1 KKKK 4

RESULT 27
US-09-997-579-46
: Sequence 46, Application US/09997579
: Patent No. US20020113203A1
: GENERAL INFORMATION:
: APPLICANT: Cambridge University Technical Services
: TITLE OF INVENTION: A novel family of beta sub unit proteins from a voltage gated sod
: TITLE OF INVENTION: Channel
: TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
: FILE REFERENCE: 674558-2001
: CURRENT APPLICATION NUMBER: US/09/997,579
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: PCT/EP00/0,364
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: 60,129,479
: NUMBER OF SEQ ID NOS: 47
: SEQ ID NO 46
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-997-579-46
Query Match          36.4%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EGGK 5
DB 1 EGGK 4

RESULT 28
US-09-860-323-1
: Sequence 1, Application US/09860323
```

```
: Patent No. US20020123471A1
: GENERAL INFORMATION:
: APPLICANT: Bavarian No. US20020123471A1dic Research Institute A/S
: APPLICANT: Uberla, Klaus
: TITLE OF INVENTION: LENTIVIRUS BASED VECTOR AND VECTOR
: TITLE OF INVENTION: SYSTEM
: FILE REFERENCE: 20239-705
: CURRENT APPLICATION NUMBER: US/09/380,323
: PRIOR FILING DATE: 1999-11-22
: PRIOR APPLICATION NUMBER: PCT/EP98/01191
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: DK 0238/97
: PRIOR FILING DATE: 1997-03-06
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Vector mutant
US-09-380-323-1
Query Match          36.4%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKK 7
DB 1 GKKK 4

RESULT 29
US-09-380-323-4
: Sequence 4, Application US/09380323
: Patent No. US20020123471A1
: GENERAL INFORMATION:
: APPLICANT: Bavarian No. US20020123471A1dic Research Institute A/S
: APPLICANT: Uberla, Klaus
: TITLE OF INVENTION: LENTIVIRUS BASED VECTOR AND VECTOR
: TITLE OF INVENTION: SYSTEM
: FILE REFERENCE: 20239-705
: CURRENT APPLICATION NUMBER: US/09/380,323
: PRIOR FILING DATE: 1999-11-22
: PRIOR APPLICATION NUMBER: PCT/EP98/01191
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: DK 0238/97
: PRIOR FILING DATE: 1997-03-06
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Vector mutant
US-09-380-323-4
Query Match          36.4%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, 1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GKKK 7
DB 1 GKKK 4

RESULT 30
US-09-813-448-2
: Sequence 2, Application US/09813448
: Patent No. US2002012346A1
: GENERAL INFORMATION:
: APPLICANT: Nestor, John
: APPLICANT: Wilson, Carol
: TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou
: FILE REFERENCE: CNS-006
: CURRENT APPLICATION NUMBER: US/09/813,448
```

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: CURRENT FILING DATE: 2001-03-20
: PRIOR APPLICATION NUMBER: US 60/190,946
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/190,996
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: US 60/141,295
: PRIOR FILING DATE: 2000-03-21
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 2
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: preferred amino acids for H2 binding domain
US-09-813 448-2

Query Match          36.4%; Score 4; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 1 KKKK 4

RESULT 33
US-09-142-043-2
: Sequence 2, Application US/09142043
: Patent No. US20020142372A1
: GENERAL INFORMATION:
: APPLICANT: MOSSAKOWSKA, Danuta Ewa Irene
: APPLICANT: EDGE, Colin Michael
: APPLICANT: SMITH, Richard Anthony Jackson
: TITLE OF INVENTION: FRAGMENTS OF PRC AND THEIR USE
: FILE REFERENCE: 86362/104
: CURRENT APPLICATION NUMBER: US/09/142,043
: CURRENT FILING DATE: 1998-12-01
: EARLIER APPLICATION NUMBER: WO PCT/EP97/00,994
: EARLIER FILING DATE: 1997-02-26
: EARLIER APPLICATION NUMBER: GB 96045142.2
: EARLIER FILING DATE: 1996-03-02
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificially Evolved Peptide
US-09-142 043-2

Query Match          36.4%; Score 4; DB 16; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 1 KKKK 4

RESULT 32
US-09-843 676-223
: Sequence 23, Application US/09843076
: Patent No. US20020164786A1
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: APPLICANT: Lingner, Joachim
: APPLICANT: Nakamura, Toru
: APPLICANT: Chapman, Karen B.
: APPLICANT: Morin, Gregg B.
: APPLICANT: Harley, Calvin
: APPLICANT: Andrews, William H.

```

```

: TITLE OF INVENTION: No. US20020164786A1el Telomerase
: NUMBER OF SEQUENCES: 225
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: United States of America
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/843,676
: FILING DATE: 26-APR-2001
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/854,050
: FILING DATE: 09-MAY-1997
: APPLICATION NUMBER: US 08/846,017
: FILING DATE: 25-APR-1997
: APPLICATION NUMBER: US 08/844,419
: FILING DATE: 18-APR-1997
: APPLICATION NUMBER: US 08/724,643
: FILING DATE: 01-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Apple, Randolph I.
: REGISTRATION NUMBER: 36,429
: REFERENCE/DOCKET NUMBER: 015389-00293005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 223:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 223:
US 09-843-676-223

Query Match          36.4%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 1 KKKK 4

RESULT 33
US-09-945-249-82
: Sequence 82, Application US/09945249
: Patent No. US20020168748A1
: GENERAL INFORMATION:
: APPLICANT: BERLIN, VIVIAN
: APPLICANT: DAMAGNEZ, VERONIQUE
: APPLICANT: SMITH, SUSAN E.
: TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
: FILE REFERENCE: MIV-074.06
: CURRENT APPLICATION NUMBER: US/09/945,249
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/041,990
: PRIOR FILING DATE: 2001-01-13
: PRIOR APPLICATION NUMBER: 08/771,212
: PRIOR FILING DATE: 1996-12-20
: PRIOR APPLICATION NUMBER: 08/631,319
: PRIOR FILING DATE: 1996-04-11
: NUMBER OF SEQ ID NOS: 89

```

```
1 SOFTWARE: PatentIn Ver. 2.1
2 SEQ ID NO: 82
3 LENGTH: 8
4 TYPE: PRF
5 ORGANISM: Artificial Sequence
6 FEATURE:
7 OTHER INFORMATION: Description of Artificial Sequence: Peptide that
8 corresponds to the C-terminus of P1ase of GC4ase
9 OTHER INFORMATION: substrates
10 US-09-945 249-82
11
12 Query Match: 36.4%, Score: 4; DB: 0; Length: 8;
13 Best Local Similarity: 100.0%; Pred. No.: 5.1e+05;
14 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
15
16 QY 5 KKKK 8
17 DB 1 KKKK 4
18
19 RESULT 34
20 US-09-805-301-40
21 Sequence 2, Application US/09805401
22 Patent No. US20020173456A1
23 GENERAL INFORMATION:
24 APPLICANT: Smith, Louis C.
25 Sparrow, James T.
26 Hauer, Jochen
27 Mims, Martha P.
28 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
29 MACROMOLECULE DELIVERY
30 NUMBER OF SEQUENCES: 139
31 CORRESPONDENCE ADDRESS:
32 ADDRESSEE: Lyon & Lyon
33 STREET: 633 West Fifth Street
34 Suite 4700
35 CITY: Los Angeles
36 STATE: California
37 COUNTRY: U.S.A.
38 ZIP: 90071-2066
39 COMPUTER READABLE FORM:
40 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
41
42 COMPUTER: IBM Compatible
43 OPERATING SYSTEM: IBM P.C. DOS 6.0
44 SOFTWARE: Word Perfect 6.1
45 CURRENT APPLICATION DATA:
46 APPLICATION NUMBER: US/09/805,301
47 FILING DATE: 12-Mar-2001
48 CLASSIFICATION: <unknown>
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: 08/584,043
51 FILING DATE: <unknown>
52 ATTORNEY/AGENT INFORMATION:
53 NAME: Warburg, Richard J.
54 REGISTRATION NUMBER: 32,427
55 REFERENCE/DOCKET NUMBER: 217/189
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: (213) 489-1600
58 TELEFAX: (213) 955-0440
59 TELEX: 67-3510
60 INFORMATION FOR SEQ ID NO: 2:
61 SEQUENCE CHARACTERISTICS:
62 LENGTH: 8 amino acids
63 TYPE: amino acid
64 STRANDEDNESS: single
65 TOPOLOGY: linear
66 MOLECULE TYPE: peptide
67 FEATURE:
68 OTHER INFORMATION: "Xaa" stands for any naturally
69 occurring amino acid and
70 analogues thereof.
71 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
72 US-09-805-301-40
73
74 Query Match: 36.4%, Score: 4; DB: 0; Length: 8;
75 Best Local Similarity: 100.0%; Pred. No.: 5.1e+05;
76 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
77
78 QY 5 KKKK 8
79 DB 1 KKKK 4
80
81 RESULT 35
82 US-09-805-301-40
83 Sequence 40, Application US/09805401
84 Patent No. US20020173456A1
85 GENERAL INFORMATION:
86 APPLICANT: Smith, Louis C.
87 Sparrow, James T.
88 Hauer, Jochen
89 Mims, Martha P.
90 TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
91 MACROMOLECULE DELIVERY
92 NUMBER OF SEQUENCES: 139
93 CORRESPONDENCE ADDRESS:
94 ADDRESSEE: Lyon & Lyon
95 STREET: 633 West Fifth Street
96 Suite 4700
97 CITY: Los Angeles
98 STATE: California
99 COUNTRY: U.S.A.
100 ZIP: 90071-2066
101 COMPUTER READABLE FORM:
102 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
103
104 COMPUTER: IBM Compatible
105 OPERATING SYSTEM: IBM P.C. DOS 6.0
106 SOFTWARE: Word Perfect 6.1
107 CURRENT APPLICATION DATA:
108 APPLICATION NUMBER: US/09/805,301
109 FILING DATE: 12-Mar-2001
110 CLASSIFICATION: <unknown>
111 PRIOR APPLICATION DATA:
112 APPLICATION NUMBER: 08/584,043
113 FILING DATE: <unknown>
114 ATTORNEY/AGENT INFORMATION:
115 NAME: Warburg, Richard J.
116 REGISTRATION NUMBER: 32,427
117 REFERENCE/DOCKET NUMBER: 217/189
118 TELECOMMUNICATION INFORMATION:
119 TELEPHONE: (213) 489-1600
120 TELEFAX: (213) 955-0440
121 TELEX: 67-3510
122 INFORMATION FOR SEQ ID NO: 4:
123 SEQUENCE CHARACTERISTICS:
124 LENGTH: 8 amino acids
125 TYPE: amino acid
126 STRANDEDNESS: single
127 TOPOLOGY: linear
128 MOLECULE TYPE: peptide
129 FEATURE:
130 OTHER INFORMATION: "Xaa" stands for any naturally
131 occurring amino acid and
132 analogues thereof.
133 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
134 US-09-805-301-40
135
136 Query Match: 36.4%, Score: 4; DB: 0; Length: 8;
137 Best Local Similarity: 100.0%; Pred. No.: 5.1e+05;
138 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
139
140 QY 5 KKKK 8
141 DB 1 KKKK 4
142
143 RESULT 36
144 US-09-805-301-40
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Sequence 96, Application US/0905540;  
Patent No. US20020173456A1  
GENERAL INFORMATION:  
APPLICANT: Sparrow, James E.  
Hauer, Jochen  
Mims, Martha P  
TITLE OF INVENTION: MICROBIAL PROPERTIES OF R  
NUMBER OF SEQUENCES: 139  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Gyor & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM PC, DOS 6.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/99/800,431  
FILING DATE: 12 Mar 2001  
CLASSIFICATION: C08K046  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/643,643  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburton, Richard J.  
REGISTRATION NUMBER: 52,427  
REFERENCE/DOCKET NUMBER: 217/189  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-5600  
TELEFAX: (213) 955-5440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MODULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NOS: 96  
US-09 805-501-96  
Query Match 96.4% Score 43 Pos 100 Mismatches 0  
Best Local Similarity 100.0% Prod No 51005  
Matches 4: Conservative 0 Mismatches 0 Gaps 0  
QY 5 KKKK 8  
Lb 1 KKKK 4  
RESULT 47  
US-09-813-214A 2  
Sequence 2, Application US/09813214A  
Patent No. US20020177200A1  
GENERAL INFORMATION:  
APPLICANT: Tucker, Kenneth  
APPLICANT: Plosila, Laura  
TITLE OF INVENTION: MORAXELLA CATABOLICAL OUTER MEMBRANE PROTEIN-1% POLYPEPTIDE, GEN  
TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
FILE REFERENCE: 7969-089-999  
CURRENT APPLICATION NUMBER: US/09/514,214A  
CURRENT FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: 08/968,485  
PRIOR FILING DATE: 1997-11-12  
NUMBER OF SEQ ID NOS: 20

Sequence 43, Application US/99-438-485-223  
Patent No. US20030309019A1  
GENERAL INFORMATION:  
APPLICANT: Cecchi, Thomas R.  
APPLICANT: Linsner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen R.  
APPLICANT: Morin, Greg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: NO: US20030309019A1el Telomerase  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111-4934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/99/438,486  
FILING DATE: 12-Nov-1999  
CLASSIFICATION: 546  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 58/851,843  
FILING DATE: 06 MAY 1997  
CLASSIFICATION: 546  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/845,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 58/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 546  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 58/724,643  
FILING DATE: 01-SEP-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-0029310S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0400  
INFORMATION FOR SEQ ID NO: 223:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
US-09-813-214A 2  
Query Match 96.4% Score 43 Pos 100 Length 8;  
Best Local Similarity 100.0% Prod No 51005;  
Matches 4: Conservative 0 Mismatches 0 Gaps 0;  
QY 5 KKKK 8  
Lb 5 KKKK 8  
RESULT 48  
US-09-438-485-223  
Sequence 223, Application US/99-438486  
Publication No. US20030309019A1  
GENERAL INFORMATION:  
APPLICANT: Cecchi, Thomas R.  
APPLICANT: Linsner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen R.  
APPLICANT: Morin, Greg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: NO: US20030309019A1el Telomerase  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111-4934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/99/438,486  
FILING DATE: 12-Nov-1999  
CLASSIFICATION: 546  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 58/851,843  
FILING DATE: 06 MAY 1997  
CLASSIFICATION: 546  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/845,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 58/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 546  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 58/724,643  
FILING DATE: 01-SEP-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-0029310S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0400  
INFORMATION FOR SEQ ID NO: 223:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid



1 STRANDEDNESS:  
2 TOPOLOGY: linear  
3 MOLECULE TYPE: peptide  
4 US 09-438-486-223

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 41  
US 09-999-724 1  
Sequence 1, Application US/09999724  
Publication No. US20030040472A1  
GENERAL INFORMATION:  
APPLICANT: WICKHAM, THOMAS J.  
APPLICANT: KOVESDI, IMRE  
APPLICANT: BROUGHT, DOUGLAS E.  
TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER  
FILE REFERENCE: 212960  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: US 09/101,175  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: WO 96/0519160  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 08/730,846  
PRIOR FILING DATE: 1996-08-21  
PRIOR APPLICATION NUMBER: US 06/701,124  
PRIOR FILING DATE: 1996-08-21  
PRIOR APPLICATION NUMBER: US 08/463,468  
PRIOR FILING DATE: 1995-11-28  
NUMBER OF SEQ ID NOS: 94  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO: 1  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US 09-999-724 1

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 40  
US 09-882-291-63  
Sequence 63, Application US/09882291  
Publication No. US20030040472A1  
GENERAL INFORMATION:  
APPLICANT: Zealand Pharmaceuticals A/S  
TITLE OF INVENTION: 007-2001  
FILE REFERENCE: 007-2001  
CURRENT APPLICATION NUMBER: US/09/882,291  
CURRENT FILING DATE: 2001-06-15  
SOFTWARE: Patent In Release #1.0, Version #1.30  
SEQ ID NO: 63  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence

US-09-882-291-63

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 41  
US-09-882-291-73  
Sequence 73, Application US/09882291  
Publication No. US20030040472A1  
GENERAL INFORMATION:  
APPLICANT: Zealand Pharmaceuticals A/S  
TITLE OF INVENTION: No. US20030040472A1 Peptide Conjugates  
FILE REFERENCE: 007-2001  
CURRENT APPLICATION NUMBER: US/09/882,291  
CURRENT FILING DATE: 2001-06-15  
SOFTWARE: Patent In version 3.1  
SEQ ID NO: 73  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence  
US-09-882-291-73

Query Match 36.4% Score 4; DB 11; Length 8;  
Best Local Similarity 100.0%; Pred. No. 5, le-05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8  
DB 1 KKKK 4

RESULT 42  
US-09-911-569-3  
Sequence 3, Application US/09911569  
Publication No. US20030069173A1  
GENERAL INFORMATION:  
APPLICANT: HARLEY-NEELSON, PAMELA  
LAN, JIANGING  
SEIH, POJEN  
JENSE, JOEL A.  
SCHIFFER, KEVIN P.  
GEHEBER, GILGAT  
TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GREENLEE, WINNER & SULLIVAN  
STREET: 5370 MANHATTAN CIRCLE, SUITE 201  
CITY: BOULDER  
STATE: CO  
COUNTRY: US  
Zip: 80303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/911,569  
FILING DATE: 23-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/039,780  
FILING DATE: 16-MAR-1998  
ATTORNEY/AGENT INFORMATION:



```
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Mus sp.
? FEATURE:
? OTHER INFORMATION: Murine HNF-1beta
US 09-876 9CA-485

Query Match 36.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5,1e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKKK 10
DB 2 KKKK 5

RESULT 47
US-09-791-524-139
? Sequence 139, Application US/09791524
? Publication No. US20030143209A1
? GENERAL INFORMATION:
? APPLICANT: Aventis Pharmaceuticals Products Inc.
? TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
? FILE REFERENCE: A3319A
? CURRENT APPLICATION NUMBER: US/09/791-524
? CURRENT FILING DATE: 2001-02-22
? PRIOR APPLICATION NUMBER: 60/09828
? PRIOR FILING DATE: 1998-08-27
? NUMBER OF SEQ ID NOS: 150
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 139
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Adenovirus
US-09-791-524-139

Query Match 36.4%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5,1e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 1 KKKK 4

RESULT 48
US 10-073-333A-26
? Sequence 26, Application US/1007333A
? Publication No. US20030134788A1
? GENERAL INFORMATION:
? APPLICANT: Kevin Baker et al.
? TITLE OF INVENTION: HUMAN TUMOR NEUROGENESIS FACTOR RECEPTOR ER16
? FILE REFERENCE: PF514P1
? CURRENT APPLICATION NUMBER: US/10/073-333A
? CURRENT FILING DATE: 2002-06-18
? PRIOR APPLICATION NUMBER: 60/268-364
? PRIOR FILING DATE: 2001-02-14
? PRIOR APPLICATION NUMBER: 09/637-856
? PRIOR FILING DATE: 2000-08-10
? PRIOR APPLICATION NUMBER: 60/148-348
? PRIOR FILING DATE: 1999-08-12
? PRIOR APPLICATION NUMBER: 60/148-681
? PRIOR FILING DATE: 1999-08-13
? PRIOR APPLICATION NUMBER: 60/148-758
? PRIOR FILING DATE: 1999-08-16
? PRIOR APPLICATION NUMBER: 60/148-870
? PRIOR FILING DATE: 1999-08-13
? PRIOR APPLICATION NUMBER: 60/149-181
? PRIOR FILING DATE: 1999-08-17
? PRIOR APPLICATION NUMBER: 60/149-453
? PRIOR FILING DATE: 1999-08-18
? PRIOR APPLICATION NUMBER: 60/149-498
? PRIOR FILING DATE: 1999-08-18

? NUMBER OF SEQ ID NOS: 43
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 26
? LENGTH: 8
? TYPE: PRT
? ORGANISM: human
US-10-073-333A-26

Query Match 46.4%; Score 4; DB 12; Length 8;
Best Local Similarity 103.0%; Pred. No. 5,1e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKKK 8
DB 4 KKKK 7

RESULT 49
US-10-200-879-3
? Sequence 3, Application US/0200879
? Publication No. US20030144230A1
? GENERAL INFORMATION:
? APPLICANT: HANLEY-NELSON, PAMELA
? INVENTOR: HANLEY-NELSON, PAMELA
? INVENTOR: SHIH, PO-JEN
? INVENTOR: JESSE, JOEL A.
? INVENTOR: SCHIFFERLI, KEVIN P.
? INVENTOR: GEBEYEHU, GULILAT
? TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
? NUMBER OF SEQUENCES: 120
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: GREENLEE, WINNER & SULLIVAN
? STREET: 5370 MANHATTAN CIRCLE, SUITE 201
? CITY: BOULDER
? STATE: CO
? COUNTRY: US
? ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/200,879
FILING DATE: 23-Jul-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/911,569
FILING DATE: 23-JUL-2001
APPLICATION NUMBER: US 09/039,780
FILING DATE: 16-MAR-1998
APPLICATION NUMBER: US 08/818,200
FILING DATE: 14-MAR-1997
APPLICATION NUMBER: US 08/658,130
FILING DATE: 04-JUN-1996
APPLICATION NUMBER: US 08/477,354
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: SULLIVAN, SALLY A.
REGISTRATION NUMBER: 32,064
REFERENCE/DOCKET NUMBER: 32-95E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303)499-8080
TELEFAX: (303)499-8089
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
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Search completed: September 30, 2003, 10:38 am  
Job time : 23.5 secs